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Ratio: 4.400
Percent Similarity: 100.000
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US-08-653-294-12 x HSHLABF1
   US-08-653-294-12 x HSHLABD1
                                                                                                                                   seq_name: gb_pr2:HSHLABF1
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                                                                                                                                                                    seq_documentation_block:
Locus HSHLABF1
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Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
Siriboonrit,U., Rungroung,E. and Bejchandra,S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="HLA-B"
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                                                                                                                                                                                                                                                                                                                                                                                                                      HSHLABDI 250 bp DNA PRI 22-MAR-1997 Human cell line THAI DCH010 MHC class I HLA-B gene (allele HLA-B+51V), exon 2. U90611 U90611 GI:1905865
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1 (bases 1 to 250; Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siriboonrit, U., Rungroung, E. and Bejchandra, S. Burbles, G. Uppublished
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Percent Identity: 90.000
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Percent Identity: 90.000
1. .250
/gene="HLA-B"
/number=2
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a 83 t 32 t
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a 82 c 80 g 32 t
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                                                                                                                                                   Quality: 44.00
Ratio: 4.400
Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-12 x HSHLABB1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Siriboonrit,U., Rungroung,E. and Bejchandra,S.
Lupublished
2 (bases 1 to 250)
E Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D., Siriboonrit,U., Rungroung,E. and Bejchandra,S.
Direct Submission
L. Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
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LOCUS HSHLABG1 250 bp DNA PRI 25-MAR-1997
DEFINITION Human cell line TRAI DCH011 MHC class I HLA-B gene (allele
ACCESSION U90615
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Human cell line THAI DCH028 MHC class I HLA-B gene (allele
HLA-B*51V), exon 2.
U90613.1 GI:1906033
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Gaps: 0
Percent Identity: 90.000
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    250
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Percent Similarity: 100.000
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US-08-653-294-12 x HSHLABI1
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1. 250
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                                                                                                                                                                                          Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Sirikong, M., Longta, K., Srinak, D., Sirikong, D., and Bejchandra, S. Direct Submission Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Chasea i to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Unphilished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 200)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E.; Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
Unpublished
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Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
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Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
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Gaps: 0
Percent Identity: 90.000
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U90422.1 GI:1905834
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Ratio: 4.400
Percent Similarity: 100.000
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US-08-653-294-12 x HSHLABG1
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LOCUS HSHLABI1
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KEYWORDS
SEGMENT
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Direct Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
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Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Direct Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSHLABJ1 250 bp DNA PRI 22-MAR-1997
Human cell line THAI DCH028 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
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Rungroung,E. and Bejchandra,S.
Bl5 alleles (B*1513)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 90.000
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2 (bases 1 to 255)
Grimsley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-5EP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 255)
Grimsley.c., Mather, K.A. and Ober, C.
H.A.-H: a pseudogene with increased variation due to balancing selection at neighboring loci
MOL Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                         seq_documentation_block:
LOCUS AF022159 255 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
ACCESSION AF022159
VERSION AF022159.1 GI:2655062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF022160 259 bp DNA PRI 05-JAN-1999
Homo sapiens isolate 034 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
AF022160.1 GI:2655063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note-"African-American individual"
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 202 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 231
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/map="6p21.3"
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/note="MHC clas
/codon_start=1
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/gene="HLA-H"
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Ratio: 4.400
Percent Similarity: 100.000
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US-08-653-294-12 x AF022159
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                                                         seq_name: gb_pr4:AF022159
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LOCUS AF022160
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Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Enugroung, E., Bejchandra, S., Juji, T. and Tokunaga, K.
Direct Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., B15 alleles (B*1513)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                           HSHLABT1 250 bp DNA PRI 22-MAR-19
HUMAN Cell line THAI DCH009 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
U90418
U90418.1 GI:1905826
                                                                                                           Length: 10
Gaps: 0
Percent Identity: 90.000
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Gaps: 0
Percent Identity: 90.000
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/cell_type="lymphoblastoid"
/cell_line="THAI DCH009"
1. 250
/gene="HIA-B"
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83 c 80 g 32 t
/product="MHC class I HLA-B"
55 a 83 c 80 g 32 t
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1. 250
/ Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="VI"
                                                                                                                                                                                                                                           to: 250
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                                                                                                                                                                                                                                                                             1 ArgGluAspLeuArglleAlaLeuArgTyr 10
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                                                                                                         Quality: 44.00
Ratio: 4.400
Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-12 x HSHLABJ1
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US-08-653-294-12 x HSHLABT1
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LOCUS HSHLABT1
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Length: 10 Gaps: 0 Percent Identity: 90.000

38

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86

class I antigen HLA-H"

KEYWORDS

us-08-653-294-12.rge

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Ratio: 4.400
Percent Similarity: 100.000
                                                                                                      alignment_block:
US-08-653-294-12 x I14590
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US-08-653-294-12 x I14591
                                                                                                                                                                                                                                  seq_name: gb_pat:I14591
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S Grimsley, C., Mather, K.A. and Ober, C.

Grimsley, C., Mather, K.A. and Ober, C.

Direct Submission

1100 Fairview Ave. N., M374, Seattle, WA 98109, USA

Location/Qualifiers

I. 259

/organism="Homo sapiens"

/isolate="034"

/db_xref="taxon:9606"

/chromosome="6"
/map="6p21.3"

/note="African-American individual"

/note="African-American individual"
Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 259)
Grimsley,C., Mather,K.A. and Ober,C.
HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
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1 (bases 1 to 270)

Apple,R.J., Bugawan,T.L. and Erlich,H.A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 67 19-SEP-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 44.00 Length: 10
Ratio: 4.400 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
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114590.
114590.1 GI:997073
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US-08-653-294-12 x AF022160
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Locus I14590
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TITLE
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Unknown.
Unclassiffed.
Unclassiffed.
Unclassiffed.
Unclassiffed.
Unclassiffed.
Apple,R.J., Bugawan,T.L. and Erlich,H.A.
Apples,R.J., Bugawan,T.L. and Erlich,H.A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 68 19-SEP-1995;
Patent: US 5451512-A 68 19-SEP-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
Unclassified.
Unclassified.
I (bases 1 to 270)
Apple,R.J., Bugawan,T.L. and Erlich,H.A.
Apples and reagents for HLA class I A locus DNA typing Methods and reagents for HLA class I A locus DNA typing Patent: US 5451512-A 69 19-SEP-1995;
Pocation/Qualifiers
Location/Qualifiers
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              Percent Identity: 90.000
Gaps:
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                                                                                                              to: 270
                                                                                                                                                seq_documentation_block:
LOCUS 114592 270 bp DNA
DEFINITION Sequence 69 from patent US 5
ACCESSION 114592 1 GI:997075
KEYWORDS OURCE UNKNOWN.
                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS
LOCUS
LOCUS
DEFINITION Sequence 68 from patent US 5
ACCESSION
114591.1 GI:997074
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alignment\_scores:

Quality: 44.00 Length: 10
Ratio: 4.400 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000

alignment\_block: US-08-653-294-12 x I14592

Align seg 1/1 to: I14592 from: 1 to: 270

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transmembrane recepto
C epsilon exon. New 1
IGE Fc chain (amino a
IGE Fc chain (amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic non-human mammalian HLA-Bw 52 gene - useful for analysis of expression of gene structure, and prodn. of malysis of expression of gene structure, and prodn. of prosession of human disease

Disclosure; Fig 1; 8pp; Japanese.

The sequence shows the exon 2 alpha-1-domain of the human leukocyte antigen-Bw 52 gene. The complete gene may be introduced into non-man mammals, pref. rat or mouse, or their encestors at the primary developmental biological step via transplantation into the zygote or embryo to generate transgenic non-human mammals incorporating the con-human mammals contq. HLA-Bw 52 gene in both their germ cells and somatic cells. Transgenic non-human mammals contq. HLA-Bw 52 are useful for the analysis of expression of the gene, its structure, and prodn. of mouse models of human disease.

See also Q29166-72.

Sequence 270 BP; 59 A; 88 C; 86 G; 37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The High Call of the Hi
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                                                                                                                                                                                                                                                                                                                                                                                           00-MAR-1993 (first entry)
HLA-Bw 52 exon 2 alpha-1 domain.
Human leukocyte antigen; transgenic; germ cells; somatic cells;
        Seven t
Human (
Human )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 44.00 Length: 10
Ratio: 4.400 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
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1284
1308
1308
560.20
626.34
639.44
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Probe; HLA class I DNA; immunogen; ss.
100.15
99.28
99.12
99.12
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ID Q01834 standard; DNA; 1086 BP.
AC Q01834;
                                                                                                                                                                                                                                                                                                                029167 standard; DNA; 270 BP. 029167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-WAR-1992.
03-AUG-1990; 207329.
03-AUG-1990; JP-207329.
(OLYU ) OLYMPUS OPTICAL CO.
WPI; 92-342893/42.
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31.00
31.00
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                                                                                                                                                                                               seq_name: N_Geneseq_36:Q29167
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US-08-653-294-12 x Q29167
                                                                                                                                                                                                                                                                                   seq_documentation_block:
N_Geneseq_36:Q66170
N_Geneseq_36:V21328
N_Geneseq_36:Q87474
N_Geneseq_36:Q91170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J04091731-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1992
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Sequence encoding HLA-B51 anti
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HLA-BW52 gene for production of
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| Enterococcus faecalis genome c | Mycobacterium species nucleic | CD40 associated protein (CAP) | LMP1 associated protein LAP1 | Human CRAF1 (TRAF-3) cDNA. Pro | DNA encoding soluble mannose in thizobium species symbiotic | Human secreted protein gene 17 | Infectious rubella virus RNA. | Infectious rubella virus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae coding
Repeat sequence of cps gene loc
Beta-glucuronidase-contg insex
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| Staphylococcus aureus contig
| Continuation (8 of 17) of
| | Continuation (14 of 17) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) CH2'-CH4 coding se
seven transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter sequence and N-termin
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                                                                                                                                                                                                                                                                  Command line parameters:
-MODEL-frame+-p2n.model -DEV-xlp
-MODEL-frame+-p2n.model -DEV-xlp
-G-/cgnll_J/USPTO_SPOOl/VS08653294/runat_04022000_160701_15807/app_query.fasta.1
-DB-N_Geneseq_36 -OFWT-fastap -SUFFIX-rng -GAPOF=12.000
-GAPEXT-4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GGAPOF 4.500 -OGAPEXT=0.050 -XGAPOF=10.000 -XGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOF=10.000 -YGAPEXT=0.500
-FGAPOP-6.000 -DELEXT=7.000 -YGAPOF=10.000 -TAPAXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFMT-Pfs -NORM=ext -MINLEN-0
-MAXLEN-1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLFXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome fragment.
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Human V28 se
                                                                                                                                                              About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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Database length: 125096042
Search time (sec): 590.520000
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Query: US-08-653-294-12
Query length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: N_Geneseq_36:*
                                                                               Date: Feb 8, 2000 1:27
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N_Geneseq_36:V30459_0 +
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N_Geneseq_36:T310773
N_Geneseq_36:T31273
N_Geneseq_36:T910123
N_Geneseq_36:Q24977
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N_Geneseq_36:N70935
N_Geneseq_36:N70225
N_Geneseq_36:T61639
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N_Geneseq_36:005701
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_Geneseq_36:X33945
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N_Geneseq_36:X13670
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N_Geneseq_36:V84507
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N_Geneseq_36:Q97686
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N_Geneseq_36:V37348
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10-Aug-1989.
11-Aug-1989; JP-200758.
(OLYU) Olympus Optical Co., Ltd.
(ALYU) Olympus Optical Co., Ltd.
(Alyu) Olympus Optical Co., Ltd.
WPI: 90-046289/07.
P-PSDB: R03142.
New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2: ppil-12; 23pp; English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;
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                                                          Quality: 44.00 Length: 10
Ratio: 4.400 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
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Ratio: 4.400 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
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                                                                                                                                                                                                                      to: 1086
                                                                                                                                                                                                                                                                                       19-MAY-1991 (first entry)
Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
Homo sapiens.
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1. .1086
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID Q01822 standard; DNA; 1086 BP.
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ID Q05693 standard; DNA; 1089 BP.
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US-08-653-294-12 x Q01834
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Quality:
Ratio:
                                       alignment_scores:
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Allotype specific monoclonal anti- HLA antibodies prodn. - using
Thickpe specific monoclonal anti- HLA antibodies prodn. - using
Thybridomas derived from transgenic animals carrying HLA gene and
Thybridomas derived from transgenic animals carrying HLA gene and
The human is a 1 A-G; 20pp; English.
The human HLA-B51 gene was injected into fertilised mouse eggs and
then these introduced into the uterus of a pseudo pregnant mouse.
The young were tested to ensure incorporation of the gene into the
Chromosome, and one of them mated 3 times with a normal male to
produce 16 young, seven of which carried the HLA-B51 gene.
The transgeneic offspring were immunised with HLA antigen.
The spleen lymphocytes were fused with myeloma cells. Hybridomas
C producing antibodies were selected.
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03-JAN-1991 (first entry)
HLA-Bw52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-Bw52 gene; ss.
Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                           note-"alpha 1-domain"
344. .619
                                                                                                                                                                                                                /note="alpha 3-domain"
896. .1012
                                                                                                                                 'note="alpha 2-domain"
520. .895
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ID 005701 standard; DNA; 1089 BP.
AC 005701;
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                                                                                                                                                                                                                                                                                                                                                  /*tag= f
/number=6
1043. .1089
/*tag= g
/number=7
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22-AUG-1990;
07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OFTICAL KK.
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/*tag= f
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/number=5
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/number=1
74. .343
/*tag= b
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/number=2
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/number=4
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US-08-653-294-12 x Q05693
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WPI; 90-255479/34.
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Such DNA, antigen of antibody Claim 2: Page 4: 5pp: German.

Claim 2: Page 4: 5pp: German.

Lamb DNA may be used as a hybridisation probe for detecting the HLA B27 gene, e.g. for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay.

Sequence 1026 BP; 213 A; 307 C; 344 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CdS 1. 1026
DE3542024-A.
DE3542024-A.
28-NOV-1985; 542024.
28-NOV-1985; DE-542034.
21-DEC-1985; DE-545576.
Riethmuller G, Meo T, Weiss E, Szots H; WPI: 87-157893/23.
P-PSDB; P70590.
DNA coding for antigen HLA B27 - and diagnostic reagents contg.
                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27.
Sequentic disorder; genetic screening; diagnosis;
ankylosing spondylitis; ss.
Homo sapiens.
 Claim 1; Page 1; 11pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-BW53 antigen. See also J03112485 and J03112486.
Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;
                                                                                                                                              Quality: 44.00 Length: 10
Ratio: 4.400 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
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Ratio: 4.875 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                       295 CGAGAGCTGCGGATCGCGCTCCGCTAC 324
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1. .1026
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ID N70935 standard; DNA; 1026 BP.
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ID N70225 standard; DNA; 3874 BP.
                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:N70935
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US-08-653-294-12 x Q12114
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US-08-653-294-12 x N70935
                                                                                                                             alignment_scores:
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    8400000
                                                                                                                                                                                                                                                                                                                                                                                                      The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.

The human HLA-BWS2 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-BW53 gene, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
/note="alpha 1-domain
                                                                /note="alpha 2-domain'
520. .895
                                                                                                                               /note="alpha 3-domain'
896. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluAspLeuArglleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q05701 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID 012114 standard; DNA; 1089 BP.
AC 012114;
                                                                                                                                                                                                                                         1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                                                                                                                                      22-AUG-1990.
07-FEB-1990: 102424.
08-FEB-1989: JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
Takiguchi M;
WPI; 90-255479/34.
                                                                                                                                                                                            1013. .1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1991.
22-SEP-1989; 247697.
22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
                                                                                                                                                              /*tag= e
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39-AUG-1991 (first entry)
                                    /*tag= c
/number=3
                                                                                                                                                                                                                          /number=6
                  344. .619
                                                                                                             /number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg_name: N_Geneseg_36:Q12114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 4.400
Percent Similarity: 100.000
                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-12 x Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R12463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J03112487-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                      EP-383183-A.
                                                                                  intron
                   exon
                                                                                                                                                                                              exon
                                                                                                                                                                                                                                            exon
                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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x51732;
                    mrna
 DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.

Claim 1, p6; 13pp; German.

THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 lavels in human serum, e.g., for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.

Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
3968. .6653
/*tag= a
/note= "HIA-B27 3' flanking region, downstream of 3' untranslated region"
4112. .4556
/*tag= b
        03-APR-1991 (first entry)
Sequence of genomic DNA encoding human histocompatibility antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA B27 consensus sequence.
HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                     21-NOV-1986; 116139.
01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
5204S H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G; WPI: 87-171468/25.
                                    Ankylosing spondylitis; rheumatic disorder; diagnosis; Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                        Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941 CGAGAGGACCTGCGGACCCTGCTCCGCTAC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluAspLeuArgIleAlaLeuArgTyr 10
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID T61639 standard; DNA; 6553 BP.
                                                                                      , 10. 1506
/*tag= c
1932.
                                                                                                                            /*tag= d
2450. .2566
/*tag= e
3009. .3041
                                                                                                                                                                  /*tag= f
3148. 3191
/*tag= g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1997 (first entry)
                                                                          a = .
989.
                                                                . 590
                                                                                                                                                                                                                                                                                                                                                                                       39.00
4.875
80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T61639
                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: N70225
                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-12 x N70225
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                             EP-226069-A
                            HLA-B 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T61639;
N70225
                                                                intron
                                                                                                                      intron
                                                                                                                                        intron
                                                                                   intron
                                                                                                   intron
                                                                                                                                                          intron
                                                                                                                                                                            intron
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Detecting pre-disposition to seronegative spondylarthropathies -
Trom the absence of a C residue at a specific position in the
Trom the absence of a C residue at a specific position in the
3'-flanking region of the HLA B27 allele
C claim 1; Page 52-56; 68pp; English.
Genetic predisposition to seronegative spondyloarthropathies (SNSA)
is detected by determining the absence of a cytosine nucleotide in
the 3' flanking region (see also T61647-48) of an HLA-B3 gene at a
position corresponding to nucleotide 4495 of the HLA-B37 consensus
sequence given in T61639. Probes and primers (see also T61640-46)
c based on this region can be used in diagnostic assays to detect the
genetic predisposition to SNSA, and permit the distinction of B27+
individuals who are resistant to SNSA from B27+ normal individuals
who are susceptible (but as yet unaffected) to such diseases.
Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;
                                                                                        /*tag= b
/note= "3' flanking region diagnostic for genetic
predisposition to SNSA"
/note= "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN'1999 (first entry)
DNA encoding a human secreted protein.
Human secreted protein; immune disorder; infection;
Human secreted protein; cancer; immune disorder; tumour; atheroscierosis;
restenosis; autoimmune disorder; Alzheimer's disease;
peripheral neuropathy; trauma; sphinal cord injury; allergy;
hematopoietic disorder; skeletal disorder; neurological disorder;
arthritic disorder; asthma; immunodeficiency disease; AIDS;
                                                                                                                                                                                                                                                              /note- "absence of cytosine at this site indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.00 Length: 10
4.875 Gaps: 0
80.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 6553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 CGAGAGGACCTGCGGGACCCTGCTCCGCTAC 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgGluAspLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: T61639 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID X51732 standard; DNA; 978 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                       1270. .4556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:X51732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplant rejection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-058974.
US-057626.
US-057663.
                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                              US-522942
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12-SEP-1997; US-058666
12-SEP-1997; US-058673
12-SEP-1997; US-058973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-12 x T61639
                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-1996; U13256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-1998; U18360.
12-SEP-1997; US-0589
05-SEP-1997; US-0576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyan DB;
WPI; 97-192924/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1999
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ΰ 526

437

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BP;
 2056
                                                                                                       Percent Similarity:
                                                   alignment_scores
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T79497;
 g
                                                                                                                                                                                                                                                                                                                                                           EH CKW KKW ELD
                                                                                                                                  x51701-55 encode human secreted proteins. The polynucleotides and their corresponding secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene treating or ameliorating medical conditions or a per protein or gene conditions and also be diagnosed by determining the presence of mutations in the new polynucleotides. Specific uses are presence of mutations in the new polynucleotides, Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atheroscierosis, restenosis, autoimmune disorders, alzheimer's disease, peripheral neuropathies, trauma, spinal cord injuries, allergy, hematopoietic disorders, asthma, immunodeficiency diseases, AIDS and transplant rejection. The polypeptides are also useful for identifying their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes
(Claim 2; Page 126-129; 184pp; English.
This sequence represents a human gene of the invention, that is induced
to express by both HCWV and interferon (IFN), designated HCMV-inducible
genes (cig or cigs). The invention also relates to genes that are
repressed in the presence of HCMV infection, designated HCMV-repressible
genes (crg or crgs). The products can be used to obtain agents which can
be used for anti-viral therapy, particularly anti-HCMV therapy. They can
also be used for the development of drugs that would allow for higher
dosage IFN treatments without the concomitant toxicity normally
associated with administering high levels of IFN. The products can also
be used for detection, diagnosis and drug screening.
                                                                  New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. neurological disorders, tumours, immune disorders, inflammation or haematological disorders Claim 1: Page 170: 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HCMY inducible gene, SEQ ID NO 17.
HCMV inducible gene; cig; human; human cytomegalovirus; interferon;
anti-viral therapy; anti-HCMV therapy; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                            240 T;
 Lafleur DW, Moore PA, Olsen HS, Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 978
                                                                                                                                                                                                                                                                                                                                                                                                                          197 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: X51732 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                            256 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgGluAspLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 AGGGAGGAGCTGAGAATCCAACTGCGGTGG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID X33945 standard; DNA; 2056 BP.
AC X33945;
                                                                                                                                                                                                                                                                                                                                                                                                                          285 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-12 x X51732/rev
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08-SEP-1998; U18638.
22-SEP-1997; US-059725.
08-SEP-1997; US-058180.
(UYRR-) UNIV PRINCETON.
CONG J, SCHENK T, Zhu H; WPI; 99-243729/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:X33945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.00
 Brewer LA, Ebner R,
Rosen GA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                        binding partners.
Sequence 978 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug screening; ds.
Homo sapiens.
WO9913075-A2.
                               WPI; 99-204988/17.
P-PSDB; Y12945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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Quosoft (first entry)

28-AUG-1990 (first entry)

Turkey herpes virus (HVT) homologue of the VZV62/HSV-1 IE 175 gene.

Infectious laryngotracheitis virus; ILTV; Marek's disease virus; MDV; Herpes virus of turkeys; HVT; vaccine; ribonucleotide reductase; ds. Turkey herpes virus.

W09002802-A.

32-AMR-1990.

13-SEP-1988; GB-021441.

(ANIM-) Inst Animal Health.

(ANIM-) Inst Animal Health.

Griffin AM, Ross LJN, Scott SD, Binns MM;

P-PSDB; R05832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meripilus giganteus galactanase cDNA.
Meripilus giganteus; galactanase; EC 3.2.1.89; arabinogalactanase;
endo-1,4-beta-galactanase; transformant; viscosity; wine production;
arabinogalactan endo-1,4-beta-galactosidase; fruit juice;
vegetable juice; animal feed; depectinisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-essential viral neucleotide sequences -
identified in Herpes virus of turkeys, Marek's disease virus and
infectious larymotrachatis virus.
Disclosure: Fig 11; 111pp; English.
The gene products may be used as antigens to provide in part a
multivalent vaccine, protecting against ILTV, MDV and HVT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Others;
  Ŧ,
                                                                                          Length: 10
Gaps: 0
Percent Identity: 70.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 8
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 G;
                                                                                                                                                                                                                                                                   Align seg 1/1 to: X33945 from: 1 to: 2056
  ပ်
                                                                                                                                                                                                                                                                                                                                                             1665 AGGGAAGCTTTGCATGTTGCTCTAAGGTAC 1694
                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: Q03811 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GACCTCCGAGTGGCATTCCGCTAC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AspLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T79497 standard; cDNA; 1026 BP.
645 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 003811 standard; DNA; 217 BP. 003811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                seg_name: N_Geneseg_36:Q03811
                                                                                                                      3.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:T79497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.250
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.00
                                                                                             35.00
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US-08-653-294-12 x X33945
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US-08-653-294-12 x Q03811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meripilus giganteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
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                                                                                             Quality:
Ratio:
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Trivial managed and a sequence encoding fungal galactanase - useful in production of wine or modification of animal feed, e.g. depectinisation, and reducing viscosity of plant cell wall derived material claim 1; Pages 34.36; 49pp; English.

Traducing viscosity of plant cell wall derived material claim 1; Pages 34.36; 49pp; English.

This cDNA sequence encodes a novel galactanase isolated from a fine constructed in E. coli. Positive cDNA inserts were dentified on SC-agar plates using the AZCL xylan assay. cDNA inserts were amplified directly from yeast colonies. In order to express the galactanase in Aspergillus, the DNA was digested with appropriate restriction enzymes, size fractionated on a gel and a fragment corresponding to the galactanase gene purified. The gene was subsequently ligated into pHA414 and digested with appropriate restriction enzymes to give pA2655. After amplification of the DNA in E. coli the plasmid was transformed into Aspergillus oryzae and transformant activity was analysed. The galactanase can be used to reduce the viscosity of plant cell wall derived material, thus having implications in wine production, the preparation of fruit or vegetable juice or for the modification of animal feed allowing a significant in the in vivo breakdown of plant cell wall material e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 99-081273/07.

New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis claim 1; Page 799-800; 1150pp; English.
X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                     Clausen IG, Kauppinen MS, Kofod LV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 9
4.250 Gaps: 0
88.889 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: T79497 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 C;
                                                        /product= galactanase
/EC_number= 3.2.1.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GluAspLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _documentation_block:
X20647 standard; DNA; 1145 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998.
23-JUN-1998; U13041.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
/*tag= a
55. .1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-12 x T79497/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:X20647
                                                                                                                                          28-FEB-1997; DK0091.
01-MAR-1996; DK-000234.
(NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme production; ds.
Treponema pallidum.
WO9859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1026 BP;
                                                                                                                                                                                                                      WPI; 97-448685/41.
P-PSDB; W23140.
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Percent Similarity:
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                                                                                                                                                                                                         Andersen LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                  WO9732013-A1
                  mat_peptide
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diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes. Sequence 1145 BP; 242 A; 267 C; 374 G; 257 T;
                                                                                                                                                                                                                                               Cladosporium oxysporum glucose oxidase encoding DNA.
Glucose oxidase; Cladosporium oxysporum; enzyme; bread improver;
antimicrobial agent; toothpaste; detergent; stain removal;
dough additive; hydrogen peroxide generator; ss.
Cladosporium oxysporum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   1. .350

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/product= "glucose oxidase"

/*tag= bredicted signal sequence"

/*tag= d

2190. .2386

/*tag= e
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Gaps: 0
Percent Identity: 77.778
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                                                                                                                                                                         839 AAAGAICITAGGATAGCICTTGCGTAC 813
                                                                                                                                                        2 GluAspLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                           seq_documentation_block:
ID V35645 standard; DNA; 2386 BP.
AC V35645;
                                                                                                                                                                                                                                       08-SEP-1998 (first entry)
                                                                                                            alignment_block:
US-08-653-294-12 x X20647/rev
                                                                        Ouality: 34.00
Ratio: 4.250
Percent Similarity: 88.889
                                                                                                                                                                                           seq_name: N_Geneseq_36:V35645
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                                                                 alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                       CDS
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581 G; 707 C; 583 A; SQ Sequence 2386 BP;

515 T;

alignment\_scores:

Quality: 34.00 Length: 9
Ratio: 4.250 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 77.778

alignment\_block: US-08-653-294-12 x V35645

Align seg 1/1 to: V35645 from: 1 to: 2386

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! AV045270 AV045270 Mus muscul
! AI768731 wh25d12.x1 NCI_CGAP
! AA594208 nn29e02.s1 NCI_CGAP
                                                                                                                                                                                                                                                                                                                    Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996) 96299762 On Oct 24, 1995 this sequence version replaced gi:1040105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .232.

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/organism="Homo sapiens"

/olone="3NHC2454"

/clone="3NHC2454"

/dev_stage="adult"

/note="Organ: heart; normalized directionally cloned cDNA

from adult heart; normalized 32 t
                                                                                                           C03945 232 bp mRNA EST 30-JUL-1996 C03945 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC2454, mRNA sequence.
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
Tanaka, T., Ogiwara, A., Uchiyama, I., Takagi, T., Yazaki, Y. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS
AA151891
LOCUS
DEFINITION ZO01[60.r1 Stratagene colon (#937204) Homo sapiens CDNA clone
INAGE:566435 5' similar to 9b:M15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108,
 255
294
340
144.65
166.72
192.74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusukeelims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 CGAGAGCATCTGCGGATCGCGCTCCGCTAC 69
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131.63
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EST.
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C03945.1 GI:1467196
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US-08-653-294-10 x C03945
                                                                                              seq_name: gb_est8:C03945
                                                                                                                                                                                                                            Homo sapiens
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Ratio:
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gb_est31:AV045270
gb_est33:AI768731
gb_est16:AA594208
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                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA151891 zoO1f06 r1 Stratagene
AA15189 zoO1f06 r1 Stratagene
AA263188 PWY0534 KG1-a Lambda Z
D82221 HUMHBC4626 Human pancrea
AA147151 zo32d06.r1 Stratagene
A1359260 qy27b07.x1 NCI_CGAP_Br
A1595864 wc74h11.x1 NCI_CGAP_Br
AA332511 EST36483 Embryo, 8 wee
AL036690 DKFZp564D2463_r1 564 (
AQ163964 HS_2270_B1_A09_MF CIT
AQ163964 HS_2270_B1_A09_MF CIT
AQ163964 HS_213_B1_B00_SP6E RF
AA899542 am64602.s1 Barstead sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D82189 HUMHC4524 Human pancrea AW092666 EST285866 tomato mixed Ad456126 GG EST285866 tomato mixed Ad456126 GG EST285866 tomato mixed Ad456126 GG EST285866 tomato mixed Ad5620 GG EST285866 tomato TCCPR AG721173 HS_564_A2_A04_T7A RPC AG721173 HS_564_A2_A04_T7A RPC AG7560 TRNS1864 T. cruzi epin Ad36510 EST71241 Pancreas tumc Ad860199 EST192966 NORMALIZE GL TZ9557 EST6446 Human Colon Hom Ad718827 mt68h02. Il Scratagene AG73595 z173004.rl Stratagene AA093595 z173004.rl Stratagene AA093910 z18h06.rl Stratagene AA093910 z18h06.rl Stratagene AA093196 mx89004.rl Soares mous AA74846 ny06904.zl NCL_GGAP_CG
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AQ319711 RPCI11-105J20.TJ RPCI-
AV209680 AV209680 RIKEN full-le
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AI813806 wk79912.x1 NCI_CGAP_Pe
B96290 T24D5TFB TAMU Arabidopsi
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A1172015 EST218010 Normalized
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AU014732 AU014732 Mouse two-cel
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                                                                                                                        -MODEL=frame+p2n.model -DEV=xlp
-Q-Cgnl_1/USPTO_spool_VUS0653294/runat_04022000_160700_15770/app_query.fasta.1
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                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        out_format : pfs
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Query: US-08-653-294-10
Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
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gb_est38.AL036690
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gb_est27.A1124815
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gb_est2:m13904
gb_est24:A117201
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gb_est6:D82221
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gb_est10:AA178827
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gb_est39:AV209680
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gb_gss4:AQ721173
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gb_est8:C03945
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expressed within the human hematopoietic hierarchy Genomics 50 (1), 44-52 (1998)
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                                                                                                                                                    The Toronto Hospital
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4.889
90.000
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PMY0534 KG1-a Lambda Zap Express cDNA library Homo sapiens cDNA 5'
                                                                                 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807\text{-}828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Stratagene colon (#937204)"
/fab_host="Solx cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI: Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. T-64 colonic epithelial cell line. Average insert size=: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 cone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifilers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 283)
Claudio, J.O., Liew, C.C., Dempsey, A.A., Cukerman, E., Stewart, A.M., E., Atkins, H.L., Iscove, N.N. and Hawley, R.G.
Identification of sequence-tagged transcripts differentially
             Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.
                                                                                                                                                                                                                                                                                   On May B, 1995 this sequence version replaced g1:800234 Contact: Wilson RK
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Gaps: 0
Percent Identity: 90.000
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/db_xref="GDB:4590888"
/db_xref="taxon:9606"
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AA263158
AA263158.1 GI:1898964
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US-08-653-294-10 x AA151891
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Locus AA263158
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Institute for Molecular and Cellular Regulation, Gunma University 339-15 Showa-machi, Maebashi Gunma 371, Japan Tel: 272-20-8856 Fax: 272-20-8896
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                                                                                                                                                                                                   CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada Tel: 416 3403834
Fax: 416 3403834
Fax: 416 3403835
Fax: 416 340383
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 375)
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Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
On May 5, 1995 this sequence version replaced gi:797810.
Contact: Hawley RG
Oncology Research Laboratories
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Location/Qualifiers
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seg_name: gb_est26:AI359260
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LOCUS A1359260
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LOCUS A141151 581 bp mRNA B37204) Home sapiens cDNA clone
DEFINITION 2032006.rl Stratagene colon (#937204) Home sapiens cDNA clone
IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.
                  /clone_lib-"Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size." 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 581)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
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97044478
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 272.
Location/Qualifiers
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/db_xref="GDB:4620889"
/db_xref="taxon:9606"
/clone="IMAGE:588587"
/clone=lib="Stratagene colon (#937204)"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK; Site_1:
EcoRI: Site_2: xhoIr; cloned unidirectionally. Primer:
Oligo dT. T-84 colonic epithelial cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
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Washington University School of Medicine
W444 Forest Park Parkway, Box 8501, St. Louis, MO (414 Forest 11: 314 286 1810
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4.889 Gaps: 0
90.000 Percent Identity: 90.000
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/db_xref="taxon:9606"
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AA147151.1 GI:1716526
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US-08-653-294-10 x D82221
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Ratio:
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COMMENT

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Bonaldo, Ph.D. con A. Library Arrayed by: Greg Lennon, Ph.D. con A. Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qy27b07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.
  -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases Primates; Catarrhini; Hominidae; Homo.

1 (bases to 618)

NCI/NINDS-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

CONTACT: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                      others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                      15
                                                                                                                                                                               44.00 . Length: 10
4.889 Gaps: 0
90.000 Percent Identity: 90.000
  'n
sequence: 5' GAATTCGGCACGAG (CTCGAGTTTTTTTTTTTTTT 3'" 162 c 185 g 85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Std Error: 0.00
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High quality sequence stop: 458.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 CGAGAGCAGCTGCGGATCNCGCTCCGCTAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
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                                                                                                                                                                                                                                                                                                                                                               to: AA147151
                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-10 x AA147151
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from: 1

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137 CGAGAGCTGCGGATCGCGCTCCGCTAC 166
                                         1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
to: A1696864
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                                                                                                                          seq_name: gb_est13:AA332511
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  Align seg 1/1
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (Dassa 1 to 748)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

On Mar 16, 1998 this sequence version replaced gi:2961758.

Contact: Robert Strausberg@nih.gov

Infe Technologies catalog #: 11548-013

DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:

LOCUS A1696864 748 bp mRNA EST 03-JUN-1999

LOCUS A1696864 748 bp mRNA character conversation wordshi.xi NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324421 3'

Similar to qb:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

B-51(B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                       to: 618
                                                                                                                              Gaps: 0
Identity: 90.000
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Percent Identity: 90.000
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                                                                                                                                                                                                                                                       from: 1
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  137
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High quality sequence stop: 424.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                  319 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 290
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                                                                                                                                                                                                                                                                                                1 ArgGluAsnLeuArgIleLeuLeuArgTyr
    δ
                                                                                                                                                    Percent
    182
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US-08-653-294-10 x AI359260/rev
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US-08-653-294-10 x AI696864
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Ratio:
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  128
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                                                                                     alignment_scores:
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  BASE COUNT
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AUTHORS
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KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sases I to 360)

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man'Wai, C., Calton, M.D., Calton, Rai, Cotton, M.D., Calton, Rai, Cotton, M.D., Calton, Raich, J. Gocayne, J.D., Fitzgerald, L.M., Fitzhugh, W.M., Colleman, E. Hinkle, P. Socht, J.L., Saudek, D.M., Shiley, R. Melan, F. Li, Y., Bednarik, D.F., Greene, J.M., Gruber, J., Hudson, P., Collins, E.J., Hudson, P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Raymond, L., Wel, Y.E., Wing, J., Yil, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.E., Wang, M. N., Kosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
seq_documentation_block:
LOCUS AA332511 360 bp mRNA EST 21-APR-1997
DEFINITION EST36483 Embryo, 8 week I Homo sapiens cDNA 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 9712 Medical Center Drive, Rockville, MD 20850 USA Fer: 3018699056 Bensil: arkerlav@tigr.org Bensil: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-;
/note="Corgan: Embryo, 8 weeks; Vector: pBluescript SK-;
114 c 67 g 67 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 18, 1995 this sequence version replaced gi:811192.
Other_ESTs: THC188992
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 9
Gaps: 0
Percent Identity: 88.889
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                                                                                                                          AA332511
AA332511.1 GI:1984775
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Similarity: 100.000
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Holzman,T., Adams,M.D. and

ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 414)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .351
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LOCUS
AI124815
414 bp mRNA
EST
II-SEP-1998
DEFINITION am56e06.x1 Johnston frontex Homo sapiens cDNA clone
IMAGE:1539586 3' similar to gb:MZ4038_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains
ACCESSION
AI124815
VERSION
AI124815. GI:3593329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Col1 DH108" 12 c 47 g 128 t 1 others
                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 351)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.
                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2270 row: B column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 9
Gaps: 0
Percent Identity: 77.778
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Location/Qualifiers
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AQ163964
AQ163964.1 GI:3562159
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Percent Similarity: 100.000
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US-08-653-294-10 x AQ163964
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LOCUS AQ163964 351 bp DNA GSS 16-OCT-1998
DEFINITION HS_2270_Bl_A09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=17 Row=B, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. Wiemannedkfz- heidelberg.de;
sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                               seq_documentation_block:
LOCUS AL036690 171 bp mRNA EST 27-SEP-1999
DEFINITION DKF2p564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKF2p564D2463_s', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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53 c 60 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5866258.
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 171)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:6606"
/clone="DKF2p56402463"
/clone=lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 80.000
                      to: 360
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                                                                                                                                                                   seq_name: gb_est38:AL036690
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Percent Similarity:
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                      Align seg 1/1
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source

FEATURES

BASE COUNT ORIGIN

us-08-653-294-10.rst

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to: AQ614213
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US-08-653-294-10 x AQ614213
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Quality:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 498)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECORI: Stanley Neuropathology Consortium

Www.stanleylab.org) brains S-58, S-65, S-67, S-78.

Random + Oligo-dT primed into ECORI site of ZAP II Vector.

Mass excised. Avg insert length 1.9kb. Custom library

provided by Dr. Nancy Johnston [(410) 614-3918,

nli@welchilnk.welch.jhu.edu].
                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Er from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ614213 498 bp DNA GSS 15-JUN-1999 HS_5123_B1_B06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=699 Col=11 Row=D, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled frontal lobe"
Ade_stage="adult"
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/note="Organ: brain; Vector: Bluescript SK-; Site_1:
WashU-NCI human EST Project
Ompublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1899887
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744
99380589
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1539586"
/clone=lib="Johnston frontal cortex"
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AQ614213.1 GI:5075489
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4.875
80.000
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US-08-653-294-10 x AI124815
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j

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Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library avallability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu,. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:

LOCUS AAA98942 402 bp mRNA EST 02-JUN-1998

LOCUS MAA980402.s1 Barstead spleen HPLRB2 Homo sapiens CDNA clone

DEFINITION am64d02.s1 Barstead spleen GD:LO5093 60S RIBOSOMAL PROTEIN L18A
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1 (bases 1 to 402)

Hillari, Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Morte, B., Schellenberg, K., Steptoe, M., Tan, F., Theislang, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Wash T., More 1997)

Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine
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This clone is available royalty-free through LLNL ; contact the
This Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 121\ c 98 g 150 t
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                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=699 Col=11 Row=D"
/clone_lbb="RPCI-11 Human Male BAC Library"
/sex="male"
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 77.778
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                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 498.
Location/Qualifiers
                                                                                                                                                                                                                              Plate: 699 row: D column: 11
Seq primer: SP6
Class: BAC ends
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AA989542.1 GI:3174906
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Ratio:
Percent Similarity:
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                                                                                                                Align seg 1/1
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KEYWORDS
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                        3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. " 106 c 132 g 92 t
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/db_xref="taxon.9606"
/db_xref="taxon.9606"
/db_xref="taxon.9606"
/dclone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences clone
133 g 61 t 8 others
                                                                                                                                Human pancreatic islet ESTs.

Human pancreatic islet ESTs.

Unpublished (1995)

On Apr 14, 1993 this sequence version replaced gi:785206.

Contact: Jun Takeda

Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan

Tel: 272-20-8856

Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMHBG4524 Human pancreatic islet Homo sapiens cDNA similar to HLA-B, mRNA sequence.

B02189 G1:1183662
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 402
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1576803"
/clone_lib="Barstead spleen HPLRB2"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                  Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                            /dev_stage="adult, 17 years"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
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US-08-653-294-10 x AA989542/rev
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Ratio: 4.222
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est6:D82189
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                                                                                                                                                                                                                                                                                      BASE COUNT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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Length:

38.00

Quality:

alignment\_scores

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/cloue_tube="tenato mixed elicitor, BTI"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
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/note="Vector: pBlueBcript SK(-); Site_1: EcoR1; Site_2:
Xho1; cLET - Inoculated with a variety of disease response
elicitors: plants exposed to 2,6 dichloroisonicotinic
acid, BTH, jamenoic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Potatoe; Lycopersicon.

1 (bases 1 to 440)
D'Ascenzo, M. He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Caraven,M.B., Fulii,C.Y., Bowman,C.L., Netman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                 Glovannonl, J. Generation of ESTs from tomato leaf tissue Ceneration of ESTs from tomato leaf tissue Ompublished (1999) On Jun 22, 1998 this sequence version replaced gi:3246706. Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .440.
/organism="Lycopersicon esculentum"
/oultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="clET21F6"
  Gaps: 0
Percent Identity: 80.000
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Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to reverse of: AW092686 from: 1
                                                                                                                                                                                                                                      279 CGAGAGAACCTGNGGATCGCGCTCCGNTAC 308
                                                                                                                                                                                                         1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
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t
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US-08-653-294-10 x AW092686/rev
4.750
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                                                                                                                                                      to: D82189
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US-08-653-294-10 x D82189
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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2000, 01:29:37 ; Search time 122.56 Seconds (without alignments) 1.933 Million cell updates/sec æ February Run on:

US-08-653-294-11 Perfect score: Title:

1 YRLLIRLNER 10

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Immunomodulatory p	Immunomodulatory p	Immunomodulatory p	HLA-B2702 CTL modu	CIL		HLA-B2702 84-75-84	Immunomodulating d	Immunomodulating d	Peptide B2702.84-7	Immunomodulatory p	HLA-B2702 CTL modu	HLA-B2702 CTL modu	HLA-B2702 84-75T/7	B2702.	Peptide B2702.84-7	S. aureus gidB pro	gidB	FRAG1 prote	gc.	). sensit	orotein	Smad6 p	otei		$^{\circ}$	SGF-	ion		윢	#4 used	TCR alpha chain of	an 5' EST s	TCR alpha-chain va
COLUMNIES	ID	W47268	W47266	W47272	R92909	R92911	R92907	R95428	က	m	33	W47270	R92910	R92908	R95430	W33791	3	W74405	W74406	W41592	R20796	R63199	R59926	W89551	o	₹	₹*	R41333	$\sim$	m	^	m	R62906	-	$\sim$
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ф	Query	 0	σ	σ	Φ	Ġ,	σ,	9	9	9	9	σ	9	9	9	9	79.6	9	9	σ	69.4	δ.	m	÷	÷	÷	÷	ä	ä	;	6	o,	59.5	φ.	6
	Score	49	44	44	44	44	44	44	44	44	44	39	39	39	39	39	39	34	34	34	34	32	31	30	30	30	30	30	30	30	29	58	59	29	29
	Result No.	 т	7	ю	4	Ŋ	Q	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34

TCR alpha-chain va V-alpha-15 gene al H. pylori GHPO 669 Mutant E. b binding Interleukin-13 bin Gene 71 product co 3-acylation enzyme Single chain T cel Ehrlichia sp. exte Bacillus popilliae Antigen peptide de
R62905 R62907 W98457 W96075 W56254 W05730 W15629 W3659 W371199
92 112 112 112 118 118 33 33 46 46 46 46 46 46 46 46 46 46 46
00000000000000000000000000000000000000
W W W W W W A 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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77-NOV-1997.
23-APR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
NOVel immunomedulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                      transplant rejection

Claim 10: Page 36: 41pp: English.

The present rejection

Chaim 10: Page 36: 41pp: English.

The present sequence is an immunomodulatory peptide, which

comprises a class I HiA-B alpha-1 domain sequence. It can be used

in a pharmaceutical composition together with a subtherapeutic dose

of an immunosuppressant, to extend the period of acceptance of a

transplant from a major histocompatibility complex (MHC) unmatched

donor, i.e. to inhibit transplant rejection. It can also be used in

the treatment of autoimmune diseases.

Peptides using the D-form amino acids are more effective

immunomodulators than their diastereomers or enantiomers.
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                                                                                                                                                                                    7..10
/note= "at least one of the amino acids is D-isomer
                                                                                  Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                     Location/Qualifiers
                                   ¥.
                              W47268 standard; peptide; 10
                                                                   (first entry)
                                                                                                                                                                                     Misc_difference 1
                                                                                                                                       Homo sapiens.
Synthetic.
                                                                 22-MAY-1998
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Gaps ö Query Match 100.0%; Score 49; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00023; Matches 10; Conservative 0; Mismatches 0; Indels

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1 YRLLIRLNER 10 ò g

RESULT

W47266 standard; peptide; 10 AA. W47266; 

22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
Homo sapiens.
Synthetic. Key Location/Qualifiers Misc\_difference 1. .10

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12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of tran
                                                                                                                                                                                                                                                                                                                                                                     Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                             R92909 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R92911 standard; peptide; 20 AA. R92911;
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                                                                                                                                                                   (first entry)
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05-APR-1995; U04349.
05-APR-1994; US-222851.
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les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
1 YRLLIRLNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the patient.
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                                                                                                                                                                   16-MAY-1996
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Best Local S.
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                  R92909;
                                                                                             RESULT
R92909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Krensky AM;
WPI; 98-018220/02.
Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                   immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                   Comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharametrical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases. Peptides using the D-form amino acids are more effective immunomodulators than their disastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplant rejection
Claim 10; Page 36; 41pp; English.
The present sequence is a immunomodulatory peptide, which
comprises a Class I HAAB alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of a coeptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
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 /note= "at least one of the amino acids is the D-isomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "at least one of the amino acids is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.8%; Score 44; DB 1; Length 10; llarity 90.0%; Pred. No. 0.0025; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 1; Length 10;
Pred. No. 0.0025;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the treatment of autoimmune diseases.
Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                       22-MAY-1996, US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                    transplant rejection
Claim 10; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-isomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W47272 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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/note=
                                                                      23-APR-1997; U06705
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Best Local Similarity
Matches 9; Conserv
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| YRLAIRLNER 10
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27-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                   Novel
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RESULT

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R83061-R83085, R83090-R83096 and R82907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
HIA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 15; Page 36; 80pp; English. R83061-R92085, R83085, R83080-R83085 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                        Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC unmatched
the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 1; Length 20;
Pred. No. 0.0054;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extension of acceptance period of transplants from donor hosts - using Class I B75-84 MHC antigen of
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Krensky AM;

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18-MAY-1995.
10-NOV-1994. U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
    cytolysis; antigen presenting cell. Synthetic. W09513288-A1.
                                                                                                                WPI; 95-194027/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate (or urrent treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                   HLA-B2702 CTL modulating peptide (B2702.84-75/75-84). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
HLA: p74; alphal-helix; human-leucocyte-associated protein; HSC70; APC;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extension of acceptance period of transplants from MHC unmatched donor hosts \, -using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                       Score 44; DB 1; Length 20; Pred. No. 0.0054;
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Pred. No. 0.0054;
0; Mismatches 1; Indels
                                                                                                                                                                                   1; Indels
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
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                                                                                                                                                                                                                                                                                                            R92907 standard; peptide; 20 AA.
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                                                                                                                                                        89.8%;
90.0%;
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Best Local Similarity
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05-APR-1994; US-222
                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
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WPI; 95-358582/46.
                                                                                                                                                                                                              1 YRLLIRLNER 10
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| YRLAIRLNER 10
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12-OCT-1995.
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WILL'S 35-1940/1/23.

WILL'S 35-1940/1/23.

WILL'S 35-1940/1/23.

Inhibit cytolytic activity and differentiation of CTLS.

Example, Page 12: 29pp; Emplish.

Example, Page 12: 29pp; Emplish.

Example, Page 12: 29pp; Emplish.

Example, Page 13: 29pp; Emplish.

Example, Page 13: 29pp; Emplish.

Example, Page 13: 20pp; Emplish.

Example, Page 13: 20pp; Emplish.

Example, Page 13: 20pp; Emplish.

Example 14: 20pp; Emplish.

Example 15: 20pp; Emplish.

Example 16: 20pp; Emplish.

Example 20pp; Emplish.

Example
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Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R Ranfe-7TL) (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Immunomodulating dimer peptide #1.
Immunomodulating dimer immunosuppressant drug; CTL activation:
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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22-MAX-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM; 98-086530/08.
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Best Local Similarity 90.0
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| YRLAIRLNER
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WO9744351-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating
This sequence represents a specifically claimed immunomodulating
Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating
Claimed which has immunomodulating activity, including the N-terminal
acylated and/or C-terminal amidated on esterified forms of up to 60.0

acylated and/or C-terminal amidated on esterified forms of up to 60.0

acylated and/or C-terminal amidated on esterified forms of up to 60.0

where A, B -(R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a

tylaphobic or small amino acid; aa80 = I or N; aa81, aa84 = a

represents amino acid; The sequence in the brackets may optionally be
absent or truncated at any peptide type bond within the brackets. The
compounds comprise amino acid; sequences related to a Class I HLA-B

alphal domain (positions 79-84). They can be used to inhibit cyctocxic

T-lymphocytes (CTL) from undesirably attacking cells in a host or in
vitro. They can also be used in combination with antigenic peptides or
proteins of interest to activate CTLS. They can also inhibit the
products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                    ö
hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA·B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T·Iymphocytes (CTL) from undesirably attacking cells in a host or in vitro and also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunomodulating dimer peptide #2.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1997.
22-MAY-1995.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) WILY LELAND STANFORD JUNIOR.
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 1; Length 20;
Pred. No. 0.0054;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                     89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1998 (first entry)
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Best Local Similarity 90. ت
احد 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLLIRLNER 10
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WO9744351-Al.
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Sequence 2
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                                                                                                                                                                                                                                                                                       Sequence
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The immunomodulating dimer peptide(s) - based on a class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autofimmune diseases.

Treating autofimmune diseases.

Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating crivity. A peptide-type compound or variant is claimed which has a munomodulating activity, including the N-terminal acylated and/or c-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula A-B, where A, B = C c. terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula A-B, where A, B = C c. R and A-70-71, [aa79-84] or I, aa89 - I or N; aa81 - a hydrophobic or small amino acid; aa82 - R or I; aa83 - G or R; and as represents amino acid sequences related to a class I HiA-B alphal domain (positions at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HiA-B alphal domain (positions or yead in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in a ceptome to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating anticimmune diseases, e.g. diabetes.

The antiput atthic and lupus erythematosis. The products can also be considered to antiputing and lupus erythematosis. The products can also be considered to antiputing and lupus erythematosis. The products can also be considered to a class of the products can also be considered to antiputing and lupus erythematosis. The products can also be considered to antiputing and lupus erythematosis. The products can also be considered to antiputing and lupus erythematosis. The products can also be considered to antiputing and lupus erythematosis. The products can also be considered to antiputing and lupus erythematosis.
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                                                                                                                                                                19-JUN-1998 (first entry)
Peptide B702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer. immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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//note= "at least one of the amino acids is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulatory peptide.
Immunomodulatory: Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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Pred. No. 0.0054;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             (STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used for detection and diagnosis.
                                                                                                                    W33792 standard; peptide; 20 AA. W33792;
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Best Local Similarity
19, Conserve
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YRLAIRLNER 10
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WO9744351-Al.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-1996;
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Gaps

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Score 44; DB 1; Length 20; Pred. No. 0.0054; 0; Mismatches 1; Indels

0;

Conservative

YRLLIRLNER 10

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Query Match Best Local Similarity Matches 9; Conserva

89.8%; 90.0%;

PR PR PP PI PP PI

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R831096 and R82307-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparade to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composite computation lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example; Page 12; 29pp; English.

Example; Page 12; 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Rsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of
                                                                                                                    HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; minunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
14.0-1909 84-757/75-84T palindrome.
15.0-1909 14.7 alphal-hellx; human-leucocyte-associated antigen; inhibitor;
17-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
18 cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
19.0-1913 1918 1919 presenting cell.
19.0-1913 1918 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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Pred. No. 0.059;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
65TRD ) UNIY LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                          R92908 standard; peptide; 20 AA.
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WPI; 95-194027/25.
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 95-358582/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the patient.
Sequence 20 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clayberger C,
                                                                                                                                                                                                                                                                                                                                               WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R95430;
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          RESULT
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R83061-R83085, R83096-R83096 and R92007-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)). Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                      Novel immunomodulatory peptide-type compound - useful for inhibiting transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                 The present sequence is an immunomodulatory peptide, which comprises a class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 0.027;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.6%; Score 39; DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krensky AM, Parham P;
23-APR-1997; U06705.
22-MAY-1996; US-651650.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                            Claim 10; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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80.0%;
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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WPI; 95-358582/46.
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16-MAY-1996

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RESULT 12

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Gaps

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Treating autoimmune diseases

Example 1; Page 19; 41pp; English.

Peptides Waish4-98 and Waish78-9 were assayed for their immunomodulating crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity.

C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = C. terminal amidated comprises the formula; A-B, where A, B = C. S. N; aa39 = R or (s. aa80 = I or N; aa77 = B, S. N; aa39 = R or (s. aa80 = I or N; aand aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CIL) from undestrably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CILS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, response to anti-CD3. The peptide can be used for preventing rejection cresponse to anti-CD3. The peptide can be used for preventing rejection cresponse to anti-CD3. The peptide can be used for preventing rejection creaming atthritis and lupus erythematosis. The products can also be chematoid arthritis and lupus erythematosis. The products can also be used for derection and diagnosis.
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a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W33791;

9-JON-1998 (first entry)

Peptide B2702.84-75T/75-84 tested for immunomodulating activity.

Immunomodulating dimer; immunosuppressant drug; CTL activation;

transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Length 20; Pred. No. 0.059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               79.6%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.6
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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W33791
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Gaps

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Query Match

79.6%; Score 39; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.059;
Matches 8; Conservative 0; Mismatches 2; Indels

1 YRLLIRLNER 10

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| YRLATRLNER 10
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Search completed: February 8, 2000, 01:29:38 Job time: 1750 sec

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Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec
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                    Compugen Ltd
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                      7, 2000, 11:54:22;
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                                                                       sw model
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Gapop 10.0 , Gapext 0.5
                                                                     - protein search, using
                                                                                                                                                                           US-08-653-294-11
                                                                                                                                                                                                          1 YRLLIRLNER 10
                                                                                                        February
                                                                                                                                                                                             Perfect score:
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                                                                     OM protein
                                                                                                                                                                                                            Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

summaries

Post-processing: Minimum Match 0% Listing first 45

pir1:\* pir2:\* pir3:\*

PIR\_62:\*

Database

Minimum DB seq length: 0 Maximum DB seq length: 1000000

cylicin II - human glycoprotein gpl3 RING finger protei ret finger protein ORF2 - chicken hypothetical prote hypothetical prote hypothetical prote dolichyl-phosphate hypothetical prote YTA12 protein prec DNA-directed RNA p hypothetical prote transforming prote chromodomain-helic glycoprotein gp13 probable penicilli bud emergence prot leucine-rich repea hypothetícal prote NADH dehydrogenase probable frxA prot fibroblast growth glycoprotein gpl3 probable membrane leucine-rich repea peptide transport peptide transport ribosomal protein Description SUMMARIES B70744 S56263 S57158 A32122 F64877 S39588 B46114 S37583 TVHURF I50372 TVHURE A47392 T12615 T12048 T00914 JC6168 B45343 S64994 I37271 S54465 B33926 T14517 VGBEEH 105004 15959 T01392 В Query Match Length Score Result Š

CDC39 protein - ye probable GTPase-ac	ribosomal mo <b>bile e</b> hvpothetical <b>prote</b>	hypothetical prote	translorming proce probable thiamine	H+-transporting AT	probable flagella-	N-acetylglucosamin	ribosomal protein	ribosomal protein		ribosomal protein	ribosomal protein
S28417 RGBYI2	A21047 S27599	F70007	G70418	E64327	D75062	B69664	A33823	B33823	R5RTL5	S55912	JC1308
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2108 3079	144	176	186	206	232	242	296	296	297	297	297
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31	0 0 8 8	30	30	30	30	30	30	30	30	30	30
31 32	ა გ	35	37	38	38	40	41	42	43	44	45

## ALIGNMENTS

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C
leucine-rich repeat protein T419.11 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T01392
R;Parnell, L.D.; Gnoj, L.; de la Bastide, M.; Hameed, A.; Habermann, K.; Schutz, K.;
submitted to the EMBL Data Library, May 1998
A;Perrell, D.D.; Gnomic sequence of BAC T419 from Arabidopsis thaliana, chromosome IV, A;Reference number: 214314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-254 <LOR>
A; Caross-references: GB:U57715; NID:g1518608; PID:g1518609
A; Note: the authors translated the codon GTG for residue 56 as Cys
C; Comment: This protein plays an important role in cellular functions, and in fibrobl
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joseph Barton receptor activating protein 1 - rat fibroblast growth factor receptor activating protein 1 - rat c; Species: Rattus norvegicus (Norway rat)  
C; Species: Rattus norvegicus (Norway rat)  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 10-Sep-1997  
C; Accession: JG618  
R; Lorenzi, M.V.; Horli, Y.; Yamanaka, R; Sakaguchi, K.; Miki, T.  
Proc. Natl. Acad. Sci. U.S.A. 93, 8956-8961, 1996  
A; Title: FRAGI, a gene that potently activates fibroblast growth factor receptor h A; Reference number: JG6188; MUID:96392347  
A; Accession: JG6188
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                                                                                                                                                                                                                                            A Accession: T01392
A Status: translated from GB/EWBL/DDBJ
A Molecule type: DNA
A Residues: 1-395 CARA
A Cross-references: EMBL:AF069442; NID:g3242970; PID:g3924604
A Experimental source: cultivar Columbia
C Genetics:
A Map position:
A Note: T419.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 7.3;
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C;Keywords: growth factor receptor; osteosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.5%;
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Best Local Similarity
Matches 6; Conserv
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231 YRVLLRLNQ 239
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Length 254;

DB 2;

Score 34;

69.48;

Query Match

Matches

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C; Superfamily: herpesvirus glycoprotein F
C; Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-468/Product: glycoprotein gpl3 #status predicted <GPT>
F;43-451/Pomain: transmembrane #status predicted <TMN>
F;46,57,62,92,100,131,203,208,269/Binding site: carbohydrate (Asn) (covalent) #status
                                                                      C'Species: Homo sapiens (man)
C'Date: 12-Aug-1996 *text_change 25-Oct-1996
C'Date: 12-Aug-1996 *sequence_revision 12-Aug-1996 *text_change 25-Oct-1996
C'Accession: 137271; S52774
R;Hess, H.; Heid, H.; Zimbelmann, R.; Franke, W.W.
Exp. Cell Res. 218, 174-182, 1995
A;Title: The protein complexity of the cytoskeleton of bovine and human sperm heads: A;Reference number: 137271; MUID:95255491
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan_1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change 16-Jul-1999
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A;Molecule type: mRNA
A;Residues: 1-506 - WALL:X75343; NID:9406747; PIDN:CAA53092.1; PID:9406748
C;Superfamily: rfp transforming protein; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Cross-references: GB:S57839; NID:9298846; PIDN:AAB25944.1; PID:9298848
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                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-348 <HES-
A;Cross-references: EMBL:246788; NID:9758586; PID:9758587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: B46114
R; Matsumura, T.; Smith, R.H.; O'Callaghan, D.J.
Virology 193, 910-923, 1993
A; Title: DNA sequence and transcriptional analyses of A; Reference number: A46114; MUID:93212524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: host Equus caballus (domestic horse)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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Pred. No. 36;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.3%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N. Alternate names: glycoprotein
C. Species: equine herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein gpl3 precursor
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLLIRLNER 10
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R; Takahashi, M.
                                      cylicin II - human
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                                                                                                                                                                                                                                                                 RESULT 3
B4543
glycoprotein gpl3 precursor - equine herpesvirus 4
N;Alternate names: glycoprotein gC
C;Species: equine herpesvirus 4
C;Species: gquence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45343
R;Nicolson, L.; Onions, D.E.
Virology 179, 378-387, 1990
A;Title: The nucleotide sequence of the equine herpesvirus 4 gC gene homologue.
A;Reference number: A45343; MUD:91021040
A;Reference number: A45343; MUD:91021040
A;Reference number: A45343
A;Molecule type: DNA
A;Residues: 1-485 ANIC
A;Cross-references: GB:M58031; NID:9330894; PIDN:AAA46083.1; PID:9330896
C;Genetics
A;Gene: 16
C;Superfamily: herpesvirus glycoprotein F
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <GGP>F;31-485/Product: glycoprotein gpl3 #status predicted <GGP>F;31-485/Product: glycoprotein gpl3 #status predicted <GGP>F;60,61,66,67,72,108,116,1147,220,225,286/Binding site: carbohydrate (Asn) (covalent) #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane protein YLR145w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L3301

C;Species: Saccharomyces cerevisiae

C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 26-Aug-1999

C;Accession: S64994

R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.

Submitted to the Protein Sequence Database, May 1996

A;Reference number: S64997

A;Residues: 1-201 <RIE>

A;R
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C;Superfamily: Saccharomyces probable membrane protein YLR145w
C;Keywords: transmembrane protein
F;92-108/Domain: transmembrane #status predicted <TMM>
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 15;
       ed. No. 12;
Mismatches
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          Pred.
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60.0%;
   87.58;
                                          Conservative
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Similarity 7; Conserv
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Matches 7; Conserv
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YRLILLLNHR 24
                                                                                                                                             109 YRLLCRLN 116
                                                                                                         1 YRLLIRLN 8
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          Best Local
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Matches

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Chromodomain-helicase-DNA-binding protein, CHD-1 - mouse
Chromodomain-helicase-DNA-binding protein, CHD-1 - mouse
Chromodomain-helicase-DNA-binding protein
Cjpecies: Mus musculus (house mouse)
Cjpecies: Mus musculus (house mouse)
Cjaccession: A47392; $21568
Cjaccession: A47392; $21568
Cjaccession: A47392; $21568
Cjaccession: A47392; Multiply
Cjaccession: A47392
Ajritle: A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWI
Ajrecession: A47392
Ajrecession: A47
                                                                                                                                                                                                          N'Alternate names: ret oncogene protein
N'Contains: protein-tyrosine kinase (EC 2.7.1.112) ret
C'Species: Homo sapiens (man)
C'Jace: Bond Sapiens (man)
C'Jace: 31-Mar-1989 #sequence_revision 10-Sep-1997 #text_change 13-Aug-1999
C'Accession: A27203
R'Jakabashi, M.; Cooper, G.M.
Roll: Biol: 7, 1378-1385, 1987
A/Title: ret transforming gene encodes a fusion protein homologous to tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 'QAGA',1-801 <TAK>
A;Residues: 'QAGA',1-801
A;Notes references: GB:M16029; NID:g340025
A;Note: codons preceding the probable start codon were translated
C;Comment: The ret oncogene is the chimeric product of a translocation mutation betwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: ATP; fusion protein; oncogene; phosphotransferase; transforming protein; F;1-315/Region: transforming protein rfp F;16-792/Region: protein rtrosine kinase ret F;316-792/Region: protein kinase ATP-binding motif F;487/Active site: Lys #status predicted
                                                                                                                                                                       transforming protein RFP/protein-tyrosine kinase RET mutant fusion protein - human
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Pred. No. 1.4e+02;
1; Mismatches 1;
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A; Residues: 772-1711 CB2>
A; Cross-references: EMBL:X66028
C; Superfamily: CHD-1 protein; chromobox homology
C; Keywords: DNA binding
F; 293-336, Domain: chromobox homology CCB1>
F; 397-427, POmain: chromobox homology CCB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 63;
0; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.8
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C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Jun-1999
C; Accession: 150372
C; Accession: 150372
R; Funahashi, J.; Sekido, R.; Murai, K.; Kamachi, Y.; Kondoh, H.
Bovelopment 119, 433-446, 1993
A; Title: Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomai A; Reference number: 150222; MUID:94116444
A; Accession: 150372
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A:Map position: 6p22-6p21.3
C;Superfamily: rfp transforming protein; RING finger homology
C;Reywords: DNA binding; transforming protein; zinc
C;Reywords: bransforming protein in finc
F;1-315-Product: transforming protein rfp (fragment) #status predicted <RET>
F;12-62/Domain: RING finger homology <RNG>
F:16-127/Domain: metal and nucleic acid binding #status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: transforming protein rfp
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A28101
A: Molecule type: mRNA
A; Residues: 1-513 <TAK>
A; Cross.references: DDBJ:J03407; NID:g337371; PIDN:AAA36564.1; PID:g337372
C; Genetics:
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A;Residues: 1-560 <FUN>
A;Cross-references: GB:D14316; NID:g391639; PIDN:BAA03262.1; PID:g391640
C;Superfamily: CHD-1 protein; chromobox homology
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red. No. 44;
Mismatches 1
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R.Takahashi, M.; Inaguma, Y.; Hiai, H.; Hirose, F.
Mol. Cell. Biol. 8, 1853-1856, 188
A:Title: Developmentally regulated expression of a la. Reference number: A28101; WUID:88246464
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A;Molecule type: mRNA
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Pred. No.
C; Keywords: zinc
F;5-55/Domain: RING finger homology <RNG>
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Best Local Similarity
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191 YRLLARLEE 199
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198 YRLLARLEE 206
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KLLIRLRER 51
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02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change ion: S56263
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Job time: 24333 sec
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211 YRLLLRLH 218
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205 YRLLLRAN 212
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-221 <MUJ
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A; Reference number: A71000; MUID:98344137
A; Reference number: A71000; MUID:98344137
A; Reference number: A71000; MUID:98344137
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-151 < KAM>
A; Residues: 1-151 < KAM>
A; Residues: 1-151 < KAM>
A; Experimental source: strain of 3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank A; Gene: PH0674
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                                                                                                                                                          probable frxA protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998
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22;
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C;Species: Saccharomyces cerevisiae
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Best Local Similarity 77.8
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793 KLLIRLRER 801
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C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 05-Dec-1997 C;Accession: $55263  
R;Murakami, Y:; Naitou, M.; Haqiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas submitted to the EMBL Data Library, May 1995  
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces A;Reference number: $56186
                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D50617; NID:g836685; PID:d1009888; PID:g836763; MIPS:YFR008w
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C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 06-Feb-1998
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A;Residues: 1-239 <ROS>
A;Cross-references: EMBL:249635; NID:g1015871; PID:g1015872; MIPS:YJR135c
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N;Alternate names: hypothetical protein J2122
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R;Rose, M.; Koetter, P.; Entian, K.D.
Submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S57158
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Pred. No. 27;
2; Mismatches
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Pred. No. 29;
1; Mismatches
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Best Local Similarity 75.0
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xenopus lae
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(without alignments)
4.688 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82229 segs, 29864866 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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NUCM_PARTE
RCA1_YEAST
NOT1_YEAST
IRA2_YEAST
IRA2_YEAST
ATPE_METJA
ATPE_METJA
NAGB_BACSU
RL5_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGLC_HSVE4

KLS_BOWNO
CYLS_BOWNO
CYLS_HUMAN
RFP_HUMAN
RFP_HUMAN
RFP_MOUSE
CHD1_MOUSE
CHD1_MOUSE
YFH8_TAST
YUJD_YEAST
VJD_YEAST
VJD_YEAST
RLS_ANOGA
SAPD_ECOLI
SAPD_ECOLI
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SAPD_ECOLI
RLS_ANOGA
SAPD_ECOLI
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RLSB_XENLA
RLS_CHICK
RLS_HUMAN
RLS_RAT
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB seq length: 1000000
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LE_NEUCR RUB_ECCLI CBA_BACSU CBA_BACSU AM2_NOUSE PYO_ZYMMO AM2_NOUSE PYO_YEAST REB_SCHPO AGE_BACSU GM3_HUMAN ALIGNMENTS AS tage; Herpesviridae; virus.  FEYNRUSES GLYCOPROTEIN C ESTRUCES GLYCOPROTEIN C ESTRUCES GLYCOPROTEIN C FOTENTIAL. FOTENT	neurospora escherichia bacillus su rickettsia zymomonas m mus musculu saccharomyc saccharomyc schizosacch bacillus su homo sapien	ne herpesvirus  gc gene  perfamily.  rough a collaboration -  restrictions on its  restrictio	0; Gaps 0;
35 30 61.2 301 1 RL5_NEUCR 36 30 61.2 314 1 TRUB_ECCLI 31	059953 P09171 P091758 P1619 P1619 P76875 P78963 P13485 P13485	그 이 이 이 이 이 이 이 이 이 이 이 이 이 이 이 이 이 이 이	1; Length 48 2; Indels
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Secretary and a secretary and	0000000000	Sister of the control	ch 1 Sim 7;
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Cytoskeleton;
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P14373;
                                                                                                                                                                                          SEQUENCE
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RFP_HUMAN
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                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exp. Cell Res. 218:174-182(1995).

-!- FUNCTION: POSSTBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS. MAY

BE INVOLUDE IN SPERMATID DIFFERENTIATION.

-!- SUBCELLULAR LOCATION: CALIX; SPERM HEAD CYTOSKELETAL STRUCTURE.

-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HESS H., HEID H., ZIMBELMANN R., FRANKE W.W.; "The protein complexity of the cytoskeleton of bovine and human sperm heads: the identification and characterization of cylicin II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                          Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                     TISSUE-SILK GLAND:
YANG C.S., SEHNAL F.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY STMILARITY).
-!- FUNCTION: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 299;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM: PF00861; Ribosomal L18p; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 299 AA; 34378 MW; 7262D2FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).
                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
608 RIBOSOMAL PROTEIN L5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 1
Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 AA
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF008229; AAC24960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 50.0
nes 5; Conservative
                                                                                 STANDARD;
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                                                                                                                                                                   Bombyx mori (Silk moth)
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                      120 YRLEIHLNOR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLLIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | :: | | : : | 49 YRLIVRLSNK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYL2_HUMAN
Q14093;
                                                                              RL5_BOMMO
076190;
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CYL2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SITE 315 316 BREAKPOINT FOR TRANSLOCATION TO FORM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAKAHASHI M., INAGUMA Y., HIAI H., HIROSE F.;
"Developmentally regulated expression of a human 'finger'-containing
gene encoded by the 5' half of the ret transforming gene.";
MOI. Cell. Biol. 8:1853-1856(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i - FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
-i - SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-i - DISEASE: RECOMBINATION OF THE N-TERMINAL OF RFP WITH A PROTEIN TYROSINE KINASE PRODUCES THE RET TRANSFORMING PROTEIN.
-i - SIMILARITY: CONTAINS A C3HC4-CLAŠS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                       Structural protein; Repeat; Sperm; Spermatogenesis.

3 47 31 X 3 AA REPEATS OF K-K-X.

240 3 X APPROXIMATE TANDEM REPEATS.
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 348; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FD27FBEF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JUL-1998 (Rel. 36, Last annotation update)
ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C3HC4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
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                                                                                                                                                                                                                                                                                       EMBL; 246788; CAA86752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00643; zf-B_box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLLIRLNER 10
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78 YRSLMRISER 87
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SO

RESULT 5 RFP\_MOUSE

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REDIED SEQUENCE FROM N.A.

REDIED SEQUENCE FROM N.A.

REDIED STATEMENT STATEMENTS A.D., HIETER P., COLLINS F.S.;

WOODGGE T., BASRAI M.A., BAXEVANIS A.D., HIETER P., COLLINS F.S.;

R. "Characterization of the CHD family of proteins.";

Proc. Natl. Acad. Sci. U.S.A. 94:11472-11477(1997).

- FUNCTION: SEQUENCE-SELECTIVE DNA-BINDING PROTEIN. COULD PLAY AN IMPORTANT ROLE IN GENE REGULATION.

- SUBCELLULAR LOCATION: NUCLEAR.

- SIMILARITY: BELONGS TO THE SNR2/RAD54 HELICASE FAMILY.

- SIMILARITY: CONTAINS 2 'CHROMO' DOMAINS.

- SIMILARITY: CONTAINS 3 'CHROMO' DOMAINS.

- SIMILARITY: CONTAINS 2 'CHROMO' DOMAINS.

- SIMILARITY: CONTAINS 3 'CHROMO' DOMAINS.

- SIMILARITY: CONTAINS 
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MEDLINE; 93211972.
DELMAS V., STOKES D.G., PERRY R.P.;
"A mammalian DNA-binding protein that contains a chromodomain and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rođentia; Sclurognathi; Muridae; Murinae; Mus.
                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; rocover, Proceedings of the PROSITE; rocover, PFAM, PF00271; helicase_C; 1.
PFAM; PF00385; chromo; 2.
DNA-binding; ATP-binding; Helicase; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1; Length 1709;
Pred. No. 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CHROMODOMAIN-HELICASE-DNR-BINDING PROTEIN 1 (CHD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EC7F932A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMO DOMAIN.
CHROMO DOMAIN.
ATP (POTENTIAL).
DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1711 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1628 1632 1.
1634 1638 2.
1640 1644 3.
1709 AA; 196517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P23197; 1APO.
MIN; 602118; --
PROSITE; P500598; CHROMO_1; 2.
PROSITE; P550013; CHROMO_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF006513; AAB87381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         795 KLLIRLRER 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLLIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD1 OR CHD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHD1_MOUSE
P40201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
CHD1_MOUSE
  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 91176437.

CAO T., SHANNON M., HANDEL M.A., ETKIN L.D.;
CAO T. SHANNON M., HANDEL M.A., ETKIN L.D.;
SPECIFIC stages of mouse spermatogenesis.";
Dav. Genet. 19:309-320(1996).
-!- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTEWTIAL).
-! SIBLEARITY: CONTAINS A C34C4-CLASS ZINC FINGER.
                                                                                       Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PSO0518; ZINC_FINGER_C3HC4; 1.
PFAM: PF00097; Zf-C3HC4; 1.
PFAM: PF00627; Zf-C3HC4; 1.
PFAM: PF00643; Zf-B_box; 1.
Zinc-finger: Metal-binding: Nuclear protein; DNA-binding. Zinc-finger: Metal-binding: C3HC4-TYPE.
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                     DB 1;
18;
B BOX.
022BC859 CRC32;
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18E6E716 CRC32;
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-LUL-1998 (Rel. 36, Last annotation update)
2INC-FINGER PROTEIN RFP (RET FINGER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                   Score 33; DB:
Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1709 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 136 B
522 AA; 59550 MW;
127 I
58489 MW;
                                                                                     67.38;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L46855; AAA85354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
انتمار 77.8
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 36, (Rel. 36, 1) (Rel. 36, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
96 J
513 AA;
                                                                                                     Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                    1111 || | |
198 YRLLARLEE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 || |
207 YRLLARLEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                           1 YRLLIRLNE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLLIRLNE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (15-JUL-1998 (15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHD1_HUMAN
014646;
                                                                                                                                                                                                                                                                                                                                   RFP_MOUSE
Q62158;
DOMAIN
SEQUENCE
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                                                                                       Ouery Match
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Gaps

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RESULT 6 CHD1\_HUMAN

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RESULT 9
YFH8_YEAST
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                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GOLE S.T., BROSCH R., GAS S., BARKY C.E. III, TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., BANCKS R., BEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L.,
                                                                                    -:- SUBCELLULAR LOCATION: NUCLEAR.
-:- TISSUE SPECIFICITY: ABUNDANCE IS HIGHER IN CELLS REPRESENTING
EARLY STAGES OF THE BILWHOID LINEAGE SUCH AS PRE-B AND B CELLS,
THAN IN CELLS REPRESENTING MATURE PLASMACYTES OR OTHER CELL
LINEAGES SUCH AS FIBROBLASTS.
-:- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
-:- SIMILARITY: CONTAINS 2 'CHROWO' DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
SNE2/SW12-like helicase domain.";
Proc. Natl. Acad. Sci. U.S.A. 90:2414-2418(1993).
-1- FUNCTION: SEQUENCE-SELECTIVE DNA-BINDING PROTEIN. COULD PLAY AN IMPORTANT ROLE IN GENE RECULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                DNA-binding; ATP-binding; Helicase; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).
DEAH BOX.
3 X 5 AA REPEATS OF H-S-D-H-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1; Length 1711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 196409 MW; CB184D33 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-DEC-1999 (Rel. 39, Last annotation update)
HYPOTHETICAL 20.7 KD PROTEIN RV0487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMO DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00598; CHROMO_1; 2.
PROSITE; PS50013; CHROMO_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00176; SNF2_N; 1.
PFAM; PF00271; helicase_C; 1.
PFAM; PF00385; chromo; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L10410; AAB08486.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 67.3
Best Local Similarity 77.8
Matches 7; Conservative
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1645
1633
1639
1645
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HSSP; P23197; 1AP0.
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793 KLLIRLRER 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y487_MYCTU
Q11153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
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SITE
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Y487_MYCTU
    SOUR PRINTER P
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       RAJANDREAM M.A., ROGERS J., SQUARES S., SQARES R., SULSTON J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C / AB972;
MPDILINE; 95400292.
MURKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,
YAMAZAKI M., TASHIRO H., EKI T.;
SARAIYsis of the nuclectide sequence of chromosome VI from
Saccharomyces cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 25.9 KD PROTEIN IN MPRI-GCN20 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
9.7;
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12;
                                                                                                                                                                                                                                                                                                                                                                                                                                            11 protein.
183 AA; 20716 MW; 23C141D2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLN.
3D34764A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last anno
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SEQUENCE 221 AA; 25915 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 10:261-268(1995).
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Best Local Similarity 75.0%;
Matches 6; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 277162; CAB00948.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D50617; BAA09247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLLIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 YRFLLRRNRR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLLIRLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YFH8_YEAST
P43592;
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65 RIIVRINER 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLLIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL5_ANOGA
044248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-G3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠:
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANNOSYLTRANSFERASE)
DPM1 OR SED3 OR YPR183W OR P9705.3.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORLEAN P., ALBRIGHT C., ROBBINS P.W.;
"Cloning and sequencing of the yeast gene for dollchol phosphate mannose synthase, an essential protein.";
J. Biol. Chem. 263:17499-17507(1988):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z., FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T., HALLSWORTH K., HAMKINS J., HILLIER L., JIER M., JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S., MILLER N., NRAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D., MILCOX L., WOHLDMAN P., VAUDIN M., WAILSON R., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) (DOLICHOL-PHOSPHATE BETA-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 27.6 KD PROTEIN IN NMDS-HOM6 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 239;
13;
                                                                                                                                                                                       LIJ
SEQUENCE FROM N.A.
ROSE M., KOETTER P., ENTIAN K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                       27567 MW; OBF23C6E CRC32;
                                                            239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           65.3%; Score 32; DB 75.0%; Pred. No. 13; Live 1; Mismatches
                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                              EMBL; 249635; CAA89666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.3
Best Local Similarity 75.0
Matches 6; Conservative
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 239 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
211 YRLLLRLH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111:1 |
205 YRLLLRAN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 89034276
                                                                                                                                  YJR135C OR J2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIRLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPM1_YEAST
P14020;
                                                            YJ9D_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
DPM1_YEAST
                                               YJ9D_YEAST
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                                                                                                                                                                                                                  SUBCELLULAR LOCATION: IF THE N-TERMINUS IS A FUNCTIONAL SIGNAL SEQUENCE, THE PROTEIN IS PREDICTED TO BE ORIENTED TOWARD THE LUMEN OF THE ENDOLAGANER RETICULUM WITH BOTH TERMINI SERVING AS ANCHORS. THE LACK OF A SIGNAL SEDUENCE INDICATES THAT THE ENZYME FACES THE CYTOPLASM AND IS ANCHORED AT THE C-TERMINUS.

DOMAIN: THE N-TERMINUS OF THE PROTEIN, THOUGH NOT HYDROPHOBIC, MEETS EXISTING CRITERIA FOR YEAST SIGNAL SEQUENCES, EVEN THOUGH NO SITE EXISTS FOR CLEAVAGE BY SIGNAL PEPTIDASE.

SIMILARITY: BELONGS TO THE GLYCOSYLIRANSFERASE FAMILY 2.
nitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN THE SYNTHESIS OF THE SUGAR DONOR DOL-P-MAN WHICH IS REQUIRED IN THE SYNTHESIS OF N-LINKED AND O-LINKED OLIGOSACCHARIDES AND FOR THAT OF GPI ANNHORS.
CATALTIC ACTIVITY: GDP-MANNOSE + DOLICHYL PHOSPHATE - GDP + DOLICHYL D-MANNOSYL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORNEL A.J., KUMAR V., MUKABAYIRE O., SALAZAR RAFFERTY C.,
CORNEL A.J., KOLUZZI M., COLLINS F.H.;
PETRARCA V., COLUZZI M., COLLINS F.H.;
PUBLITTED (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A32122; A32122.
SGD; L0000524; DPM1.
PRAW: PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
15;
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F8D92784 CRC32;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 AA; 30362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J04184; AAA34578.1; -. EMBL; U25842; AAB68116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.3%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endoplasmic reticulum.
TRANSMEM 239 259
SEQUENCE 267 AA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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RESULT 14
SAPD_SALTY
ID SAPD_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P36636;
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                                                                                                                                                                                         ö
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12;
EPSTEIN W., NOELKER E., STUMPE S., TEWES R., SCHMID R., BAKKER E.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 97426617.
BLATTHER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K., ITOH T., KASAI H., KASHIMOTO K., KINUKASAWA M., MAKINO K., MINI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K., NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIWA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H., TAREDA J., TAKEMOTO K., TAKEMOTO Y., VAMAMOTO Y., HORIUCHI T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A 570-kb DNA sequence of the Escherichia coll K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                           ö
                                                                                                                                              Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 301-330 FROM N.A.
BERGLER H., EBELING A., FUCHSBICHLER S., HOGENAUER G.,
TURNOWSKY F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEPTIDE TRANSPORT SYSTEM ATP-BINDING PROTEIN SAPD.
                                                                                                                                                ï
                 EMBL; AF002238; AAB97731.1; -.
PFAM; PF00861; Ribosomal_L18p; 1.
Ribosomal protein; FRNA-binding.
SEQUENCE 327 AA, 37996 WM, F3A3EED2 CRC32;
                                                                                                                                       DB ,
                                                                                                                                         Score 32; DB pred. No. 18; Aismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 29, Created)
                                                                                                                                              65.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:363-377(1996).
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABC TRANSPORTERS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                         :||::||: |
49 FRLIVRLSNR 58
                                                                                                                                                                                                                                 1 YRLLIRLNER 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                            SAPD_ECOLI
P36635;
                                                                                                                                                                                                                                                                                                                                     RESULT 13
SAPD_COLI
IS DAD_COLI
IS DAD_COLI
IS DAD_COLI
IS DAD_COLI
IS DAD IN NOW
DT 01-NOW
DT 01-NOW
DT 01-NOW
DE PEPTID
GN BACTER
RP SEQUEN
RP S
CC
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SQ
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: INVOLVED IN A PEPTIDE INTAKE TRANSPORT SYSTEM THAT PLAYS A ROLE IN THE RESISTANCE TO ANTIMICROBIAL PEPTIDES.
-!- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE; 94038887.

PARRA-LOPEZ C., BAER M.T., GROISMAN E.A.;

"Molecular genetic analysis of a locus required for resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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0
                                                                                                                                                                                                                                                                             PFAM; PF00005; ABC_tran; 1.

PEPELIGE transport; Transport; Inner membrane; ATP-binding. NP_BIND

NP_BIND

SEQUENCE 330 AA; 37660 WW; BE0692E6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antimicrobial peptides in Salmonella typhimurium."; EMBO J. 12:4053-4062(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PEPTIDE TRANSPORT SYSTEM ATP-BINDING PROTEIN SAPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
18;
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9910EB90 CRC32
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STYGENE; SG10380; SAPD.
PROSITE; PS00211; ABC_TRANSPORTER; FALSE_NEG.
                                                                                                                         EMBL, D90766; CAB20760.1; -.
EMBL, D90767; CAB20768.1; -.
EMBL, D90768; CAB20789.1; -.
EMBL, U90768; AAA17670.1; -.
ECOGENE; EG12304; SAPD.
PROSITE; PS00211; ABC_TRANSPORTER; FALSE_NEG.
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                                                                         EMBL; X97282; CAA65940.1; -. EMBL; AE000227; AAC74373.1; -
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Best Local Similarity
Matches 6; Conserv
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Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=KENTUCKY D;
MEDLINE; 89382761.
GUO P., GOEBEL S., DAVIS S., PERKUS M.E., LANGUET B., DESMETTRE P.,
ALLEN G., PAOLETTI E.;
"Expression in recombinant vaccinia virus of the equine herpesvirus 1 gene encoding glycoprotein gpl3 and protection of immunized
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=KENTUCKY D;
MEDLINE, 88275055.
ALLEN G.P., COGGLE L.D.;
"Characterization of an equine herpesvirus type 1 gene encoding splycoprotein (spi3) with homology to herpes simplex virus 1, virol. 62:2850-2858(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equine herpesvirus type I (strain Ab4p) (EHV-1), and Equine herpesvirus type I (strain Kentucky D) (EHV-1). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                               STRAIN=AB4P;
MEDLINE; 92295566.
MEDLOND E.A.R., WATSON M.S., MCBRIDE K., DAVISON A.J.;
"The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316(1992).
                                                                                            VGLC HSVEB STANDARD; PRT; 468 AA. P12889; P36321; 01-0CT-1989 (Rel. 12, Created) 01-0CT-1989 (Rel. 12, Last sequence update) 15-UU-1999 (Rel. 38, Last annotation update) GLYCOPROTEIN C PRECURSOR (GLYCOPROTEIN 13). GC OR GP13 OR 16.
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EMBL; M86664; AAB02451.1; --
EMBL; M19966; AAA46077.1; --
EMBL; M20234; AAA46085.1; --
EMBL; S57839; AAB25944.1; --
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198 FRLLTRLNQ 206
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           1 YRLLIRLNE 9
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VGLC_HSVEB
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Pred. No. 27;
1; Mismatches 2; Indels
                                 POTENTIAL.
F = > K (IN REF. 4).
V -> A (IN REF. 4).
                                                                                                                                                    EBF20B67 CRC32;
                  ن
                  GLYCOPROTEIN
                                                                                                                                                                                                                                                                              Search completed: February 8, 2000, 00:59:52 Job time: 3781 sec
                            POTENTIAL
Signal
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Transmembrane;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
         104 YRLEIYLNOR 113
                                                                                                                                                    468 AA;
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013592 saccharomyco 023741 brassica ol 0947369 trypanosoma 057369 trypanosoma 057369 trypanosoma 057369 trypanosoma 05736 brugia paha 032098 bacilius su 067378 aquifex aeo 09542 paramectum 085823 yersinia ps 094016 myxine glut 09164 xenopus lae 092649 streptomyce 092649 streptomyce 093434 gallus gall 01360 caenorhabdi 021147 caenorhabdi 021147 caenorhabdi 021147 caenorhabdi 021147 caenorhabdi 02141

Q9y1x6 ephydatia f

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Sequence:

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Title:

Searched:

Database

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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
PARNELL L.D., GNOI L., DE LA BASTIDE M., HAMEED A., HABERMANN K.,
SCHUTZ K., HUANG E., GOTTESMAN T., DEDHIA N.N., MCCOMBIE W.R.;
"Genomic sequence of BAC T419 from Arabidopsis thaliana, Chromosome
IV, near 16.6 cM.";
                                                                                                                                                                                                                                                                                                           ol-Mar-1999 (TrEMBLrel. 10, Last sequence update)
01-Mar-1999 (TrEMBLrel. 10, Last annotation update)
PUTATIVE LEUCINE-RICH REFEAT PROTEIN.
T419.11.
T419.11.
Rubaidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta: eudicotyledons; ocre eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF069442; AAC79105.1; -.
SEQUENCE 395 AA; 43507 MW; F547BBDS CRC32;
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P70561;
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
FGF RECEPTOR ACTIVATING PROTEIN FRAGI.
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Pred. No. 15;
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Q51316
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09WI79
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01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
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66.7%;
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Best Local Similarity
Matches 6; Conserv
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1 YRLLIRLNE 9
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065654 arabidopsis
076669 caenorhabdi
086190 erwinia chr
048758 arabidopsis
093811 streptomyce
Q19125 caenorhabdi
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P70561 rattus norv
O39258 equine herp
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O42142 gallus gall
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Q12530 saccharomyc
Q62157 mus musculu
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Q22520 caenorhabdi
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3.317 Million cell updates/sec
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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P70561
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MEDLINE; 98264497.
TELFORD E.A.R., WATSON M.S., PERRY J., CULLINANE A.A., DAVISON A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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EMBL: AF030027; AAC59530.1; -
PRINTS; PRO0668; GLYCPROTEINC.
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FRAGI.
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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NICOLSON L., ONIONS D.E.;
The nucleotide sequence of the equine herpesvirus 4 gC gene
                                                                                                                                                                                 INSSUE-BRAIN;
LORENZI M.V., HORII Y., YAMANAKA R., SAKAGUCHI K., MIKI T.;
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(0).
EMBL; U57715; AAB07050.1; -.
SEQUENCE 254 AA; 29395 MW; 8470603F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                        69.4%; Score 34; DB 11; Length 254; ilarity 87.5%; Pred. No. 25; Conservative 0; Mismatches 1; Indels
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COUNTERPART OF HSV-1 GENE UL44 AND VZV GENE 14.
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J. Gen. Virol. 79:1197-1203(1998).
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                            SEQUENCE FROM N.A.
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039258
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SEQUENCE FROM N.A.
STRAIN-S28GC (AB972);
OTHNSTON M., ANDREMS S., BRINKMAN R., COOPER J., DING H., DU Z.,
DOHNSTON M., ANDREMS S., BRINKMAN R., COOPER J., KIRSTEN J., KUCABA T.,
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
MILLER N., NHAN M., PAULET A., PELUSO D., RIFKEN L., RILES L.,
MILLON R., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
WILSON R., WATERSTON R.,
Submitted (APR-1996) to the EMBL/Genbank/DDBJ databases.
                                                                                     A493L.
Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                             (1)
SEQUENCE FROM N.A.
MEDIJIRE; 96400190.
KUTISH G.F., LI Y., LU Z., FURUTA M., ROCK D.L., VAN ETTEN J.L.;
"Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: r
positions 182 to 258.";
Virology 223:303-37(1996).
EMBL; U42580; AAC96860.1; -.
EMBL; U42580; AAC96860.1; -.
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Pred. No. 30;
2; Mismatches 1; Indels
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STRAIN-228GC (AB972);
WATENSTON N. S.
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 273317; CAA97717.1; ...
EMBL; U53879; AAB82739.1; ...
SEQUENCE 201 AA; 23618 MW; FDD081D6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIEGER M., MUELLER-AUER S., BRUECKNER M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) GENOME, PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
CHROMOSOME XII READING FRAME OFF YLR145W
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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STRAIN-S288C (AB972);
FULTON L.;
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74 YRLVVRENE 82
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TISSUE-LENS:
MEDLINE; 94116444.
FUNAHARHI J., SEKIDO R., MURAI K., KAWACHI Y., KONDOH H.;
FUNAHARHI J., SEKIDO R., MURAI K., KAWACHI Y., KONDOH H.;
FUNAHARHI J., SEKIDO R., MURAI K., KAWACHI Y., KONDOH H.;
FUNAHARHI J., SEKIDO R., MURAI K., KAWACHI Y., KONDOH H.;
Denedomain protein implicated in postgastrulation embryogenesis.";
Development 119:433-446(1993).
BEMBL; D14316; BAA03262.1;
FPAM; PF00271; helicase_C; 1.
Hypothetical protein.
SEQUENCE 560 AA; 64394 MW; A54C9E16 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHNERAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SHALDON N., SMITH A., SONNHAMMER B., STADEN R., WALERSTON J.,
WALSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCMURRAY A.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL 64.4 KD PROFEIN.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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EMBL: 277135; CABO0875.1; -.
SEQUENCE 537 AA; 61447 MW; A7597F26 CRC32;
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01-NOV-1996 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
116A9.1 PROTEIN.
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Best Local Similarity
Matches 5; Conserv
                               419 YRTLIRLRE 427
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113 KLIVKLNER 121
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    1 YRLLIRLNE
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Q08781;
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                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 33; DB 11; Length 506; 77.8%; Pred. No. 79; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAKAHASHI M.;
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
EMBL: X755443. CAPA53092.1; -.
EMBL: X755483. CAPA53092.1; -.
PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ZINC FINGER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
NEOPULLARASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paenibacillus polymyxa (Bacillus polymyxa).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Paenibacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 170:41-49(1999).
EMBL: U89716; AAD05199.1; -.
SEQUENCE 3132: 1UOK.
SEQUENCE 515 AA; 58749 MW; 68075B21 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 AA; 57882 MW; AEE397C3 CRC32;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 33; DB ilarity 77.8%; Pred. No. 81; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
60.08;
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PFAM; PF00643; zf-B_box; 1.
PFAM; PF00097; zf-C3HC4; 1.
DNA-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.3
Best Local Similarity 77.8
Matches 7; Conservative
                          Conservative
                                                                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
                                                                 1 YRLLIRLNER 10
                                                                                              |||::||| |
|15 YRLILLLNHR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-CECT 155; MEDLINE; 99118304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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|191 YRLLARLEE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
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SEQUENCE
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KAWARABAYASI T., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAWAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H., KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 98384483.

BRUNEL C.A., MADIGAN S.J., CASSILL J.A., EDEEN P.T., MCKEOWN M.;
BRUNEL C.A., MADIGAN S.J., CASSILL J.A., EDEEN P.T., MCKEOWN M.;
Ppcdr, a novel gene with sexually dimorphic expression in the pigment cells of the Drosophila eye.";
Dev. Genes Evol. 208:327-335.

EMBL; AF098864; AAC72391.1;
SEQUENCE 261 AA; 28302 MW; DC731F30 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                    Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                     "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DAN Res. 5:55-76(1998).
EMBL: aP0000003; BA2655.1; -.
SEQUENCE 151 AA: 17160 MW; 11AACD59 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AN-1999 (TrEMBLrel. 09, Last annotation update)
15.1Aa LONG HYPOTHETICAL FRXA PROTEIN.
PH0674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
U-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PIGMENT CELL DEHYDROGENASE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
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Pred. No. 66;
3; Mismatches
                                                                                                           151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                           PRELIMINARY;
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207 YRILDRLNKQ 216
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Best Local Similarity
                 :||||| ||
792 KLLIRLRER 800
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96 RLLIELDER 104
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SEQUENCE FROM N.A.
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RLLIRLNER 10
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096646
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058407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                             Score 33; DB 13; Length 560;
Pred. No. 88;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 67.3%; Score 33; DB 11; Length 859; Best Local Similarity 75.0%; Pred. No. 1.3e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97473516.
GRIFFITHS R., KORN R.M.;
A CHDI gene is Z chromosome linked in the chicken Gallus
domesticus.";
Gene 197:225-229(1997).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
PEARCE J.J.H., DAVIES T., GARDENER R.L.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X99384; ZAA67763.1;
SEQUENCE 859 AA; 96739 MW; 8D061D00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CHROMO-HELICASE-DNA-BINDING ON THE Z CHROMOSOME PROTEIN.
                                                                                                                                                                                                                                                                                             PALADIN.

Was musculus (Mouse).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97FE8926 CRC32
                                                                                                                                                                                                     859 AA
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                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                       PRT;
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HSSP; P23197; 1AP0
PROSITE; PS00598; CHROMO_1; 2.
PFAM; PF002365; Chromo; 2.
PFAM; PF00271; helicase_C; 1.
PFAM; PF00176; SNF2_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; Prout.,
Helicase: DNA-binding,
1808 AA; 208399 MW;
                              67.3%;
77.8%;
                                                                                                                                                                                                                 P70261;
01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-AUG-1998 (TrEMBLrel. 07,
PALADIN GENE.
                              Query Match 67.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
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                                                                                          -2 RLLIRLNER 10
                                                                                                              :|{||| ||
43 KLLIRLRER 51
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464 YRLLVELN 471
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P70261
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042142
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Gaps

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Gaps

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CA COLE S.T. BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V. EIGLMEIER K., GAS S., BARRY C.E., TERAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DESTAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DESTAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., ADALDIN N., HOLROYD S., HORNSBY T., ADACHER S., MURPHY L., OLLIVER S., OSBORNE J., QUALL M., RAJANDREAM M.A., ROGERS J., ROTTER S., SUBGEGR K., SKELIVER S., SUBRES R., SULSTON J.E., TAYLOR K., NATHERED S., BARRELL B.G.,
L. NATHEREAD S., BARRELL B.G.,
L. NATHEREAD S., BARRELL B.G.,
L. PENNCTION: CELL WALL FORMATION.
C. I- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
C. I- SUBLELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
C. INDICATION: CELL LOLAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).
C. INDICATION: CELL LOLAR BACTERIAL CLASS IA PENICILLIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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EMBL; Z80775; CAB02529.1; -.

PFAM, PF00912; Transglycosyl; 1.

PPPAM, PF00905; Transpeptidase; 1.

Peptidoglycan synthesis; Cell wall; Transmembrane.

ACLARTED BY PENICILLIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

BEVAN M., MONFORT A., CASACUBERTA E., PUIGDOMENECH P., HOHEISEL J., MENES H.W., MAYER K.F.X., SCHUELLER C.; Submitted (APR-1998) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudioots; Rosidae, eurosids II; Brassicales, Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 1.7e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PROBABLE PENICILLIN'BINDING PROTEINS 1A/1B (PBP1).
PONA OR RV0050 OR MTCY21.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AVG-1998 (TrEMBLrel. 07, Created)
01-AVG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 24.8 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO.
58CC83F1 CRC32;
                                                                 678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 AA
                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71150 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%;
                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 62.5
انتخب 5; Conservative
                                                                   PRELIMINARY;
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065654;
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                               RESULT 14
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DR EMBL; AL022605; CAA18753.1; -.
DR MENDEL; 29179; Arath;3410;29179.
KW Hypothetical protein.
SQ SEQUENCE 214 AA; 24813 MW; 110A2C72 CRC32;
Query Match 63.3%; Score 31; DB 10; Length 214;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps
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Search completed: February 8, 2000, 13:17:39 Job time: 32488 sec

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Lect Submission of Taxalo, X.

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Nov-1999) to the DDBJ/EMBL/GenBank databases. Takuji
Sasaki, National Institute of Agrobiological Resources, Rice Genome
Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Research Program; Rannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp,
URL:http://www.dna.affrc.go.jp,
URL:http://www.dna.affrc.go.jp,
The orientation of the sequence is from T7 to SP6 of the PAC clone.
Genes were predicted from the integrated results of the
following:GENSCANI.O, BLASTNZ.O, BLASTNZ.O, as well as
SplicePredictor (October 1998 version). The genomic sequence was
searched against the non-redundant database NRP (PIK, SWISSPROT,
GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at
RCP. Protein similarities of the cording regions were searched
against NRP with BLASTP2.O. ESTS represent the identified cDNA
sequences using BLASTN 2.O with the corresponding DDBJ accession
no. and RGP clone ID.
Detailed information on assemble quality together with annotation
of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeF1
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//note="ESTS D47452(S12946),C23573(S10086),C19173(E10057),AU031245(E10057),AU032455(S10086) COITESPOND to a region of the predicted gene.; Similar to PNIL34. (U37437)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGEPNORRLYQVWQGSNKFLCGGRLIFGPDAGSLFLSTVLIVAP
LVGLCCQCITKMNSISSEKQVLGLPVLIATIVLGLADLAFLLMTSSRDPGIVPRNARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PESCGGGDEEGVAGDVTTPSAEWVTAASPHLRLPRSKDVVVNGCVVKVKYCDTCLLYR
PPRASHCSICNNCVRKFDHHCPWVGQCIGLRNYRFFFLFISTSTLLCVYVFVVSWLNI
                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cione="P0003H10"
join(2901. .2951,3129. .3317,3521. .3850,4405. .4638,
5069. .5509)
/note="Similar to Arabidopsis thaliana DNA chromosome 4,
BAC clone F22K18 (AL035356)"
       HOMO
HOMO
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                                                                                                                                                              AP000815 142418 bp DNA PLN 04-DEC-1999
Oryza sativa genomic DNA, chromosome 1, clone:P0003H10.
AP000815.1 GI:6498418
                                                                                                                                                                                                                                                                                                                                                                      Poaceae; Oryza.

1 (bases 1 to 142418)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
  AC013557 E
AC011189 E
AC008537 E
                                                                                                                                                                                                                                                                             Oryza sativa (cultivar:Nipponbare) DNA, clone:P0003H10.
  178506
179611
187246
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Published Only in DataBase (1999) in press
2 (bases 1 to 142418)
  1.6e+04
1.6e+04
1.7e+04
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1. 142418
. Organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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                                                                                           seq_name: gb_pl1:AP000815
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gb_htg6:AC013557
gb_htg4:AC011189
gb_htg3:AC008537
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ACCESSION
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KEYWORDS
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TITLE
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418 1 AP000815 Oryca sativa genomi
122 180150 Caenorhabditis elegans
128 1 AC017780 Decosphila melanogas
130 1 AC005355 Derosophila melanogas
130 1 AC005355 Homo sapiens chromos
06 1 AL08912 Homo sapiens chromos
06 1 AL08013 Human DNA sequence
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15 1 AC004287 Drosophila melanogas
16 1 AC0101874 Drosophila melanogas
17 1 AC01011 Drosophila melanogas
18 1 AC010659 Homo sapiens chromos
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AC000375 Sequence of BAC F19K
AC007583 Arabidopsis thalian
AL096867 Human DNA sequence
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AF142728 Robinia pseudoacacia
Z32840 Caenorhabditis elegans
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109413 Sequence 1 from Patent
1 AF203588 Pterocarpus macrocarr
1 AF142691 Pterocarpus indicus r
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-VOOEL-frame+_p2n.model -DEV-x1p
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142418 | AP00081
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60918 | AC017780
66958 | AC005365
86130 | AC005365
97906 | AL109912
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185469 | AC00832
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.1e+03
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.4e+04
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Search time (sec): 11370.480000
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gb_htg4:AC010121
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gb_htg3:AC008847
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gb_ba1:BACRXMT
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gb_pl1:AP000815
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/note-similar to Arabidopsis thaliana chromosome II BAC /codon_start-1
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LSKPPVWALIVSHFCHNWGTFILLTWMPTYYNQVLKFNLTESGLFCVLPWLTMAVSAN
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SWDPTLVNPOTWFHYTCDRAGRYTRLDIGNSNLSGHLABELGHLEHLQYLELYRINIQ
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SSLKYIDVSNNDLGGTIPTSGPFEHIPLNNFRLEGFELGGELATYOTNC"
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translation="MHPKNHLVAAATVILVLQSPLPSSSFSNRRRRRRQCRPTIAIAT"
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53657. .53800,5464(26031. .344,56056. .56534))
region of the predicted gene.; Similar to L.esculentum
a region of the predicted gene.; Similar to L.esculentum
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complement(join(42025. .42083,43481. .43661))
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/note="hypothetical protein"
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Gaps: 0
Percent Identity: 88.889
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/note="hypothetical protein"
/codon_start=1
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                                                                                                   /note="hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAA87830.1"
/db_xref="GI:6498427"
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/db_xref="G1:6498429"
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/db_xref="GI:6498431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLYLVGTLVWNLFSTGEKIID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: AP000815
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US-08-653-294-11 x AP000815/rev
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                                                        PAAKPGTPKKRGKTEIQETLLIPRFYTTDFDEMERLFNAEINKQLNOEEFDALLQEFK
TDYNQTHFVRNPEFKAAADKMEGPLRQIFVEFLERSCTAEFSGFLLYKELGRRLKKTN
PVVAEIFSLMSRDEARHAGFLNKGLSDFNLALDLGFLTKARKYTFFKPKFIFYATYLS
                                                                                                                                                               EKIGYWRYITIFRHLKANPEYQYYPIFKYFENWCQDENRHGDFFSALLKAQPQFLNDW
KAKLWSRFFCLSYYYTWYLNDCQRTTFYEGIGLDTKEFDMHVIIETNRTTARIFPAVL
DVENPEFKRKLDRMYEINKKIIAIGESDDIPLVKNLKRIPHVAALVSEIIAAYLMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMDEVSGSASQNFSLLQĒFYQTTLKALEEAKNERLWFKTNLKLCKIWFDMGEYGRMSK
ILKELHKSCQREDGSDDQKKGTQLLEYYAIEIQMTTETKNNKKLKELYTKALSIKSAI
PHPRIMGIIRECGGKMHMAERQWADAATDFFEAFKNYDEAGNPRRIQCLKYLVLANML
MESEVNFFDGQEAKPYKNDFEILMANTLIAAYQKNDIMEFEKILKSNRRTIMDDFIR
NYIEDLIKNIRTQVLKLIKPYTRIRIPFISQKWCMKIISNMELWYILVLFHGTLVYT
RAILGSCKKYSLKLDLFLSCAQTRVQLKSCALNRADFMLFTEVNLLSYSVQDALSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSMFCMELNPPEKDVEQLLVSLILDNRIOGHIDQVNKLLERGDREIPSHRQVEYSAE
EHLPNGVQQSWVREIAGCLGCTALGTCLHVLLWMMLGFCPELNLSANSNPSETILASM
ARNFWFCWHCRTSKFWYGRENVWFRVKYAPGTRHTANIVPLPSSDSVANQSLSNONEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MADQLTDDQIAEFKEAFSLFDKDGDGCITTKELGTVMRSLGQNP
TEAELQDMINEVDADGNGTIDFPEFLNLMARKMKDTDSEEELKEAFRVFDKDQNGFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAELRHVWINLGEKLIDEEVEEMIREADVDGDGQINYDEFVKVWAAK"
complement(join(24778, 24897,25615, 25722,25808, 25893,
26090, 26177,26435, 26638,27519, 277581,27708,
28329, 28389,28512, 28552,29058, 29225,30476, 31136))
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TDERRAPGHSHKPSIILMWIQTTKPARRGANVLARHCGDDRRRRCKSQCAVARRQE
ALPIQSLFPYLYFMIRDLKVAKEEQDIGFYAGFVASCIVQAYASEVCRKEHQALGISL
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GHTKSLLKNWQLMSAITLYCVFSLHPTAYLEIFSLMAVSSRXYRGLSTTSQDVGIVLA
GHTKSLLKNWQLMSAITLXCVFSLHPTAYLEIFSLMAVSSRXYRGLSFTSQDVGIVLA
ASLLKNWFANKKEMTNQSISLLDAGFHGRKSTLLGGSYQVRQQGSSKP"
complement(join(34468. .34544,37202. .37385))
/note="hypothetical protein"
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join (4034) 40358, 40468) ,
/note-"hypothetical protein"
                            /translation-"MASSAMELSLLNPAAMRGLSAAKPRVVSSRRIVRFRVASSAAAP
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TRGHALAEPEPHASPRLVGHRGSRRRSPSPPSPPPLPVTARCEEEHRRRHRCSSLPPR
RQMRRGAPPPDPASPCPDLATLGVGRRWKKWDAAEEGVGVAEEEEERWARGRARQLRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MEDYGFEYSDDEPEEQDYDIENQYYNSKGMVETDPEGALAGFDQ
VVRMEPEKAEWGFKALKQTVKLYYKLGKYKEMMDAYREMLTYIKSAVTRNYSEKCINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KESPFLSYTTDQQALNLQREHTTLSDNVINLSEGSYRPLAPSSHLGHPVYTIFYVDDN
                                                                                                                                                                                                                                                                                                  join(13373. 13457,15836. 15914,17237. 17477,17560. 177766. 17726. 17860,18400. 18587,18681. 18749,18826. 18916, 19028. 19162,19323. 19379,19349. 19441,19450. 19509, 19523. 19585,19589. 19701,19800. 19941,20057. 20294, 21399. 21586)
//note="ESTS AU081256(C53656),AU081257(C53656), AU0812236(R7784),AU081351(E61905),AU031587(E61905),AU031587(E61905),AU081361(R3784),Correspond to a region of the predicted gene; Similar to alien-like protein. (AC005623)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(22475. .22550,23332. .23705)
/note="ESTS AU031013(E50493),AU081341(E50493) correspond
to a region of the predicted gene.; Similar to O.sativa
gene encoding calmodulin. (Z12828)
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/db_xref="G1:6498422"
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                                                                                                                                                                                                                                                                             ESGSVDFAEFEPQLVY"
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/ Gene="Teacher.)

/ Gene="Teacher.]

/ Astone binding protein (SW:P06180); CDNA EST EMBL:214755

comes from this gene; CDNA EST EMBL:214820 comes from this

gene; CDNA EST EMBL:10134 comes from this gene; CDNA EST

EMBL:T02164 comes from this gene; CDNA EST EMBL:M79494

comes from this gene; CDNA EST CEMSA18R comes from this

gene; CDNA EST EMBL:D3193 comes from this gene; CDNA EST

EMBL:D35959 comes from this gene; CDNA EST EMBL:D71778

comes from this gene; CDNA EST EMBL:D72307 comes from this

gene; CDNA EST EMBL:D72719 comes from this gene; CDNA EST

EMBL:D74467 comes from this gene; CDNA EST EMBL:D55270

comes from this gene; CDNA EST EMBL:D65270

comes from this gene; CDNA EST EMBL:D65270

comes from this gene; CDNA EST EMBL:D65258

gene; CDNA EST EMBL:D67440 comes from this gene; CDNA EST

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comes from this gene; CDNA EST EMBL:D69258

gene; CDNA EST EMBL:C12197 comes from this gene; CDNA EST EMBL:D65420

comes from this gene; CDNA EST EMBL:D692070 comes from this

gene; CDNA EST EMBL:C12197 comes from this gene; CDNA EST EMBL:D69218

comes from this gene; CDNA EST EMBL:D69210

comes from this gene.
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STATURKTASENSPTEAADSTNIIAHDKETIAKNVDSTGEEKVAMTNVAEETTPSTD
STATURKTASENSPTEAAADSTVAVAEDSTGSGETNSSSETSPAVEDERSKASMEYSIGT
SIEDSETSOREIEGELVVPENRVVEETSPEOKRKSIENIIAGRRFKATDVPURAVDVL
SVAASIAAEVFGDAHEDTFEANFLYGKALLEVGKLEDRVLANALTDVPKMAEGEEEVV
DGIVENPEDVPODEERAEIKOKVEEALGVASEEPETVADEAVKTEOKRAEBEEEVV
NSDEQNOEEEEVVBEATVOPTEDVEMEGVEEVNDEKEVGGTAEVDGEAEED
EADSMALAWELLETSROIADKRAASLAAESTVDGEAIKWMKINLADVLTSLGEHGIAD
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ERNWRKEIGGYKMKRQRLFAIIGRQKAMLLQVMDRTKWPQGSVDRQKVADKVNLAYHQ
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ASEXMVMLISSPPFRSLSQFFLFGLHLLGKYQSEGGCVVVREEAXIABIRQNDEBKRQ
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KKELEGAAAMLAKVADVTEATDISSMVRRPTKRPASEEAPEETKKRKSGDGVDVAVVT
EEQVVESTEEPTPINE"
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FRYVBASATKKRKKTPRSSPKKMRKSESPLAUKAPREDEDLSYAJILKP
RRKVVKTADEVGLCAPIFVMQSELKKFREEVQRRYAEGSSASQQERVRNMYYBAYDN
IYHINRLSANEGPRILISDQKLVMQQYKTTFRQGPTFAEETESDVEEEEEKKVVEVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6483,6532. .7116,7207. .7428,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(2944. .3651,3698. .4050,4106. .4395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(9672. .10594)
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complement(join(9672. .10406,10454. .10594))
         /gene="C50B6.1"
/note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                            ITHQYRVHPENQMYMQNSKRQTREKITVSY"
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/pln(6195. .6268,6321. .64
7495. .7971,8025. .8084)
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/gene="C5086.2"
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bin/display?db-wormaceGclass-Sequence &object=C50B6
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
IMPORTANT: This sequence is not the entire insert of clone C50B6.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa: Nematoda; Secernentea; Rhabditia; Rhabditida; Eukaryota: Metazoa: Nematoda; Secernentea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis. I Chases I to 4132,R. 'Anderson,K.' Baynes,C.' Berks,M.' Bonfield,J.' Burton,J.' Connell,M.' Copsey,T.' Cooper,J.' Cooper,J.' Cooper,J.' Cooper,J.' Gradner,A.' Gradner,P.' Hawkins,T.' Hiller,L.' Jier,M.' Johnston,L.' Gardner,P.' Hawkins,T.' Hiller,L.' Jier,M.' Latreille,P.' Lightning,J.' Lloyd,C.' McMurray,A.' Mortimore,B.' O'Callaghan,M.' Parsons,J.' Percy,C.' Rifken,L.' Roopra,A.' Staden,R.' Shownkeen,R.' Smaldon,N.' Smith,A.' Sonnhammer,E.' Staden,R.' Sutson,J.' Thiery-Mieg,J.' Thomas,K.' Waudin,M.' Waterston,R.' Waltson,A.' Wellston,D.' Therry-Medistock,L.' Waltson,Sproat,J. and Wohldman,P.' Wallstoner, Sproat,J. and Wohldman,P.' Wallstoner,D.' Wallston,A.' Wallston,B.' Mallston,A.' Wallston,A.' Wallston,A.' Wallston,A.' Wallston,B.' Wallston,A.' Wallston,A.' Wallston,A.' Wallston,A.' Wallston,B.' Wallston,A.' Wall
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The true left end of clone C50B6 is at 1 in this sequence. The true right end of clone C50B6 is at 2293 in sequence 281524.
The true left end of clone F32H5 is at 41219 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this sequence (41219. .41322) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
gesteanger.ac.uk or rwenematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ပ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                       seq_documentation_block:
LOCUS CEC50B6 41322 bp DNA INV 02-SE
DEFINITION Caenorhabditis elegans cosmid C50B6, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         880. .1777
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join(880. .1077,1532. .1639,1685. .1777)
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/db_xref="taxon:6239"
/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368 (6466), 32-38 (1994)
94150718
Location/Qualifiers
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Z81050.1 GI:1627685
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Direct Submission
                                                                                                                                      seq_name: gb_in1:CEC50B6
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TITLE
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TITLE

COMMENT

FEATURES

CDS

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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
15775 a 13372 c 13641 g 18030 t
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Gaps: 0
Percent Identity: 88,889
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t2
38600 TATAGGATACTGCTCCGATTGAATGAA 38626
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1. .60818
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Drosophila melanogaster,
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HTG; HTGS_PHASE1.
fruit fly.
                                                                                                                                                                                                                  AC017780.1 GI:6553410
HTG; HTGS_PHASE2.
fruit fly.
                                                                                                                       60818 bp
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Percent Similarity: 100.000
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                                             seq_name: gb_htg7:AC017780
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                                                                                                seq_documentation_block:
LOCUS AC017780 (
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LOCUS AC009355 (
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Quality:
Ratio:
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TITLE
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                   join(11061. 11221,11307. .11452,11897. .12333,12385. .12463,
1211. .12677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jóin(13581. 13654,13709. 13834,13884. 14029,14205. 14272,
14327. 14642,14708. 14952)
/gene="C50B6.6"
                                                                                                                                                                                                                  /db_xref-"SPTREMBL:011686"

/translation="MSAKTLVYGASYLSGFAILGCVFTVGYIFNDINEFYEOTMETMD

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GQPGSDGGPGEAGAPGAPGAPGAPGOPGQDGGAAGAPGODGORSTGFPGAAGAPGPAGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KHFLVWHTASNLISEIYNAMFLAPKVHLPYPLIRFTAIMTQLGFSGLFQFYTINALIH
QTGYSIIEMYMFRFKASTYNFQSTCFYVYLQINLYIYRITLVLFFVVNITTYNISLGQ
QIISKQNLLIQHPEAPWLVNCDSVVVAAPFTDPISMFNVVWIVIIFVASTSTFSTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLOKHLSKSEHHSPAVLRMHRMLLITLFVORALHAVNLGIPNSMFITAVFFERRHEFL
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13581. .14952
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ALINNCPKTLKEYRXYLWHTLGNLLFELYISLFMLPYTLPYPVFRGAGFLKYLDIS
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PVFTPLMTLIPMAMLLAATIIPOTELTIWKTLDQLSKHLSKKTIQLQKMLLYSLFIQA
VIHGVMLGAPLIGFIYAVVFVLDYNYIAYMLLLISFHGSFSTIAMIAFTKPIREGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB02856.1"
| Dackein_id="G1:3875058"
| Ab_xref="SPTRBML: P9198"
| Ab_xref="SPTRBML: P9198"
| Atranslation="MLKHLFLFIRSSIAYNFYWYDKTQTLQNRQTMVHLFEWKWAD
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/translation="MDCSLISTAEYLDVLHFLFIVSFPIYTVAIIALFRTKSTYFETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9. .15902,
.17122,
                    /note="predicted using Genefinder; similar to collagen;
CDNA BST EMBL:065564 comes from this gene; cDNA EST
EMBL:D69046 comes from this gene; CDNA EST yk366bl2.3
comes from this gene; cDNA EST yk366bl2.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similarity to Shrimp amylase (TR:Q26193); cDNA EST
EMBL:214343 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(15021. .15502,15568. .15753,15799.
15954. .16171,16221. .16634,16680. .16871,16918. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLFQSLFPFLILSEPRTEKIMVVTSTTSASTKQRDSIFMSNKNSFLSV" complement(15021. .17567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to RNA binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 9
Gaps: 0
Percent Identity: 77.778
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/gene="C50B6.5"
                                                                                                                                                codon_start=1
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Ratio: 4.444
Percent Similarity: 100.000
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CDS

CDS

to: 41322

from: 1

Align seg 1/1 to: CEC50B6 alignment\_block: US-08-653-294-11 x CEC50B6

1 TyrArgLeuLeuIleArgLeuAsnGlu 9

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DNA HTG 09-DEC-1999
*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 66958)

1 Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., Rocroe, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S. R., Karra, R., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 60818)
Adams, M. and Venter, J.C.
Direct Submitssion
Submitted (19-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was identified as CDM:10212069 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This is a "working draft' sequence. * This sequence will be replaced. * by the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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COMMENT

us-08-653-294-11.rge

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unknown length
g of 1542 bp in length
f unknown length
g of 1591 bp in length
if unknown length
g of 1386 bp in length
g of 1784 bp in length
g inknown length
g inknown length
                                                                                                                                                                                                                                            d unknown length of 2107 bp in length of 1968 bp in length of unknown length of 555 bp in length of unknown length of 550 bp in length of unknown length
                                                            g of 1414 bp in length
f unknown length
g of 1322 bp in length
g of 1756 bp in length
g of 1756 bp in length
f unknown length
unknown length
of 914 bp in length
unknown length
of 962 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g of 750 bp in length
f unknown length
g of 646 bp in length
f unknown length
g of 580 bp in length
i unknown length
g of 606 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f unknown length
9 of 622 bp in length
f unknown length
9 of 571 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                     of 591 bp in length
unknown length
of 555 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
of 597 bp in length
unknown length
                                                                                                                                                                                                                                   of 961 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                             of 328 bp in length
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of 581 bp in length
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unknown length
of 624 bp in length
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unknown length
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54453
54533
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                                                                                                                                                       Direct Submission

Submitted (17-Aug-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, UGA

On Sep 20, 1999 this sequence version replaced gi:5748857.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft' sequence record is a robitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
                     Unpublished

(Calniker,S.E., Accaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Hummasti,S.R., Karra,K., Kearney,L.,
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Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Misra, M. and Deaven, L.

Direct Submission
Submission
Submitted (01-407-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
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28059. .28174

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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Drimates; Catarrhini; Hominidae; Homo.

Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Misra, M. and Deaven, L.
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LOCUS AC005365 86130 bp DNA
DEFINITION Homo sapiens chromosome 16, Pl clone 79-2A (LANL), complete
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US-08-653-294-11 x AC009355/rev
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Percent Similarity: 100.000
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Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Cambridgeshire, CB10 1SA, UK. E-mail enquires:

CB 12, 1999 this sequence requests: clonerequest (Sanger.ac.uk on Sep 12, 1999 this sequence version replaced gi:5777438.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may be sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tation_block:

HIG 23-NOV-1999
HOMO SAPIESO 97906 bp DNA
HOMO SAPIESO 97906 bp Clone RP5-1141E20, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.

AL109912
AL109912.4 GI:5870369
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sims, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                         from: 1 to: 86130
66995 . 67262
/rpt_family="Alu"
67741. .68036
/rpt_family="Alu"
complement (69213. .69456)
/rpt_family="Alu"
70077. .70906
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/rpt_family="Alu"
74915, .75035
/rpt_family="L1"
75843, .76122
                                                                                                            0077. ./USUS
rpt_family="LTR1"
                                                                                                                                     2. .72045
family="L1"
8. .72876
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76105, 7611
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76635. .76655
/note="(A)21"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /note="(A)41"
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294-11 x AC005365
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us-08-653-294-11.rge

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31856:
31936:
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31108
31188
                       COMMENT
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopteryqota; Diptera; Brachycera;
Muscomorpha: Endopteryqota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
E 1 (bases 1 to 122061)
S Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomctan, M.A., Mazda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.
Sylicss, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC008324 122061 bp DNA HTG 06-AUG-1999
Drosophila melanogaster chromosome 2 clone BACR25K01 (D854) RPCI-98
25.K. l map 25C-25D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
***, 81 unordered places:
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Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celuiker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Chempe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Chue, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Petiffer, B., Poon, L., Sequeira, A., Sethi, H., Sair, E., Sairskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
segments. Unfinished: dJ1141E20 Contig_ID: 00340 acc=AL109912 Length: 64235 bp Unfinished: dJ1141E20 Contig_ID: 00618 acc=AL109912 Length: 13202 bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                          1602 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 97906
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chomosome="6"
/clone="RP5-1141E20"
/clone=lib="RPCI-5"
a 18298 c 18016 g 29795 t
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                                                                                                                                                                Location/Qualifiers
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HTG; HTGS_PHASE1.
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LOCUS AC008324 1:
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                                                                                                                                                                                                                                                                                        30195 a
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Ratio:
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DEFINITION
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VERSION
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JOURNAL
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AUTHORS
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AUTHORS
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently * consists of 81 contigs. The true order of the pieces is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of unknown length contig of 1140 bp in length gap of unknown length contig of 651 bp in length gap of unknown length length gap of unknown length contig of 943 bp in length gap of unknown length gap of unknown length contig of 732 bp in length gap of unknown length contig of 682 bp in length gap of unknown length contig of 733 bp in length gap of unknown length gap of unknown length contig of 808 bp in length gap of unknown length gap of unknown length contig of 815 bp in length gap of unknown length contig of 815 bp in length gap of unknown length l
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of 1268 bp in length
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unknown length
of 917 bp in length
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unknown length
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of 1375 bp in length
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1223 bp in length

unknown

unknown length

gap of

1349 bp in length

length

of 669 bp in length

unknown length

contig gap of contig gap of

unknown length

of 507 bp in length unknown length

contig gap of contig gap of

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unknown length
of 1491 bp in length
unknown length
of 1262 bp in length
                                                                                                                                                           unknown length
of 849 bp in length
unknown length
of 1924 bp in length
unknown length
of 1734 bp in length
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of 2565 bp in length
unknown length
of 3388 bp in length
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of 3516 bp in length
unknown length
of 4927 bp in length
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of 1695 bp in length
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of 1360 bp in length
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of 1514 bp in length
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of 1343 bp in length
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2883 bp in length
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of 4613 bp in length
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unknown length
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requests: clonerequest@sanger.ac.uk
on Sep 6, 1999 this sequence version replaced gi:5791529.
During sequence assembly date is compared from overlapping clones.
During sequence assembly date is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

EMBL; Sww. SWISSROT; Tr.; TREMBL; Wp:, WORNPEP; information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is the entire insert of clone 112D6. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger centre chromosome 6 when the contract of bacterial clone and the bacterial clone and the bacterial clone contigs of the backer and the contract of bacterial clone contigs of the backer and the contract of the backer and the contract of the backer centre chromosome 6 when the contract of bacterial clone contigs of the backer and the contract of the backer centre chromosome 6 when the contract of the contract of backer centre chromosome 6 when the contract of the c
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Direct Submission
Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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LOCUS HSJ1112D6-135305 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from clone 1112D6 on chromosome 6q21-22.2,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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tunknown length
g of 708 bp in length
f unknown length
f unknown length
g of 758 bp in length
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SOURCE
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AUTHORS
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Mapping Group. Further informatiohttp://www.sanger.ac.uk/HGP/Chr6

ORIGIN

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bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
        the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently consists of 188 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 880 bp in length
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N Drosophila melanogaster chromosome 2 clone BACR14K04 (D859) RPOI-98
14.K.4 map 27C-27C strain y; cn bw sp, *** SEQUENCING IN PROGRESS
***, 188 unordered pleces.
AC008327
AC08327.2 GI:5748862
HTG: HTGS_PHASE1.
fruit fly.
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1112D6 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2. Location/Qualifiers
1. .135305
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1 (bases 1 to 189469)

1 celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G., Chew, M., Cisaloika, E., Botanpe, M., Chavez, C., Chew, M., Cisaloika, E., Boyle, C. M., Farfan, D. E., Ghavez, C., Chew, M., Chane, M., Chane, M., Chavez, C., Chew, M., Chane, M., Chane, M., Chane, M., Chavez, C., Chew, M., Chane, L. L., Chane, M., Chane, L. L., and Chane, M., Chane, M., Chane, M., Chane, L. L., and Chane, M., Chane, M., Chane, M., Chane, L. L., and Chane, M., Chane, M., Chane, M., Chane, L. L., and Chane, M., Chane, M., Chane, M., Chane, L. L., and Chane, M., 
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                                                                                                                                          /organism="Homo saplens"
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/clone_lib="RPCI-5"
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a 26002 c 26091 g 4
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Drosophila melanogaster
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US-08-653-294-11 x HSJ1112D6/rev
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LOCUS AC008327 1
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Ratio:
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KEYWORDS
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SOURCE

COMMENT

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contig of 1203 bp in length app of unknown l
gap of unknown length contig of 1395 bp in length gap of unknown length contig of 438 bp in length gap of unknown length contig of 1187 bp in length gap of unknown length contig of 732 bp in length gap of unknown length gap of unknown length
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DNA HTG 09-DEC-1999
, *** SEQUENCING IN PROGRESS ***, in ordered
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N PACO17912.
AC017912.
AC017912.1 GI:6553278
HTG; HTGS_PHASE2.
Fruit fly.
Ends.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
E 1 (bases 1 to 49261)
S. Adams, M. and Venter, J. C.
Direct Submission
L. Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was identified as CDM:10212607 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
1. 49261
gap of unknown length gap of unknown length s. contig of 2491 bp in length gap of unknown length contig of 2122 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 3984 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 4754 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 597 bp in length contig of 597 bp in length
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                                                                                                                                                                                                                                                                                   Percent Identity: 88.889
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9975 c 9922 g 14492 t
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Drosophila melanogaster,
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88181:
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99919:
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US-08-653-294-11 x AC017912/rev
                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-11 x AC008327/rev
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Percent Similarity: 100.000
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LOCUS AC017912 4
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AUTHORS
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8116 TATAAACTCTTGATCAGGATCAATAGCCGA 8087

seq\_name: gb\_pr2:AC002465 .documentation\_block: AC002465.1 GI:2337862

human.

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

DEFINITION

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complement(join(<17894. .18158,35353. .35630,40849. .41075,
43189. .43271))
/gene="WNT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDYGIKFARAFVDAKERKGKDARALMILHNNRAGRKAVKRFLKQECKCHGVSGSCTLR
TCWLAMADFRKTGDYLWRKYNGAIQVVMNQDGTGFTVANERFKKPTKNDLVYFENSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(17893. .18003)
//otce="match to human EST T99653 (NID:g749390) ye67a02.rl*
complement(17893. .18004)
/note="match to human EST W78848 (NID:g1389395)
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RSSRESAFVYAISSAGVVFAITRACSOGEVKSCSCDPKKMGSAKDSKGIFDWGGCSDN
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'protein_id-"AAB67043.1"
'db_xref-"G1:2337863"
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complement(17529. 17751)
/rpt_family="ALU"
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(24726.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (20-AUG-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE INFORMATION:
This clone is from a release of the human BAC library. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, linc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RG343P13;
this clone
                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15581)
Connell,M and Cordes,M.
                                                                                                                       20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone contains STS's SWSS847 (NID:91916380), SWSS846 (NID:91916379).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The actual start of this clone is at base position 1 of actual end is at 155881 of RG343P13. The orientation of is unknown.
                                                                                               AC002465 155881 bp DNA PRI 20-F
Human BAC clone RG343P13 from 7q31, complete sequence.
AC002465
                                                                                                                                                                                                                                                                                                                                                                              The sequence of H. sapiens BAC clone RG343P13
Unpublished (1997)
2 (bases 1 to 155881)
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confirmed by restriction digest.

MAPPING INFORMATION:

mailto:sapiens@watson.wustl.edu

Genome Sequencing Center Department of Genetics Washington University St. Louis MO 63108, USA http://genome.wustl.edu/gsc

1. .155881
/organism="Homo sapiens"
/db\_xref="taxon:9606"
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Location/Qualifiers

source

FEATURES

NEIGHBORING SEQUENCE INFORMATION:

Selection: chloramphenicol

pBeloBAC11

Inc. (ht VECTOR:

NNA HTG 16-NOV-1999 \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered

DNA

seq\_documentation\_block: LOCUS AC015280 159468 bp D DEFINITION prosophila melanogaster,

seq\_name: gb\_htg5:AC015280

AC015280 AC015280.1 GI:6436055 HTG; HTGS\_PHASE2. fruit fly.

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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Percent Identity: 70.000
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/rpt_family-"ALU"
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55051. 55074
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5554. 55791
55902. 55935
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7144. .57227
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3980. .64398
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2528. .52987
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                                         misc_feature
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Length: 10 Gaps: 0 Percent Identity: 70.000

Ouality: 39.00 Ratio: 3.900 Percent Similarity: 100.000

alignment\_scores:

source

FEATURES

BASE COUNT

ORIGIN

alignment\_block: US-08-653-294-11 x AC015280

to: 159468

to: AC015280 from: 1

Align seg 1/1

Irult Ligy.

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Erachycera;
Muscomorpha; Ephydroidea; Drosophila.

Drosophila.

RS Adams, M. and Venter, J.C.

Direct Submission

AL Submission

Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

Brockville, MD, USA

This sequence was identified as CDM:10213506 by the submitter.

For further information on this sequence e-mail to fly@celera.com.

\* NOTE: This is a 'working draft' sequence.

\* This sequence will be replaced

\* by the flished sequence as soon as it is available and

\* the accession number will be preserved.

Location/Qualifiers

// Ab xref="taxon/727"

// Ab xref="taxon/727"

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fruit fly.

Drospphila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophildae; Drosophila.

I (bases 1 to 171979)

Strain, D.E., Galler, A. Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harriss, N.L., Hoskins, R.A., Hummasti, S.R., Karra, K., Kaarney, L., Kim, E., Lee, B., Lewis, S.L., P., Lomotan, M. A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Shir, E., svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
                                                                      seq_documentation_block:
LOCUS ACO7054 171979 bp DNA HTG 13-OCT-1999
LOCUS ACO7054 171979 bp DNA HTG 13-OCT-1999
DEFINITION Drosophila melanogaster chromosome 2 clone BACR45018 (D527) RPCI-98
45.0.18 map 41E-41E strain y; cn bw sp, *** SEQUENCING IN PROGRESS
ACCESSION ACO7054
VERSION ACO7054
COTOS4.22 GI:6041715
KEYWORDS HTG; HTGS-PHASE1.
SOURCE fruit fly.
seq_name: gb_htg4:AC007054
                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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from: 1

Align seg 1/1 to: AC002465

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be preserved
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                                                                                                                                                                                                                                                                                                                              DEFINITION
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                            Laboratory, MS 64-121, Berkeley, CA 94720, USA
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Oct 15, 1999 this sequence version replaced 91:5922045.
For further information about this sequence, including its location and relationship to other sequence, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.perkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.
* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                         Centifer, S.E., Adbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciestolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., Karray, K., Kerrney, L., Kim, E., Lee, B., Lewis, S., 11, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Sylrskas, R., Wan, K.H., Welnburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
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Drosophila melanogaster BAC library, partial EcoRI in
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731: gap of unknown length
1409: contig of 678 bp in length
1489: gap of unknown length
1920: gap of unknown length
1920: gap of unknown length
2426: contig of 550 bp in length
2506: gap of unknown length
71748: contig of 69242 bp in length
71828: gap of unknown length
67244: contig of 69346 bp in length
67344: gap of unknown length
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gap of unknown length
contig of 790 bp in length
gap of unknown length
contig of 652 bp in length
gap of unknown length
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Percent Identity: 70.000
Sequencing of Drosophila melanogaster
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Percent Similarity: 100.000
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AUTHORS
TITLE
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Pterygote; Mectaca; Endopterygote; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases I to 17595)
S (clinker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,R.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Spirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                        AC006467 175695 bp DNA HTG 27-OCT-1999 Drocophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.1.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. It currently * NOTE: This is a "working draft' sequence. It currently * consists of 9 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uppublished

2 (bases 1 to 17595)

2 (bases 1 to 17595)

2 (bases 1 to 17595)

3 (bases 1 to 17595)

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Karney, E., La, F., Humesti, S.R., Karraw, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Petifer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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f unknown length
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g of 698 bp in length
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g of 1443 bp in length
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2 (bases 1 to 216649)

So DoE Joint Genome Institute.

Direct Submission

L Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jgi.doe.gov.

* NOTE: This 1s a "working draft' sequence. It currently

* consists of 63 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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clone CIT978SKB_54G2, *** SEQUENCING IN
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//organism-"Drosophila melanogaster"
/strain-"y: cn bw sp"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/chcmosome="2"
//map="40A_40C"
/clone="BACR03L08 (b532) RPCI-98 03.L.8"
/clone="BACR03L08 (Roswell Park Cancer Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216649)

DOE Joint Genome Institute.

Gequencing of Human Chromosome 5
3: gap of unknown length
5: contig of 16550 bp in length
6: gap of unknown length
7: contig of 731 bp in length
7: gap of unknown length
7: contig of 458 bp in length
7: gap of unknown length
7: gap of unknown length
7: gap of unknown length
7: contig of 813 bp in length
                                                                                                                                                                                                                                                   641 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637: contig of 637 bp in length
gap of unknown length
1631: contig of 994 bp in length
gap of unknown length
1553: contig of 922 bp in length
                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                              to: 175695
                                                                                                                                                                                                                                                   35773 c 35603 g 51919 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AC008682 216649 bp DNA
DEFINITION Homo sapiens chromosome 5 clone CI
PROGRESS ***, 63 unordered pieces.
ACCESSION AC008682
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuLeuIleArgLeuAsnGluArg 10
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
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HTG; HTGS_PHASE1.
                                                     174344:
                                                                              174882:
                            73533:
                                           174264:
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                                                                                                                                                                                                                                                                                                                   Quality: 39.00
Ratio: 3.900
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-11 x AC006467
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174265
174863
174883
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                                                                                                                         source
                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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JOURNAL
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AUTHORS
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/organism="Homo sapiens"
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50932:
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ORIGIN
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SOURCE
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alignment\_scores:

Length: 10 Gaps: 0 Percent Identity: 70.000 Quality: 39.00
Ratio: 3.900
Percent Similarity: 100.000 Align seg 1/1 to reverse of: AC008682 from: 1 to: 216649

1 TyrArgLeuLleArgLeuAsnGluArg 10

alignment\_block: US-08-653-294-11 x AC008682/rev

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Temp. sensitive autolysing
Human GAP-SH3 domain bindin
DNA encoding glycine rich p
      Mouse G3BP cDNA. New
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21-MAY-1992; 877976.

R 24-MAY-1992; 877976.

R 28-JAN-1992; 877876.

R 28-JAN-1992; 877876.

R 28-JAN-1992; US-878816.

R 28-JAN-1994; US-188581.

R 28-JAN-1997; US-188581.

R 28-JAN-1994; US
                                                                                                                                                                                                                                                                                                                                  19-NOV-1996 (first entry)
Bacillus thuringlensis ssp. israelensis CryIVD protein DNA.
CryIVD; toxic protein; crystal toxin; expression construct;
transformed cyanobacteria; phycocyanin beta; cpcB; promoter;
insecticide; dipteran larvae; mosquito; blackfly; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N90712 standard; DNA; 2100 BP.
N90712;
O9-JAN-1990 (first entry)
CYD protein; Bacillus thuringiensis; biopesticide.
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Gaps: 0
Percent Identity: 77.778
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T29774;
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Percent Similarity: 100.000
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US-08-653-294-11 x T29774/rev
                                                                                                                                                                         seq_name: N_Geneseq_36:T29774
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N_Geneseq_36:V73474
N_Geneseq_36:Q77686
N_Geneseq_36:T31725
N_Geneseq_36:N91438
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Documentation...

Cryb gene. Bacillus thuringies in cryb gene. Bacillus thuringies in the poly all 72kpa cry insecticida in the poly all 72kpa cry insecticida in the poly who creted protein gene 15 in the poly who could sequence from the poly poly view sector DNA fragm in thuman gene signature HUMGS01151 is staphylococcus aureus contig SE aureus gidB coding sequence. S. aureus gidB coding sequence. No. S. aureus gidB coding sequence. In the coding a gidAl protein. Staphylococcus aureus contig sequence from the coding a gidAl protein. Helicobacter pylori 76 kDa pol Staphylococcus aureus contig setaphylococcus aureus contig setap
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Human brain Expressed Sequence
Human gene signature HUMGS01887
Thaumatin like gene PR-5mz. New
Bacillus thuringiensis transcri
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A.altocetigenes membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a Staphylococcus
Staphylococcus aureus contig
                                                                                                                                                                                                                                                             -MODEL-frame-p2n.model -DEV-x1p
-0-/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
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-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORMeext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                       About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
                                                                     Date: Feb 8, 2000 1:27 PM
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Query: US-08-653-294-11
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N_Geneseq_36:V20767
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N_Geneseq_36:X20531
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N_Geneseq_36:Q14809
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N_Geneseq_36:Q99805
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N_Geneseq_36:V75169
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N_Geneseq_36:X02018
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seq_documentation_block:
ID Q14810 standard; DNA; 2901 BP.
                                                                seq_name: N_Geneseq_36:Q14810
                                                                                                                              Bacillus furingiensis var israelansis cry D toxin gene and proteins used for producing insecticide compsns.active against Dipteran species. Claim 1; fig 12:58pp; English. cryb gene is inserted into plasmid and used to transform a microorganism. The 67kD protein encoded by the gene has insecticidal activity against dipteran larvae. Sequence 2100 Bp; 746 A; 316 C; 378 G; 660 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This fusion gene comprises sequences isolated from the PG14 strain of B.thuringiensis subsp. morrisoni. The cytA gene encodes a cytOlytic protein which has high affinity for the lipid portion of cell membranes. After ingestion by insects, the 27 kba Cyt A protein is cleaved by midgut proteases to a relatively resistant core of 25 kba. The Cyt A coding sequence is combined with the Cry toxin, also from B.thuringiensis.
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Extending host range or toxicity of insecticidal proteins - using protein capable of binding to gut epithelium of insects Claim 34; Fig 21: 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-1992 (first entry)

Btm PG14 72kDa Cry insecticidal protein/25kDa Cyt A fusion gene.

chimeric; fusion protein; insecticide, Lepidoptera larvae;

midgut targetting; bacterial endotoxin; ss.

Bacillus thuringiensis subspecies morrisoni.
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Ratio: 4.111 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 77.778
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Bacillus thuringiensis var.israelesis.
WO8907605-A.
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02-MAY-1991.
03-MAY-1990; UG-518575.
(REGC ) UNIV OF CALIFORNIA.
Sivasubramanian N, Federici A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q14809 standard; DNA; 2802 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-11 x Q14809/rev
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US-08-653-294-11 x N90712/rev
                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 4.111
Percent Similarity: 100.000
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                                                                  17-FEB-1989; U00663.
19-FEB-1988; US-158176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block
                                                                                                             (ECOG) Ecogen Inc.
                                                                                                                                                      WPI; 89-263682/36.
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Ratio:
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                                                 24-AUG-1989.
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                                                                                                                                     Donovan WP
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Human secreted protein; gene 150 clone HMSKQ35.

Human secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; itssue; cancer; tumour; neurodegenerative disorder; leukemia;

developmental abnormality; focatal deficiency; blood; allergy; renal; diffiamune system; asthma. lymphocytic disease; brain; hepatic; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schlarophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This fusion gene comprises sequences isolated from the PG14 strain of B.thuringlensis subsp. morrison. The cytA gene encodes a cytolytic protein which has high affinity for the lipid portion of cell membranes. After ingestion by insects, the 27 kDa Cyt A protein is cleaved by midgut proteases to a relatively resistant core of 25 kDa. The Cyt A coding sequence is combined with the Cry toxin, also from B.thuringlensis. 1023 A; 462 C; 503 G; 913 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Extending host range or toxicity of insecticidal proteins · using protein capable of binding to gut epithelium of insects Claim 33; Fig 22; 61pp; English.
10-FEB-1992 (first entry)

Btm PG14 72kDa Cry insecticidal protein/27kDa Cyt A fusion gene.

chimeric: fusion protein; insecticide: Lepidoptera larvae;

midgut targetting; Cry A; bacterial endotoxin; ss.

Bacillus thuringiensis subspecies morrisoni.
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Gaps: 0
Percent Identity: 77.778
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LO V84560 standard; DNA; 1842 BP.

AC V84560;
DT 01-MAR-1999 (first entry)
DE Human secreted protein gene 150 c
KW Human; secreted protein; fusion is diagnosis; tissue; cancer; tumoun kW diagnosis; tissue; cancer; tumoun kW inflammation; ischaemic shock; M inflammation; ischaemic shock; M cognitive disorder; schizophrenia cathma; Lymphocytik kW cognitive disorder; schizophrenia cathma inflammation; ischaemic shock; M cognitive disorder; schizophrenia cathma inflammation; uschaemic shock; M cognitive disorder; schizophrenia coloronosis; arthritis; testis; KW wolespense; metabolism; regulation os Homo sapiens.

PR NOBE-1998 U11422.

PR 18-DEC-1999; US-070923.

PR 06-JUN-1997; US-048881.

PR 06-JUN-1997; US-048881.

PR 06-JUN-1997; US-048881.

PR 06-JUN-1997; US-048899.
                                                                                                                                                                                                                       14-NOV-1991.
02-MAY-1991; U03008.
02-MAY-1990; US-518575.
(REGC ) UNION OF CALIFORNIA.
Slvasubramanian N, Federici A;
WPI; 91-353775/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-11 x Q14810/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 37.00
Ratio: 4.111
Percent Similarity: 100.000
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PT We isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cencers, neurological tissuedars, immune diseases, inflammation or blood disorders classes, inflammation or blood disorders claim 4: Page 412-413; 772pp; English.

Claim 4: Page 412-413; 772pp; English.

CC closeding human secreted proteins (W88534 to W88756). The secreted protein gene sequences are deposited with the ArCC under deposit numbers ArCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209000, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209000, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209009, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 209008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200008, 200
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New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis (Lim 1; Page 388-370; 1150pp; English.

X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DS-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouality: 35.00 Length: 8
Ratio: 4.375 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 75.000
             W88683, W89013, W89014, W89015, W89016
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30-DEC-1998.
23-JUN-1998, U13041.
24-JUN-1997, US-050667.
(HUMA-) HUMAN GENOME SCI INC.
Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: V84560 from: 1
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ID X20531 standard; DNA; 3858 BP.
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US-08-653-294-11 x V84560
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             (HUMA-) HUMAN GENOME SCI INC.

Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,
Brewer LA, Ferrie AM, Fischer CL, Florence C,
Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,
Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
Shi Y, Soppet LBR, Wei Y, Young P, Yu G, Zeng Z;
WPI; 99-083965/05.
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US-057763.
US-057769.
US-057774.
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US-048971.
US-049019.
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US-057627
US-057634
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06-JUN-1997; U6-JUN-1997; U6-JU
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
06-JUN-1997;
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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05-SEP-1997;
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05-SEP-1997;
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 $\begin{array}{c} \mathbf{q} \\ \mathbf$ 

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Okubo K;
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EP-786519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-11 x T20013
                                                                                          WPI; 95-206931/27
  Homo sapiens.
WO9514772-Al.
                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                 Matsubara K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-1997
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                                                                                                                                           tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fowl poxyirus-originated 5 kb DNA vector with hetrologous genes - useful as a vaccine, providing large copy number per cell, with superior preventive efficacy claim 2; page 36-39; Sapp; Japanese.

This sequence is used in the construction of a new vector originated from fowlpox virus which can duplicate poxyirus in infected cells. The part occurs of the poxyirus including orthopoxvirus and chicken poxyirus. The DNA vector is about 5 kb and is concomitant. It can grow in on-poxyirus-infective cells. It has a large copy number per cell, making the vaccine very effective.

Sequence 5243 BP; 1826 A; 882 C; 1026 G; 1508 T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1996 (first entry)
Human gene signature HUMGS01151.
Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                     25-JAN-1999 (first entry)
FOWLDOX Virus vector DNA fragment.
Vector; poxvirus; infection; treatment; prevention; copy number; promoter; vaccine; ds.
Fowlpox virus.
            1116 T;
production of biosynthetic products such as enzymes.
Sequence 3858 BP; 659 A; 777 C; 1306 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0 Gaps: 0 Percent Identity: 66.667
                                                                                                                                        to: 3858
                                                        Length: 9
Gaps: 0
Percent Identity: 77.778
                                                                                                                                        Align seg 1/1 to reverse of: X20531 from: 1
                                                                                                                                                              Align seg 1/1 to: V65691 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID T20013 standard; cDNA to mRNA; 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeuIleArgLeuAsnGlu 9
                                                                                                                                                                                                                                  seq_documentation_block:
ID V65691 standard; DNA; 5243 BP.
                                                        35.00
4.375
88.889
                                                                                                     alignment_block:
US-08-653-294-11 x X20531/rev
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4.375
88.889
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                                                                                                                                                                                                            seq_name: N_Geneseq_36:V65691
                                                                                                                                                                                                                                                                                                                                        08-OCT-1998.
26-MAR-1998; J01358.
28-MAR-1997; JP-094875.
                                                                                                                                                                                                                                                                                                                                                                        (JAPG ) NIPPON ZEON KK
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US-08-653-294-11 x V65691
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Fowl poxvirus-oric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                          Quality:
Ratio:
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                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                            WO9844093-A1.
                                             alignment_scores:
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  ပ္ပင္တ
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PE 11.*NOV-1931; 01316.

PR (ANXER) ANTERDARA K.

PA (MAYER) ANTERDARA C.

PA (MAYER) ANTERDARA
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memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
the Saureus DNA sequences allows putative functions to be assigned so
that protein-encoding or regulatory regions of commercial, therapeutic or
industrial importance can be obtained. Specifically, sequences which are
likely to encode antigens have been identified and these polypeptides can
be used in a vaccine composition against Saureus infection. The
colypeptides can also be used in a kit for the immunodetection of
Saureus in a sample. Saureus is implicated in numerous human diseases,
including cellulitis, eyelid infections, food poisoning, osteomyelitis,
skin and surgical wound infections, scalded skin syndrome, toxic shock
syndrome, etc. Organisms transformed with the DNA sequences can be used
for recombinant production of the polypeptides. The new DNA sequences
(and their fragments) are useful as primers or probes for isolating
computer readable medium.

Sequence 394 BP; 109 A; 85 C; 71 G; 126 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes the Staphylococcus aureus gidB protein of the invention. GidB polymucleotides and polypeptides are useful for invention. GidB polymucleotides and polypeptides are useful for diagnosing susceptibility to diseases by detecting mutations or polymorphisms in the GidB gene or analysing for the presence of amount of gidB polypeptide expressed in a patient sample. GidB PCR probes are useful for diagnosing diseases, and can characterise the response of the infectious organism to drugs. GidB polypeptides and polymucleotides are also useful for screening for antagonists and antagonists are infectious micro-organisms. GidB agolists and antagonists are bacteriostatic and bacteriocidal compounds which can be used in treatment to enhance or block GidB activity, therefore treating diseases caused by microbial infection, especially S. aureus diseases including microbial infection, especially S. aureus diseases including costeomyelitis, septic arthritis, septic thrombophlebitis, acute bacterial endocarditis and bacteraemia in cancer patients. Epitopes of GidB colypeptides and polynucleotides are useful immunogens for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1999 (first entry)
S. aureus gidB coding sequence.
GidB; mutation detection; bacteriostatic; bacteriocidal compound;
microbial infection; osteomyelitis; septic arthritis; gene therapy;
septic thrombophlebitis; acute bacterial endocarditis; bacteraemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Staphylococcus aureus GidB polypeptides and polynucleotides - useful as diagnostic reagents and for prevention and treatment of Staphylococcus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.00 Length: 10
3.778 Gaps: 0
90.000 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1999; 305175.
12-JUN-1998; US-097072.
01-JUL-1997; US-886638.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
BUIDHAM WRK, Kallender H, Palmer LM, Ward J;
WPI: 99-083572/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: V77268 from: 1 to: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TyrArgLeuLeuIleArgLeuAsnGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:X18185
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US-08-653-294-11 x V77268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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20-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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Pure transmission of the staphylococcus aureus gids protein of the claim 2; Page 23; 39pp; English.

Claim 2; Page 24; Page 25; Page 25; Page 25; Page 26; Pag
                                                                                          for
anti-GidB antibodies for prevention of bacterial infections, and GidB polynucleotides can be used in genetic immunisation to prevent infections. GidB polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial infection. GidB polypeptides and polynucleotides may also be used as reagents for differential screening methods.

295 h; 113 C; 158 G; 244 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1999 (first entry)
S. aureus gidB ORF sequence
GidB) mutation detection; bacteriostatic; bacteriocidal compound;
microbial infection; osteomyelitis; septic arthritis; gene therapy;
septic thrombophlebitis; acute bacterial endocarditis; bacteraemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burnham MKR, Kallender H, Palmer LM, Ward J;
WHY1 99-083572/08.
P-PSDB; W7440coccus aureus GidB polypeptides and polynucleotides -
New Staphylococcus aureus GidB polypeptides and polynucleotides -
useful as diagnostic reagents and for prevention and treatment of
                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 TATCGTTTACTTGTTGAATGGAAAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuleulleArgLeuAsnGluArg 10
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30-JUN-1998; 305175.
11-JUN-1998; US-097072.
01-JUJ-1997; US-886638.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X18186 standard; DNA; 900 BP. X18186;
                                                                                                                                                                                                                                                                                                                                         3.778
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US-08-653-294-11 x X18185
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                                                                                                                                                                                                                                                                                       alignment_scores
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     888888888
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Polynucleotide(s) and proteins derived from Staphylococcus aureus retorated on computer readable medium and used in the production of auti-S.aureus vaccines

Pratics.aureus vaccines

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

Cof the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access

Cof the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access

Cof the invention. The DNA sequences are recorded on a computer readable the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or the protein-encoding or regulatory regions of commercial, therapeutic or that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences contained on the computer readable medium.

Computer readable medium.

Sequence 1398 BP; 461 A; 197 C; 186 G; 494 T;
                                                                                                                                                                                                                                                                                                                                                                                              "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                  Staphylococcus aureus contig SEQ ID #662.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JÄN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.00 Length: 10
3.778 Gaps: 0
90.000 Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1064 TATAAGAAGATTGTCCGATTAAATCAGCGC 1035
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1261. .1320
/*tag= a
/note= "these bases r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrargLeuLeuIleArgLeuAsnGluArg 10
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ID Q20995 standard; DNA; 1560 BP.
AC Q20995;
                                                seq_documentation_block:
ID V74973 standard; DNA; 1398
                                                                                                                                     (first entry)
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US-08-653-294-11 x V74973/rev
seq_name: N_Geneseq_36:V74973
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                                                                                                                                                                                                                                                                                               Staphylococcus aureus
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-786519-A2.
                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                  16-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Isolated gidal polypeptide from Staphylococcus aureus - used to diagnose, treat and prevent bacterial infections e.g. S. aureus and diagnose, treat and prevent bacterial infections e.g. S. aureus and diagnose, treat and associated cancers, ulcers and gastritis
Claim 2: Page 5-6; 43pp; English.

The present sequence encodes a partial gidal protein of Staphylococcus aureus. Gidal proteins, nucleic acids and agonists are used to treat conditions requiring increased activity or expression of gidal, while conditions (particularly bacterial infections) requiring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.MAR.1999 (first entry)
DNA encoding a partial gidAl protein.
GidAl: bacterial infection; meningitis; Helicobacter pylori infection;
cancer; ulcer; gastritis; antibacterial; in-dwelling device;
wound treatment; bacterial adhesion; matrix protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibition of gidal are treated by administering an antagonist, inhibitory nucleic acid or competitive polypeptide. The products are used to treat S. pneumoniae infection, particularly meningitis and gastritis. These antibacterial agents may also be used to treat in-dwalling devices to prevent infection or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. Sequence 1300 Bp; 477 A; 195 C; 262 G; 365 I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a /*tansl_except= (pos: 848. .850, aa: Xaa) / /transl_except= gidAl /note= "Xaa= unspecified amino acid"
                                                                                 Gaps: 0
Percent Identity: 60.000
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3.778 Gaps: 0
90.000 Percent Identity: 60.000
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(SMIK ) SMITHKLINE BEECHAM PLC.
BUINHAM M. KAllender H, Lenox AL, Palmer LM;
WPI; 99-062660,06.
P-PSDB; W89446
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                                                                                                                                                                                                                                         to: 900
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3.778
90.000
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US-08-653-294-11 x X18186
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US-08-653-294-11 x V82078
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30-JUN-1998; 305180
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Percent Similarity:
                                                                                                    Percent Similarity:
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                                                           Quality:
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                             alignment_scores:
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to: 1398

19-MAY-1992 (first entry)

1249 TATCGTTTACTTGTTGAATGGAATGAAAG 1278

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25-MAR-1999 (first entry)

DNA encoding a gidAl protein.

GidAl; bacterial infection; meningitis; Helicobacter pylori infection; cancer; ulcer; gastritis; antibacterial; in-dwelling device; wound treatment; bacterial adhesion; matrix protein; ds.
                                                                                                                                                                                                                                                                                                                      Claim 1: Page 23; 29pp; English.

Equine dermal cells (NBL-6) were infected with EHV-4 strain 1942
Viral DNA, purified and a BamHI library constructed in pUC9.
Calcium shocked E. coli DHT cells were transformed with the
recombinant plasmids. Additional clones were derived from a
restriction digest of pUC9 contg. the BamHI G fragment. The
nucleocide sequence of a region of BamHI G fragment. Spanning the gC
gene was determined. by analysis of overlapping sequences (SEQ ID no
2). Vaccines can be prepd. using this sequence, and they may be used
to protect horses against EHV-4 infection, inducing a higher level
See also Q20934.
                                                                                                                                                    23-JAN-1992.
04-JUL-1991; G01091.
06-JUL-1990; GB-014950.
(UNIU ) UNIV OF GLASGOW.
(EQUI-) EQUINE VIROLOGY RES FOUN.
MICOLSON L, Onions DE;
WPI; 92-056812/07.
P-PSDB; R20796.
Nucleic acid sequence encoding EHV-4 gH or gC protein - used to produce a vaccine for protection of horses against EHV-4.
EHV-4 gC gene.
Equine herpes virus-4; glycoprotein gC; antigenic; vaccine;
alphaherpesvirus; respiratory disease; cellular attatchment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 T;
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3.778 Gaps: 0
90.000 Percent Identity: 70.000
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30-JUN-1998: 305180.
01-JUL-1997: US-052758.
(SMIX ) SMITHKLINE BEECHAM CORP.
(SMIX ) SMITHKLINE BEECHAM PLC.
Burnham M, Kallender H, Lenox AL, Palmer LM;
WPI: 99-062660/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q20995 from: 1 to: 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 C;
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109. .1986
/*tag= a
/product= gidAl
                                                                        Location/Qualifiers
52. 1509
/*tag= a
                                                                                                              /*tag= a
/product= EHV-4_gC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID V82077 standard; DNA; 2132 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 A;
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Key Locati
CDS 109. .
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US-08-653-294-11 x Q20995
                                              pathogenic; ss.
Equine herpesvirus-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1560 BP;
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Ratio:
Percent Similarity:
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                                                                                                                                          WO9201057-A
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PP PPSDB; W89445.

PT New isolated gidAl polypeptide from Staphylococcus aureus - used to diagnose, treat and prevent bacterial infections e.g. S. aureus and PT H. Pylori and associated cancers, ulcers and gastritis

Claim 2; Page 3-4; 43pp; English.

CC The present sequence encodes a gidAl protein of Staphylococcus

CC aureus. GidAl proteins, nucleic acids and agonists are used to contitions requiring increased activity or expression of gidAl, while conditions requiring increased activity or expression of gidAl, while conditions requiring increased activity or expression of gidAl, while conditions requiring increased activity or expression of gidAl, confinibition of gidAl are treated by administering an antagonist, inhibition of gidAl are treated by administering an antagonist, consect to treat S. pneumoniae infection, particularly meningitis and class Helicobacter pylori infections e.g. related cancers, ulcers and cancer indeed to prevent infection or generally as wound creatments to prevent adhesion of bacteria to matrix proteins.

SQ Sequence 2132 BP; 791 A; 311 C; 430 G; 600 T;
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Align seg 1/1 to: V82077 from: 1 to: 2132

alignment\_block: US-08-653-294-11 x V82077

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AA864515 Oh55b03.sl NCI_CGAP
AI233666 EST230354 Normalize
AI246027 qk44g11.xl NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Konno, H., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukudishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Fukuda, S., Fukudishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Fukuda, S., Fukudishi, Y., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawat, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Namura, M., Oda, H., Odazaki, Y., Shibata, Y., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokhino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al.)

On May 18, 1998 this sequence version replaced gi:3137751.

Genome Exploration Research Group, Life Science Tsukuba Center, Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
                                                                                                                                                     Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,X., Izawa,M., Kawai,J., Owazaki,Y. and Hayashizaki,Y.

Owazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sal1; Site_2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 246)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
     285
287
293
  255.29
257.10
262.54
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/lab_host="DH10B"
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/clone-"4831414015"
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  127.20
127.15
126.98
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                                                                                                                                                                                                                                                                                                                                      AV242923.1 GI:6230332
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                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
     gb_est20:AA864515
gb_est24:AI233666
gb_est25:AI246027
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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B57891 CTT-HSP-2010015 TR CIT-H
AQ586481 HS.5543B2_A12.SP6E RF
AQ557396 n181h06.51 NCI_CGAP_BT
AQ146935 HS_2248_AZ_B10_MR CIT
AQ215203 HS_210_A1_H08_MR CIT
AQ216648 HS_2190_A1_B03_T7 CIT
AQ186906 HS_3113_BZ_E07_T7 CIT
AQ685122 HS_2160_A1_F05_T7 CIT
A1772130 EST253230 tomato resis
A1772130 EST253230 tomato resis
A1772130 EST25320 tomato resis
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AQ735952 HS_2261_A1_F09_T7C CIT
AL097957 Drosophila melanogaste
AQ157379 nbxb00009118r CUGI Rice
AQ271001 nbxb00015A11f CUGI Rice
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AI658427 AEMTBM58 Aedes aegypti
AI65844 AEMTBM57 Aedes aegypti
AL051558 Drosophila melanogaste
AA911731 oi15e06.sl NCI_CGAP_GG
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AI866895 W112e12.X1 NCL_CGAP
AA729926 nX40f01.s1 NCI CGAP
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                                                                                                                                                                                                   -MODEL-frame-f-D2n.model -DEV-x1p
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.1
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-MINAATCH=0.100 -LOOPCL=0.000 -LOOPSTT=0.000 -GAPOP=4.500
-QAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LIST=45 -DOCALIGN=200 -THR_SCORE-PCt -ALIGN=15 -MODE-LOCAL
-USTST=45 -DOCALIGN=200 -THR_SCORE-PCt -ALIGN=15 -MODE-LOCAL
-USTST=45 -DOCALIGN=20 -THR_SCORE-PCt -ALIGN=15 -MODE-LOCAL
-USTST=45 -NORM-ext -MINIEN-0 -MAXIENTST-00000 -USER-US08653294
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     out_format
                                                                                                     About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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1327.78
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Database length: 1887831982
Search time (sec): 8553.360000
OM of: US-08-653-294-11 to:
                                                     Date: Feb 8, 2000 4:02 AM
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Query: US-08-653-294-11
Query length: 10
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9b_gss11:AQ271001
9b_gss1:CNS00G7E
9b_gss1:CNS00G6
9b_gss8:AQ064329
9b_est22:A1008780
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gb_est17:AA604578
gb_est32:A1758190
gb_est36:AV188192
gb_gss9:AQ128402
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gb_gss1:CNS00S22
gb_est1:F02347
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gb_gss4:AQ675126
gb_gss8:AQ054233
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gb_est16:AA557396
gb_gss9:AQ146935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_gss10:AQ216648
gb_gss10:AQ186906
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gb_gss1:CNS00881
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gb_est35:AI866895
gb_est18:AA729926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_gss4:AQ685122
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1 TyrArgLeuLeuIleArgLeuAsnGluArg 10
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                                                           207
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                                                          BASE COUNT
ORIGIN
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ORIGIN
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 578)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ735952 578 bp DNA GSS 15-JUL-1999 HS_2261_A1_F09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2261 Col=17 Row=K, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jwallacedu, washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2261 row: K column: 17
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/do_xef="taxon:5606"
/clone="Plate=2251 Col=17 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Vol Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                        Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 246
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Location/Qualifiers
1. .578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TyrArgLeuLeuIleArgLeuAsnGlu 9
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AQ735952
AQ735952.1 GI:5507504
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                                                                                                                                                                                                                                                                                                                                         Ratio: 4.444
Percent Similarity: 100.000
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US-08-653-294-11 x AV242923
                                                                                                                                                                                                                                                                                                                           40.00
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                                                                                                                                                                                                                                                                                                                             Quality:
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ORGANISM
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COMMENT
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KEYWORDS
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.edl.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence SP6 end of BAC BACN02A09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108" 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins:
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 others
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1. .983
/organism="Drosophila melanogaster"
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                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 70.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN02A09"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrArgLeuLeuIleArgLeuAsnGluArg 10
                                                                        p
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                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL097957.1 GI:5609568
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         983 bp
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                                                                                                                                                                                          Quality: 39.00
Ratio: 3.900
Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-11 x AQ735952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS CNS002P7
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SOURCE ORGANISM

VERSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AQ271001 946 bp DNA GSS 03-NOV-1998
DEFINITION nbxb0015A11f CUGI Rice BAC Library Oryza sativa genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poaceas, Oryza.

Tobaceas, Oryza.

Wing,R.A. and Dean,R.A.

**RAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

Tol Orotach Hall, Clemson, SC 29634, USA

Fax: 864 655 4293
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Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Location/Qualifiers
1. .946
                                                                                          /strain="Japonica"
/cultivar="Nipponbare"
                               to: AQ157379 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ271001.1 GI:3824316
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4.222
90.000
                                                                                                                                                                                                                                    seq_name: gb_gss11:AQ271001
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JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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//organism="Crypa sativa"
//organism="Crypa sativa"
//db.xref="Lasponica"
//clone="lib="CuGI Rice BAC Library"
//clone="lib="CuGI Rice BAC Library"
//clone=lib="CuGI Rice BAC Library"
//clone=lib="CuGI Rice BAC Library"
//clone="lib="CuGI Rice BAC Library"
//clone=lib="CuGI Rice BAC Library"
//clone=lib="CuGI Rice BAC Library"
//clone=lib="CuGI Rice BAC Library"
//clone=lib-"Loaf
//clone=lib="CuGI Rice BAC Library"
//clone=lib-"CuGI Rice BAC Library"
//clone=library road composition or rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a happioid genome equivalent of 431 Mbp (Arumyanathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library from Oryza sativa, Nipponbare variety. The library contains $6.864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents.

The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                              Poeceae: Oryza.

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
On Sep 10, 1998 this sequence version replaced gi:3554404.
Contact: Wing RA Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 70.000
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/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 2
High quality sequence stop: 389.
Location/Qualifiers
Email: rwing@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                   AQ157379
AQ157379.1 GI:3592495
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Percent Similarity: 100.000
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US-08-653-294-11 x AQ157379
                                                                                          seq_name: gb_gss10:AQ157379
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source

FEATURES

alignment\_scores:

BASE COUNT

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthbria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 403)
Mahairas, G.G.; Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                   1 (bases 1 to 399)
Salabacubat,M., Cholsne,N., Artiguenave,F., Brottier,P., Wincker,P., Unpublished
                                                                                                                                                                         thale cress. Arabidopals thallana Embryophyta; Embryophyta; Tracheophyta; Eukaryota; Viiddiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:

LOCUS AQ064329 403 bp DNA GSS 04-AUG-1998

LOCUS AQ064329 403 bp DNA Genomic Sperm Library D Homo
DEFINITION HS_2200_A1_MF_E07 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2200 Col=13 Row=1, genomic survey
CNSOOPG6 399 bp DNA GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence T7 end of BAC F801 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
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Gaps: 0
Percent Identity: 87.500

    .399
    /organism="Arabidopsis thaliana"

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High Throughput Sequencing Center
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/db_xref="taxon:3702"
/clone_lib="IGF"
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AL084468.1 GI:5285608
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AQ064329.1 GI:3378867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission of Submisted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecord digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                    DOSOPhila melanogaster genome survey sequence T7 end of BAC:
BACR32013 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RECI-98"
/clone="BACR32013"
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Gaps: 0
Percent Identity: 70.000
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                                                                                                                              1 TyrArgLeuLeuIleArgLeuAsnGluArg 10
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247 c 22
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  alignment_block:
US-08-653-294-11 x AQ271001/rev
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Ratio: 3.800
Percent Similarity: 100.000
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SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS

DEFINITION

BASE COUNT ORIGIN

FEATURES

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74

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144 a
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                                                                                               Quality:
Ratio:
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                        ORIGIN
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EST203231 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMBD17 3' end, mRNA sequence.
                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="plate=2200 Col=13 Row=I"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      & Rat
                                                                                                                                                                                                                                                                                                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lbe"Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT/T3Pac; Site_1: EcoRI; Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
Rattus sp.
Battus sp.
Eukaryosa, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (Dases I to 405)
Lies. N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J.,
Rerlavage, A. R. and Adams, M. D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat Genome Project: Generation of a Rat EST (REST) Catalog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
On Jan 17, 1998 this sequence version replaced g1:2044445.
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Exa: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2200 row: I column: 13
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                      1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus sp."
/db_xref="ATCC (inhost):2016965"
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                                                                                                                                                                                                                                                                                                                                      ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AQ064329 from: 1
                                                                                                                                                                                                                                                                                                                                    132
                                                                                                                                                 High quality sequence stop: 403. Location/Qualifiers
1. 403 /Organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
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AI008780.1 GI:3222612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nhlee@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-11 x AQ064329/rev
                                                                                                                                                                                                                                                                                                                                    88
C
                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 37.00
Ratio: 3.700
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
Locus A1008780
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ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)

2 hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

Map Building

Lonpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Enkaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850

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Fax: 401 838 0200

Fax: 401 838 0200

Fax: 401 838 0200

Fax: 401 838 0200

Fax: 501 838 0200

Fax: 501 838 0200

Fax: 501 838 0200

Fax: 401 838 0200

Fax: 501 838 0200

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LOCUS AQS83741 552 bp DNA GSS 07-JUN-1999
DEFINITION RPCI-11-434G5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-434G5,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphocytes"
/cell_type="lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 117 c 70 g 220 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                               Percent Identity: 66.667
                                                                                                                                                                                                               Length:
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/clone="RPCI-11-43465"
/clone=1hb="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 TACAAAATACTTTTGAGGTTAAATGAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AI008780 from: 1
63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArgLeuAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ583741
AQ583741.1 GI:5010851
    υ
                                                                                                                                                                                                                                                            Ratio: 4.111
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-11 x AI008780
                                                                                                                                                                                                               37.00
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Ratio: 3.700
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_gss14:AQ583741
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SOURCE ORGANISM

VERSION KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL COMMENT

```
seq_documentation_block:
LOCUS AA604578 325 bp mRNA EST 08-OCT-1997
DEFINITION no76b01.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112713 3',
ACCESSION AA604578
                                                                                                Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 325.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                    1..304
/organism="Brugia malayi"
/organism="Exrain="TRS Labs"
/db_xref="taxon:6279"
/clone="SW3ICAL954"
/clone=llb="Brugia malayi infective larva cDNA (SAW94WL-BmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                            Eukaryota; Metazoa; Nematoda; Secer
Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeuIleArgLeuAsnGluArg 10
 AA185851
AA185851,1 GI:1769739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA604578.1 GI:2445442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est17:AA604578
                                                           Brugia malayi.
Brugia malayi
                                                                                                                                                     Williams, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saptens
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Mixed"
/dev_stage="Egg"
/note="vector: Uni-Zap XR vector, Stratagene (pBluescript XR); Site_1: EcoRI; Site_2: XhoI; mRNA was extracted from eggs and the library was constructed and excised according to the manufacturer's instructions."

16 c 69 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                  Olivelra.G.C. and Baba, J.
Cataloguing Schistosoma mansoni genes with expressed sequence tags
Cataloguing Schistosoma mansoni genes with expressed sequence tags
Unpublished (1998)
On Feb 18, 1999 this sequence version replaced gi:4296741.
Contact: Olivelra, Guilherme
Lab. Parasitologia Cel. e Mol.
Centro de Pesquisas Rene Rachou - FIOCRUZ
Av. Augusto de Lima 1715 Barro Preto, Belo Horizonte, MG, CEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:6183"
/clone_lib="Egg stage cDNA expression library in Lambda
ZAPII"
                                                                                                                                                                                       seq_documentation_block:
LOCUS A1820472 254 bp mRNA EST 09-JUL-1999
DEFINITION ME000422.FOR Egg stage cDNA expression library in Lambda ZAPII
ACCESSION A1820472
VERSION A1820472.1 GI:5439551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AAA8851 304 bp mRNA EST 08-JAN-1997
DEFINITION SW3ICA1954SK Brugia malayi infective larva cDNA (SAM94WL-BML3)
Brugia malayi cDNA clone SW3ICA1954 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                               Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma
1 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                               Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: oliveira@netra.cpgrr.flocruz.br
Insert Length: 254 Std Error: 0.00
Seg primer: M13 Reverse Universal Sequencing primer.
Location/Qualifiers
                                         to: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 254
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Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Schistosoma mansoni"
/strain="LE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                       Align seg 1/1 to reverse of: AQ583741 from: 1
                                                                                                10
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                                                                            1 TyrArgLeuLeuIleArgLeuAsnGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-11 x AI820472/rev
   US-08-653-294-11 x AQ583741/rev
                                                                                                                                                                                                                                                                                                                             Schistosoma mansoni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 55 31 2953566
Fax: 55 31 2952115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 4.000
Percent Similarity: 100.000
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
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FEATURES

BASE COUNT

1000

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Ratio: 3.600
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-11 x AI758190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est36:AV188192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                      CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/db_xref="taxon:9606"
/clone=libe"Nus.112713"
/clone=libe"Nus.12020,841"
/tissue_type="adrenal adenoma"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: adrenal gland; Vector: Bluescript SK-;
Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
Primer: Oligo dr. Two pooled bulk adrenal adenomas. 5'
adaptor sequence: 5' CTGGAGTTTTTTTTTTTTTTTTT 3' Average insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LQCUS A1758190 337 bp mRNA EST 23-JUN-1999
DEFINITION ty70e05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2284448 3',
mRNA sequence.
ACCESSION A1758190
VERSION A1758190.1 GI:5151913
  Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primetes; Catarrhini; Hominidae; Homo.

1 (bases 1 to 337)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                               cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                  Tumor Gene Index
Onpublished (1997)
On Special 2, 1996 this sequence version replaced gi:1405116.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Dec 20, 1995 this sequence version replaced gi:1133827.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 682 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 217.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 g
  Cancer Institute,
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Percent Similarity: 100.000
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US-08-653-294-11 x AA604578
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TITLE
                                         JOURNAL
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KEYWORDS
SOURCE
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TITLE
                                                                  COMMENT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IxMGE:2284448"
/clone=lib="NGI_GAP_Kid11"
/lab_host="NGI_GAP_Kid11"
/lab_host="DH108"
/note="Organ: kidney: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NGI_GGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PGR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatina Bonaldo.
                                                                                               CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Koharan,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugimoto,A., Nomoto,H.
                                    ď
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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LOCUS AY188192 360 bp mRNA EST 22-JUL-1999
DEFINITION AV188192 YUJI Kohara unpublished cDNA.Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk520912 5', mRNA
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Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137896.
Contact: Yuji Kohara
Gene Library Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
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Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
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Location/Qualifiers
1. .337
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50 c 5
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Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

1.360

/organism="caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk220g12"
/clone="yk220g12"
/clone="laxon:10"
/dev_stage="embryo"
/de
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Align seg 1/1 to reverse of: AV188192 from: 1 to: 360

alignment\_block: US-08-653-294-11 x AV188192/rev

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Key Location/Qualifiers
Misc_difference 1. .10
Misc_difference
                                                                                                                                                                                                                                                                                                                 Homo sapiens
Synthetic.
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22-MAY-1998
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W47270
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HIA-B2702 CTL modu
HIA-B2702 84-75/7
Peptide B2702.84-7
Bovine p32 11-cis-
Bovine p32 11-cis-
Bovine p32 11-cis-
A p32 protein whic
KOD-1 heat shock p
Thermococcus sp. K
EHV-4 9C. Nucleic
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HLA-B2702 CTL modu
HLA-B2702 CTL modu
HLA-B2702 84-75-84
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Large polyprotein
Bacillus subtilis
Immunomodulatory p
Peptide #2 used in
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Immunomodulatory p
Immunomodulatory p
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Immunomodulating d
Beta 7 integrin S3
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Immunomodulating d
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Mabinlin MBLIII fr
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Immunomodulatory p
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                                                                                                     (without alignments)
1.933 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #2 used
HLA-B2702 84-79-
                                                                                         Search time 122.56 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                           Compugen Ltd.
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
             GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                   188963 seqs, 23686106 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                         8, 2000, 01:29:38
                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                  sw model
                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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W47266
W47272
R92909
R92911
R92907
R95428
W33778
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W47268
R92910
R92908
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Y01994
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W33791
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R62504
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W47263
W33781
R95429
W33799
W19361
W23586
W23588
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                                                                 · protein search, using
                                                                                                                                            US-08-653-294-13
                                                                                                                                                                     1 YRLAIRLDER 10
                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 1000000
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Match Length
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Maximum DB
                                                                 OM protein
                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                     Searched:
                                                                                         Run on:
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23-ARP-1997; UG6705.
22-MAY-1996; US-651650.
22-MAY-1996; US-651650.
22-MAY-1996; US-651650.
21 (Clayberger C, Krensky AM; SP -010220/0.2.
21 (May -1) (
                                                                                                                                                                                      Nicotiana plumbagi
Streptococcus pneu
Ethylene response
                                                                                                                                                                                                                                                                                               Ethylene response
Ethylene response
A. thaliana ethyle
   Carbonic anhydrase
                                          Chlamydomonas carb
                                                                         H. pylori GHPO 121
                                                                                                                Toxoplasma gondii
Thermococcus sp.
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1. .10
/note= "at least one of the amino acids is D-isomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-WAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W47266.
22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.00014; Pred. No. 0.0014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
R21416
R21417
W98786
R25534
W67798
W65105
R69849
R69853
R69853
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Best Local Similarity 100.
Matches 10; Conservative
376
3377
3377
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                                                                                                                                                      Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                   Claim 10; Page 36; 41pp; English.
The present sequence is an immunomodulatory peptide, which comprises a Class I HiA-B alpha-I domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 36; 41pp; English.

The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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/note= "at least one of the amino acids is the
D-isomer
 one of the amino acids is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                     the treatment of autoimmune diseases.
Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                       Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1;
Pred. No. 0.0016;
1; Mismatches (
                                                                                22-MAY-1996; US-651650..
(STRD ) UNIV LELAND STANFORD JUNIOR
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/note= "at least
D-isomer
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90.0%;
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                                                                                                                   Clayberger C, Krensky AM;
WPI; 98-018220/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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                                                                                                                                                                     transplant rejection
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23-APR-1997; U06705.
                                                              23-APR-1997; U06705
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLAIRLDER 10
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Gaps

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Score 44; DB 1; Length 10; Pred. No. 0.0016; 0; Mismatches 1; Indels

89.8%; 90.0%;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

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R83061-R83085, R83090-R83096 and R82907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a rectipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abstinct comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of
R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequent
class I major fresidues 75-84 of the alpha-1 domain of the class I MHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extension of acceptance period of transplants from donor hosts - using Class I B75-84 MHC antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOSSACTORY OF THE STATE OF THE 
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                           standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1996 (first entry)
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1 YRLAIRLDER 10
                                                                                  1 YRLLIRLDER 10
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WPI; 95-358582/46.
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WO9526979-A1.
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Matches
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R92909
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R92911
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18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
cytolysis; antigen presenting cell. Synthetic.
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WO9744351-A1.
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Synthetic.
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R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class inajor histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
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HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                       16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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HIA-B2702 84-75-84 palindrome.
HIA-B2702 84-75-84 palindrome.
HIA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA: p74: alphal-helix; numan-leucocyte-associated profein; Hsc70: APC;
T-cell lysate; membrane protein; mammal; heat shock profein; Hsc70: APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Krensky Am, rulling Clayberger C, Krensky Am, rulling S5-358582/46.
Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                     Score 44; DB 1; Length 20;
Pred. No. 0.0035;
1; Mismatches 0; Indels
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Pred. No. 0.0035;
1; Mismatches 0; Indels
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90.0%;
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Best Local Similarity
9; Conserv
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                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                             1 YRLAIRLDER 10
                                                                                                                                                                                                                             YRLAIRLDER 10
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                                                                                              patient
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                                                                                                               Sequence
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ID R9
AC R9
DT 112
DE HI
KW HI
KW T
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This is a comprising lymphoid surface membrane proteins - which may finibit cytolytic activity and differentiation of CTLS.

PS Example; Page 12: 29pp: English.

Example; Page 13: 2pp: English.

Example; Page 13: 2pp: English.

Example; Page 14: 2pp: English.

Example; Page 14: 2pp: English.

Example; Page 15: 2pp: English.

Example 15: 2pp: English.

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Claim 16; Page 35; 41pp; English.
This sequence represents a specifically claimed immunomodulating dimer peptide of the Invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 acylated dis, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 0.0035;
1; Mismatches 0; Indels
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22-MAX-1997; U08689.
24-MAX-1996; US-653294.
(STRD ) UNIY LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W33778 standard; peptide; 20 AA.
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Best Local Similarity 90.0°
Local 9; Conservative
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Treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating

This sequence represents a specifically claimed immunomodulating

dimer peptide of the invention. A peptide-type compound or variant is

claimed which has immunomodulating activity, including the N-terminal

acylated and/or C-terminal amidated or esterified forms of up to 60.

Claimed which has immunomodulating activity, including the N-terminal

acylated and/or C-terminal amidated or esterified forms of up to 60.

Claimed which has immunomodulating activity, including the N-terminal

acylated and/or C-terminal amidated or esterified forms of up to 60.

Claimed which has immunomodulating as 20 or 8; and 20 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
hydrophobic or small amino acid; aa82 - R or L; aa83 - G or R; and aa arepresents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-1ymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenc peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rhemmatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunomodulating dimer peptide #2.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-1997; U08689.
24-MAY-1996; US-653294.
26-MAY-1996; US-653294.
STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Claybriger C, Krensky AM;
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1; Length 20;
Pred. No. 0.0035;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W33779 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W33779;
19-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0v
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WO9744351-A1.
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DEPLOY R. Claybergor S. Krensky AM;

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

WPI: 98-086530/08.

Treating dutoimmune diseases

Example 1; Page 19; 41pp; English.

Peptides W3784-98 and W37378-9 were assayed for their immunomodulating activity, including the N-terminal arclated and/or immunomodulating activity, including the N-terminal acylated and/or companies the peptide-type compound comprises the formula: A-B, where A, B = C. C. terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = C. C. R and 67-771, [ang)-94) or (ang 47-9) (Lan77-76R); and a represents amino acid sequences in the brackets may optionally absent or truncated acid. The sequences related to a class I HiA-B alphal domain (positions and on a sequences related to a class I HiA-B alphal domain (positions on the sequences related to a class I HiA-B alphal domain (positions on the compounds comprise amino acid sequences related to a class I HiA-B alphal domain (positions of activity actacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate cTLs. They can also inhibit the proliferation of T cells in a ceponse to anti-CD3. The peptide can be used dor preventing rejection of characteristics and lupus erythematosis. The products can also be considered to anti-CD3. The public can be used for preventing rejection of characteristics.

The amino acid sequences relating autoimmune diseases, e.g. diabetes, considered to anti-CD3. The peptide can be used for preventing rejection of characteristics.
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                                                                                                                                                                                                                                                                                                     19-JUN-1998 (first entry)
Peptide B2702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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/note= "at least one of the amino acids is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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Pred. No. 0.0035;
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22-MAX-1997; U08689.
24-MAX-1996; US-653294.
24-MAX-1996; US-653294.
25TRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                         W33792 standard; peptide; 20 AA.
W33792;
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90.0%;
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Query Match
Best Local Similarity
Matches 9; Conserv
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WO9744351-A1.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rejection.
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                                                                                                                                                  RESULT 10
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Gaps

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89.8%; Score 44; DB 1; Length 20; 90.0%; Pred. No. 0.0035; ive 1; Mismatches 0; Indels

Conservative

1 YRLAIRLDER 10

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Query Match Best Local Similarity Matches 9; Conserv

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-B2702 84-75775-841 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of
                                                                                                                 HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
class I MHC; HIA-B2702.
Synthetic.
W09526979-A1.
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HIA-B2702 84-757/75-64T palindrome.
HIA-B2702 84-757/75-64T palindrome.
HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composis, comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example, Page 12, 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I 875-84\ \mathrm{MHC} antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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Pred. No. 0.04;
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                                                                                                                                                                                                                                                                                                                                                            Krensky AM, Parham P;
                                                                                                                                                                                                                                                              12-OCT-1995.
05-ARR1995; 004349.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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10-NOY-1994; U12985.
10-NOY-1993; US-150493.
GSTRD ) UNIV LELAND STANFORD JUNIOR.
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                                                   R92908 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.6%;
80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                             16-MAY-1996
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  RESULT
R92908
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R83061-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                         Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                claim 10; Page 36; 41pp; English.

The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunomosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.

Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 0.019;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
23-APR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R92910 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.6%;
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80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                       Clayberger C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      class I MHC; HLA-B2702
                                                                                                                                               transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
1.75 8; Conserv?
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| YRLLIRLNER 10
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WO9526979-A1.
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12-OCT-1995

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RESULT 12

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Gaps

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a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by sufficient to compete with p74 for the binding of the p74 ligand. Sequence 20 AA; 888888888888888

Gaps ö Score 39; DB 1; Length 20; Pred. No. 0.04; 0; Indels 1; Mismatches 79.68; 88.98; Query Match
Best Local Similarity 88.9
Matches 8; Conservative

1 YRLAIRLDE 9 

w33791;
19-JUN-1998 (first entry)
19-JUN-1998 (first entry)
Inmunomodulating activity.
Immunomodulating dimer: Immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; W33791 standard; peptide; 20 AA. RESULT

27-NOV-1997. 22-MAY-1997; U08689 Homo sapiens. Synthetic 

24.MAT.1996; US-653294.

(STRD ) UNIV LELAND STANFORD JUNIOR.

(STRD ) UNIV LELAND STANFORD JUNIOR.

(STRD ) 98-086530/08

WPI; 98-086530/08

New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-I domain, used for preventing rejection of transplants or

treating autoimmune diseases

Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity.

C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (C-terminal amidated comprises the formula: A-B, where A, B = (C-terminal amidated comprises the formula: A-B, where A, B = (C-terminal amidated compound completes to the peptide type bond within the brackets and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets or proteins of interest to need in combination with antigenic peptides or proteins of interest to activate CILS. They can also inhibit the proliferation of T cells in response to anti-CDS. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, chematoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.

ö Gaps ö 79.6%; Score 39; DB 1; Length 20; 80.0%; Pred. No. 0.04; Live 1; Mismatches 1; Indels Conservative Query Match Best Local Similarity Matches 8; Conserva

1 YRLATRLNER 10 셤 Search completed: February 8, 2000, 01:29:38 Job time: 1750 sec

1 YRLAIRLDER 10

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Sequence

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Query Match 71.4%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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hypothetical prote
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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hypothetical protein transcription fact transcription regul hypothetical protein glycoprotein D preim protein preim protein pr	MENTS	shii Aug-1998 #text_change 14-A H.; Haikawa, Y.; Hino, Y.; ; Kudoh, Y.; Yamazaki, J.;	organization of the genome of a hyper-thermophili 344137 sequence not shown; translation not shown D:g3236130; PID:d1030708; PID:g3257082	im accession for a sequence replaced by GenBa 37; DB 2; Length 151; No. 1.8; matches 1; Indels 0; Gaps 0;		.) -Jan-1995 #text_change 16-Jul-1999 er 1993 747; PIDN:CAA53092.1; PID:G406748 RING finger homology
139689 112615 306117 606515 106523 106529 106523 1168311 112704	ALIGNMENT	cus horikoshii 1 evision 14-Aug Horikawa, H.; Tanaka, T.; K	98 98 id	n inter Score Pred. 0; Mis		rfp - mouse (fragment) lus (house mouse) #sequence_revision 06-Jan L Data Library, October 1' 837583 X AK> EMBL:X75343; NID:g406747; ransforming protein; RING
понововновно		Shift Shift	C a c a c a c c a	6.5 9.5 9.5 9.5		conse (fruse mouse (ce_revis) (ce_revis) Library, Library, ming pro homology
28 28 28 28 28 28 28 28 28 28 28 28 28 2	•	- Pyrococcus horikoshil equence_revis wada, M.; Hor ashi, T.; Tan	complete sequence and te number: A71000; MUJ n: C71113 preliminary; nucleic type: DNA :: 1-151 <kan> iferences: GB:AP000003 intal source: strain on</kan>	n replaces 75.5% ty 88.9% ervative	_ <b>4</b> *	infp - mouse (frautus (house mous) #sequence_revis   #sequence_revis   BL Data Library,   837583
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	н	es: Pyrc 14-Aug: sion: C; abayasi, ifuku, Y.	Title: Complete sequence and ge Reference number: A71000; MUID: Accession: C71113 Status: preliminary; nucleic ac Molecule type: DNA Residues: 1-151 KRM> Cross-references: GBAP000003; Experimental source: strain O73	Note: this ac Genetics: Gene: PH0674 Query Match Best Local Si Matches 8;	2 RLLIRLDER            96 RLLIELDER	nger process: Mus 06-Jan. Sistem: Sistem: Sistem: Sistem: Sistem: Sistem: Sistem: Sistem: Sistem: Desire in the sistem: 1-referent family: Tomas: 2-referent family: Domain: Domain:
U W W W W W W W W W W W W W W W W W W W	RESULT C71113	probabl C;Speci C;Date: C;Acces R;Kawar M;Oh	A;Title: Complete sequence an A;Accession: C71113 A;Status: preliminary; nuclei A;Molecule type: DNA A;Kesidues: 1-151 cKAN> A;Cross-references: GB:AP0000 A;Experimental source: strain	A; Note: t C; Genetic A; Gene: P Query M Best Lo Matches	Qy	RESULT 2 837583 RING finger protein rfp - mouse C; Species: Mus musculus (house m C; Date: 06-Jan-1995 #sequence_re C; Accession: 837583 R; Takahashi, M. submitted to the EMBL Data Libra A; Reference number: 837583 A; Reference number: 837583 A; Status: preliminary A; Accession: 837583 A; Status: preliminary A; Residues: 1-506 «TAK» A; Cross-references: EMBL:X75343; C; Superfânily: rfp transforming C; Keywords: 2inc F; 5-5/Domain: RING finger homole
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Gaps

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Length 506; l; Indels

Score 35; DB 2; Pred. No. 16; 1; Mismatches

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C; Species: Mycobacterium tuberculosis
C; Decies: Mycobacterium tuberculosis
C; Decies: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C; Ccession: D7086
C; Connor, R:; Brosch, R:; Parkhill, J:; Garnier, T.; Churcher, C.; Harris, D.; Gordon
C; Connor, R:; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A; Accession: D70886
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
C;Accession: S75953
R;Kaneko, T.; Sarco, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL008883; GB:AL123456; NID:g3261490; PID:e1172958; PID:g261281
A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-87 <COL>
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66.7%;
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                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv2866
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Matches 6; Conserv
198 YRLLARLEE 206
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120 YRKLLRLDD 128
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60 YRLLYRIDD.68
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A: Molecule type: mRNA
A: Residuals: 'OAGA',1-801
A: Residuals: 'OAGA',1-801
A: Residuals: 'OAGA',1-801
A: Comment: The ret oncogene is the chimeric product of a translated
C: Comment: The ret oncogene is the chimeric product of a translocation mutation between
C: Genetics: A: Genetics: A: C: Reywords: ATP: fusion protein: oncogene; phosphotransferase; transforming protein: try
C: Reywords: ATP: fusion protein: from the first of the comming protein from the first of the comment of the comme
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Nicontains: protein-tyrosine kinase (EC 2.7.1.112) ret
Nicontains: protein-tyrosine kinase (EC 2.7.1.112) ret
Sispecies: Homo sapiens (man)
C;Species: Homo sapiens
C;Spec
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Species: Homo sapiens (man)
Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
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Pred. No. 26;
1; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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ilarity 77.8%;
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|191 YRLLARLEE 199
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hypothetical protein YPL088w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPG20w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 29-Sep-1999
C;Accession: S61978
R;Wang, Y;Ahmed, A; Bussey, H;Fortin, N;Friesen, J.D.; Hall, J.; Storms, R.K.;
submitted to the EMBL Data Library, December 1995
A;Reference number: S61959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: U43281; NID: 91151218; PIDN: AAB68211.1; PID: 91151238; MIPS: YP
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Aces: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Acession: F70548
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Cole, S.T.; Davis, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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cylicin II - human sapiens (man)

cylicin II - human sperm heads:

R; Hess, H; Heid, H; Zimbelmann, R; Franke, W.W.

Exp. Cell Ress, 218, 1144-182, 1995

Fyritle: The protein complexity of the cytoskeleton of bovine and human sperm heads:

A; Reference number: I37271

A; Accession: I37271
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60.0%; Pred. No. 45;
ive 2; Mismatches 2; Indels
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C;Superfamily: conserved hypothetical protein YPL088w
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0; Mismatches
       Pred. No. 44;
2; Mismatches
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ilarity 70.0%;
Conservative
       Best Local Similarity 60.0%;
Matches 6; Conservative
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Matches 6; Conservative
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221 YRKLYRMDKR 230
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Best Local Similarity
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A; Residues: 1-342 <WAN>
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C;Species: Chloroplast Chlorella vulgaris cuicroplast
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 22-Jun-1999
C;Accession: T07269
E;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlc
A;Reference number: 215985; MUID:97303241
A;Accession: T07269
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-52 <WAK>
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDd they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C; Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C; Accession: D48435
R; Pratt, D.; Armes, L.G.; Hageman, R.; Reynolds, V.; Boisvenue, R.J.; Cox, G.N.
Mol. Biochem. Parasitol. 51, 209-218, 1992
My: Title: Cloning and sequence comparisons of four distinct cysteine proteases expressed A; Reference number: A48435; MUID:92244291
A; Accession: D48435
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A;Cross-references: GB:AE001223; GB:AE000520; NID:g3322745; PID:g3322760
A;Experimental source: strain Nichols
C;Genetics:
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A.Note: Sequence extracted from NCBI backbone (NCBIN:98512, NCBIP:98520)
C.Superfamily: papain
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Pred. No. 6.4;
2; Mismatches
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Pred. No. 38;
0; Mismatches
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38;
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87.58;
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60.0%;
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Best Local Similarity 87.37
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Best Local Similarity 60.07
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A;Molecule type: mRNA
A;Residues: 1-341 <PRA>
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C;Keywords: chloroplast
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FLLLVELDER 26
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140 YTLLIRLD 147
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Search completed: February 7, 2000, 11:54:26 Job time: 24336 sec
                                    Query Match
Best Local Similarity 66.7
احداث 6: Conservative
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A; Molecule type: DNA
A; Residues: 1-157 < KAW>
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17 YNQLLRLDE 25
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C; Species: Streptomyces hygroscopicus
C; Species: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jul-1997
C; Accession: S2566
R; Hidaka, T :; Hidaka, M : Uozumi, T :; Seto, H.
Mol. Gen. Genet. 233, 476-478, 1992
A; Title: Nucleotide sequence of a carboxyphosphonoenolpyruvate phosphonomutase gene isol
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MUID:98295987
A; Accession: F70548
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-554 <COL>
A; Coss-references: GB:295589; GB:AL123456; NID:93261781; PID:e316800; PID:92114017
A; Experimental source: strain H37Rv
C; Genetics:
A; Genetics:
A; Superfamily: menD protein
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C:Species: Mycobacterium tuberculosis
C:Date: 17-Un-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Date: 17-Un-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Date: 17-Un-1998
R:Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. R.; Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Rajandream, M.A.: Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987
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A;Residues: 1-1400 <COL>
A;Cross-references: GB:292669; GB:AL123456; NID:93242271; PID:e1300719; PID:93242273
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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A.Cross-references: strain SF1293
C.Superfamily: enolase
C.Superfamily: enolase
C.Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
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Pred. No. 1.9e+02;
2; Mismatches 0; Indels
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A; Accession: S2566
A; MOJecule type: DNA
A; Residues: 1-30 < HID>
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Best Local Similarity 66.7
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Best Local Similarity 75.0
Matches 6; Conservative
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A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50333.1; PID:e151
A;Experimental source: strain Orsay
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submitted to the EmBL Data Library, July 1999
A;Description: Pyrococcus abyss1 genome sequence: insights into archaeal chromosome
A;Reference number: A75001
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                                                                                                                                                                                                           Species: Pyrococcus abyssi
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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                                                                                                                                                                                         hypothetical protein PAB2372 - Pyrococcus abyssi (strain Orsay)
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Length 30;
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DB 2;
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Score 31; DB 2
Pred. No. 5.8;
1; Mismatches
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32;
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63.3%;
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75.0%;
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Best Local Similarity 75.0
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 8, 2000, 00:59:53; Search time 63.71 Seconds (without alignments) 4.688 Million cell updates/sec

US-08-653-294-15 49 1 YRLLIRLDER 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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minities are united and units a license agreement (See Por Send an email to license agreement (See Por Send an email to license@isb-sib.ch).  EMBL; J03407; AAA3654.1; -  PIR; A28101; TVHURF.  MIM; 602165; -  PRAM; PF00622; SPRY; 1.  PRAM; PF00622; SPRY; 1.  PRAM; PF00643; Zf-B_DOX; 1.  Proto-oncogene; Zinc-finger; Metal-binding; Nuclear protein; DNA-binding; REP-RET ONCOGEN ZITE  ZN-FING 16 56 C3HC4-TYPE.  DOMAIN 96 127 B BOX.  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC3 Secure Match  T, 44; Score 35; DB 1 asset Local Similarity 77.84; Proceed No. 8.3; Astches 1. Mismatches	ט נ	use by non	1-proile	institu	tions as	·· ~	its content is	in no way	>-
or send an email to licensee  EMBL; J03407; AAA36564.1; - PIR; A28101; TVHURF.  MIM; 602165; - PROSTEE: PS00518; ZINC_FINGE PFAM; PF00607; Zf-C3HC4; 1. PFAM; PF00602; SPR; 1. Proto-oncogene; Zinc-finger; Nuclear protein; DNA-binding SITE 315 316 DOMAIN 96 25 SEQUENCE 513 AA; 58489 MW Suery Match 7: Conservative 77.4%;	ט כ	Potities red	IIII TPS B	1 tense	agreemen1	<u>.</u> ه د	baye by and lot	h/announce	٠.
EMBL; J03407; AAA36564.1; - PIR; A28101; TVHURE. MIM; 602165; MIM; 602165; PROSITE: PS00618; ZINC_FINGER_C3HC4; 1. PFAM; PF00607; Zf-C3HC4; 1. PFAM; PF00607; Zf-C3HC4; 1. PFAM; PF00607; Zf-C3HC4; 1. PFAM; PF00607; Zf-B.Dox; 1. Proto-oncogene; Zinc_finger; Metal-binding; Chromosomal translocation; Nuclear protein; DNA-binding. SITE RFP-RET ONCOGENE. ZN_FING 16 56 C3H44-TYPE. DOMAIN 96 127 B BOX. SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32; SEQUENCE 513 AA; F8489 MW; 022BC859 CRC32; AATChes 7: Conservative 1. Mismarches 1. Indels 0. Gans 1. Indels 1. Indels 0. Gans 1. Indels 1.	ט	or send an e	mail to	license	isb-sib.	zh).			
PIR: A28101; TVHURE.  MIM: 602165; TVHURE.  MIM: 602165; ZF-C3HC4: 1.  PROSITE: PS00518; ZI-C3HC4: 1.  PROMITE: PS005018; ZI-C3HC4: 1.  PRAM: PF00602; SPRY: 1.  PFAM: PF006022; SPRY: 1.  PFAM: PF006022; SPRY: 1.  PRAM: PF006022; SPRY: 1.  PRAM: PF006022; SPRY: 1.  PFAM: PF00602	r)								
PIR: AZB101; TVHORF.  MIM: 602165;  PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.  PRAM: PF00062; SPRY: 1.  PFAM: PF006043; Zf-B_DOx; 1.  PRAM: PF00643; Zf-B_Dox; 1.  PRAM: PF00643; Zf-B_Dox; 1.  PRAM: PF00643; Zf-B_Dox; 1.  Protco-oncogene: Zinc-finger: Metal-binding; Chromosomal translocation; Nuclear protein; DNA-binding. BREAKPOINT FOR TRANSLOCATION TO FORM THE SITE 315 The C3H44-TYPE.  ZN_FING 16 56 C3H44-TYPE.  DOMNIN 96 127 B BOX.  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  ABSEL Local Similarity 77.8%; Score 35; DB 1; Length 513;  MATCHA ASSACRATION OF GADS	<b>64</b> 1	EMBL; J03407	; AAA365	64.1;					
PROSITE: PSO(0518; ZINC_FINGER_C3HC4; 1. PRAM; PF00097; Zf-C3HC4; 1. PFAM; PF000623; SFRY; 1. PFAM; PF00623; SFRY; 1. PFAM; PF00623; Zf-E_box; 1. Proto-oncogene: Zinc-finger; Metal-binding; Chromosomal translocation; Nuclear protein; DNA-binding. BREAKPOINT FOR TRANSLOCATION TO FORM THE ZN_FING 16 56 C3HC4 TYPE.  ZN_FING 16 56 C3HC4 TYPE. DOWNIN 96 127 SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32; SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32; ALTIGN 18 17 17 18 18 50 18 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	oc o	PIR; A28101; MTM: 602165:	TVHURE.						
PEAM; PF00622; SPRY; 1. PFAM; PF00622; SPRY; 1. PFAM; PF00622; SPRY; 1. PFAM; PF00622; SPRY; 1. Profice of the state of th	4 A		10518. 913	INTO UN	י איטחניי פ	-			
PFAM; PF00622; SPRY; 1. PFAM; PF00643; zf-B_box; 1. Proto-oncogene; Zinc-finger; Metal-binding; Chromosomal translocation; Nuclear protein; DNA-binding: Chromosomal translocation; Nuclear protein; DNA-binding: BREAKPOINT FOR TRANSLOCATION TO FORM THE REP-RET ONCOGENE.  ZN.FING 16 56 C3HG4-TYPE. DOMAIN 96 127 B BOX. SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32; SEQUENCE 513 AA; 71.4%; Score 35; DB 1; Length 513; Match 7. Conservative 1 Mismatches 1 Tidels 0: Gans	4 04	PEC	7: zf-C3	304: 1.	, *) uc) _v				
PFAM, PF00643; Zf-B_box; 1.  Proto-oncogene; Zinc-finger: Metal-binding; Chromosomal translocation; Nuclear protein, DNA-binding BREAKPOINT FOR TRANSLOCATION TO FORM THE SITE 316 REP-RET ONCOGENE.  ZN_FING 16 C3HC4-TYPE.  DOMAIN 96 127 B BOX.  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  SUBJECT ONCOGENE SITE STANSING STANSING SEGURATION TO FORM THE REP-RET ONCOGENE.  AND SEGURATION TO STANSING STANSING SEGURATION TO FORM THE STANSING SEGURATION TO FORM THE STANSING SEGURATION TO STANSING SEGURATION SEGURA	ω.								
Proto-oncogene; Zinc-finger; Metal-binding; Chromosomal translocation; Nuclear protein, DNA-binding.  SITE 315 BREAKPOINT FOR TRANSLOCATION TO FORM THE ZN_FING 16 C3HC4-TYPE.  ZN_FING 16 C3HC4-TYPE.  DOMAIN 96 127  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  Query Match 71.4%; Score 35; DB 1; Length 513; A4thches 7: Conservative 1: Mismatches 1: Indials 0: Gans	· ~			box; 1.					
Nuclear protein; DNA-binding.  SITE 315 316 BREAKPOINT FOR TRANSLOCATION TO FORM THE REP-RET ONCOGENE.  ZN_FING 16 56 C3HC4-TYPE.  DOMAIN 96 127 B BOX.  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  DUETY MATCh 71.4%; Score 35; DB 1; Length 513; AA+Choc 7: Concervative 1 Mismatches 1 Tidels 0: Gans	3	Proto-oncode	ne; Zinc	-finger;	Metal-b	Inding; Ch		cation;	
SITE 315 316 BREAKPOINT FOR TRANSLOCATION TO FORM THE REP-RET ONCOGENE.  ZN.FING 16 56 C3404-TYPE.  DOMAIN 96 127 B BOX.  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  Query Match 71.4%; Score 35; DB 1; Length 513; A4thches 7: Conservative 1 Mismatches 1 Indials 0: Gans	3	Nuclear prot	ein; DNA	-binding					
ZN_FING 16 56 C3HC4-TYPE.  DOMAIN 96 127 B BOX.  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  Query Match  71.4%; Score 35; DB 1; Length 513;  Atches 7: Conservative 1: Mismatches 1: Indels 0: Gans	E	SITE	315 3.	16	BREAKPO				
ZN_FING 16 56 C34C4-TYPE.  DOMAIN 96 127  SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  Query Match 71.4%; Score 35; DB 1; Length 513;  Atches 7. Conservative 1. Missiphes 1. Indels 0: Gans	E⊢⊥			,	RFP-RET	ONCOGENE.			
DOMAIN 30 12/ B DOA. SEQUENCE 513 AA; 58489 MW; 022BC859 CRC32;  Usery Match 71.4%; Score 35; DB 1; Length 513;  Abest Local Similarity 77.8%; Pred. No. 8.3;  Matches 7. Conservative 1 Mismatches 1 Indels 0: Gans	<b>E</b> ⊣ E	ZN_FING		26	C3HC4 - T	(PE.			
SEQUENCE 513 AA; 58489 MW; 0228C859 CRC32;  Usery Match 71.4%; Score 35; DB 1; Length 513;  Best Local Similarity 77.8%; Pred. No. 81.3;  Matches 7. Conservative 1. Mismatches 1. Indels 0. Gans	<u>.</u>	!	<b>⊤</b>	/7	10				
71.4%; Score 35; DB 1; Length 513; Similarity 77.8%; Pred. No. 81.3; 7. Concervative 1: Mismatches 1: Indels 0: Gans	α		ξ	58489 MW	••	359 CRC32;		•	
Car Similaricy //.os, rick. NO. 0.3, 7. Conservative 1. Mismatches 1. Indels 0: Gans	000	ery Match		71.48;	Score 3:	DB	Length 513;		
TOTAL VELLAGE TO MISHIGH COMPANY OF COMPANY	M M	Cal Silli	ĕ	, 0	l: Misma		1: Indels 0:	Gaps 0:	

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-1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                    65.3%;
50.0%;
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                           STANDARD;
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Best Local Similarity :
                                                                                                                                                                                          1 YRLLIRLDER 10
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49 YRLIVRLSNK 58
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Q95156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                 -:- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
-:- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-:- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                           STRAIN-C57BL/6;
MEDLINE; 97176437.
CAO T., SHANNON M., HANDEL M.A., ETKIN L.D.;
"Mouse ret finger protein (rfp) proto-oncogene is expressed at specific stages of mouse spermatogenesis.";
Dev. Genet. 19:309-320(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 1; Length 522;
                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-SILK GLAND;
YANG C.S., SEHNALF;
Submitted (UNN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              BOX.
18E6E716 CRC32;
                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S RIBOSOWAL PROTEIN L5.
                            522 AA.
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1; Mismatches
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77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
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207 YRLLARLEE 215
                                                                                                                                   SEQUENCE FROM N.A.
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076190;
                  RFP_MOUSE
ID RFP_MOUSE
AC Q62158;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                            EMBL; AF008229; AAC24960.1; -.
PFAM; PF00861; Rlbosomal_L18p; 1.
Rlbosomal protein; FRNA-blnding.
SEQUENCE 299 AA; 34378 WW; 7262D2FC CRC32;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0LFACTORY RECEPTOR-LIKE PROTEIN OLF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 AA.
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240 3
39079 MW;
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Cytoskeleton; Structural prot
DOMAIN 25 347
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                                                                                   STANDARD;
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Best Local Similarity
Matches 6; Conserv
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78 YRSLMRISER 87
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  LLIRLDER 10
               RESULT 6
CYL2_HUMAN
ID CYL2_HUMAN
AC Q14093;
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            DB 1; Length 317;
21;
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Pred. No. 21;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                Indels
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EXTRACELLUAR (POTENTIAL).
5 (POTENTIAL).
CXTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                         POTENTIAL.
C16156EE CRC32;
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                                                                                                                                                                                                                            01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0LFACTORY RECEPTOR-LIKE PROTEIN OLF3.
                                                                       Score 32; DB
Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                        317 AA
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E; PS00237; G_PROTEIN_RECEPTOR; 1.
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ilarity 87.5%;
Conservative (
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Best Local Similarity 87.5%;
Matches 7; Conservative 0
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273 292
293 317
5 5 5
317 AA; 35238 M
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                                                                                                                                                                                                        STANDARD;
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317 AA;
                                                                       Query Match
Best Local Similarity
                                                                                                                    3 LLIRLDER 10
                                                                                                                                            47 LLIRLDSR 54
                                                                                                                                                                                                       OLF3_HUMAN
Q13607;
 TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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                         CARBOHYD
                                   SEQUENCE
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                                                                                                                                                                               RESULT 5
OLF3_HUMAN
                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-TESTIS;
MEDLINE; 92255491.
HESS H., HEID H., ZIMBELMANN R., FRANKE W.W.;
The protein complexity of the cytoskeleton of bovine and human sperm heads: the identification and characterization of cylicin II.*;
Exp. Cell Res. 218:174-182(1995).
-! FUNCTION: POSSIBLE ARCHITECTURAL ROLE DURING SPERMATOGENESIS. MAY BE INVOLVED IN SPERMATID DIFFERENTIATION.
-! SUBCELLULAR LOCATION: CALYX; SPERM HEAD CYTOSKELETAL STRUCTURE.
-! TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structural protein; Repeat; Sperm; Spermatogenesis. 5 347 31 X 3 AA REPEATS OF K-K-X. 7 240 3 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEH8_YEAST

YEH8_YEAST

ID YFH8_YEAST

A P4359;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last nnotation update)

DT 01-NOV-1995 (Rel. 32, Last nnotation update)
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                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).
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348 AA.
      PRT;
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STRAIN-S288C / AB972;
MEDLINE; 95400292.
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STRAIN-S288C;
MEDLINE; 95274317
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P40341;
                                                             GIDA_COXBU
P94613;
                                              GIDA_COXBU
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-G3;
CORNEL A.J., KUMAR V., MUKABAYIRE O., SALAZAR RAFFERTY C.,
PETRARCA V., COLUZIZI M., COLLINS F.H.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M., SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K., YAMAZAKI M., TASHIRO H., EKI T.; "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                    Score 31; DB 1; Length 221; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                       POLY-GLN.
3D34764A CRC32;
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PFAM; PF00861; Ribosomal_L18p; 1.
Ribosomal protein; FRNA-binding.
Ribosomal 327 AA; 37996 WW; F3A3BED2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S RIBOSOMAL PROTEIN L5.
                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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221 AA; 25915 MW;
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                                                                                                                                                                                                                                                                                                                    63.3%;
85.7%;
                                                              Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995)
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.3
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                          Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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49 FRLIVRLSNR 58
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211 YRLLLRL 217
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044248;
                                                                                                                                                                                                                                                                          SEQUENCE
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RL5_ANOGA
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    STERRARAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-COT-1996 (Rel. 34, Last sequence update)
01-COT-1996 (Rel. 34, Last sequence update)
01-COT-1996 (Rel. 34, Last annotation update)
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCAI
(EC 3.4.24.-) (TAT-BINDING HOMOLOG 12).
RCA1 OR YMR089C OR YMS982.14C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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TZAGCLOFF A., YUE J., JANG J., PAUL M.F.;
A new member of a family of ATPases is essential for assembly c
mitochondrial respiratory chain and ATP synthetase complexes in
Saccharomyces cerevisiae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.3%; Score 31; DB 1; Length 627; 75.0%; Pred. No. 70; 1; Mismatches 1; Indels
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SCHNALL R., MANNHAUPT G., STUCKA R., TAUER R., EHNLE S.,
SCHWARZLOSE C., VETTER I., FELDMANN H.;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-NINE MILE PHASE I;
WILLEMS H., JAEGER C.;
SUbmitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NOT KNOWN.
-!- SIMILARITY: BELONGS TO THE GIDA FAMILY.
                                                                                                                                                                     Coxiella burnetii.
Bacteria; Proteobacteria; gamma subdivision; Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y10436; CAA71459.1; -.
PROSITE; PS01280; GIDA_1; 1.
PROSITE; PS01281; GIDA_2; 1.
PROSITE; GIDA1; 1.
SEQUENCE 627 AA; 69951 MW; B9AF4071 CRC32;
                                                                  ul-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GLUCOSE INHIBITED DIVISION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 AA.
627 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                           SEQUENCE FROM N.A.
MEDLINE; 97470991.
MEDLINE; 97470991.
WOODAGE T., BASENAI M.A., BAXEVANIS A.D., HIETER P., COLLINS F.S.;
"Characterization of the CHD family of proteins ";
Proc. Natl. Acad. Sci. U.S.A. 94:11472-11477(1997).
-!- FUNCTION: SEQUENCE-SELECTIVE DNA-BINDING PROTEIN. COULD PLAY A IMPORTANT ROLE IN GENE REGULATION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
-!- SIMILARITY: CONTAINS 2 'CHROMO' DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Nuclear protein; DNA-binding; Helicase;
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   AAD54, ACE1/CUP2, PMR1, RCK1, AMS1 and CAL1/CDC43.";
east 11:1413-1419(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLU.
POLY-SER.
POLY-GLU.
POLY-GLU.
ATP (POTENTIAL).
DEAQ BOX.
MW; 8149887E CRC32;
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Pred. No. 1.7e+02;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1709 AA
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                                                                                                                                                                                                                                                                                                                                                  EMBL; Z48618; CAA88537.1; -. EMBL; Z72672; CAA96861.1; -. EMBL; X99960; CAA68224.1; -. PFRAM; PF00176; SNF2_N; 1. PFAM; PF00271; helicase_C; 1.
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.30,
hea 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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| 1420 YRLLVRGTIEER 1431
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259 26
300 30
568 57
675 68
731 73
841 84
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014646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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CHD1_HUMAN
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ATP-binding; Mitochondrion; Transmembrane; Hydrolase; Metalloprotease;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JAMES C.M., INDGE K.J., OLIVER S.G.; "DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosome VII reveals 19 open reading frames including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi: Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
putative ATPases with high similarity to constituents of the 26S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
DV -> EL (IN REF. 2).
I -> V (IN REF. 1).
I -> V (IN REF. 1).
MW; 69EBD054 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 171.5 KD HELICASE IN NUT1-AROZ INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 825; 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1489 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U09358; AAA62606.1; -.
EMBL; X21068; CAA56955.1; -.
EMBL; A24959; CAA89236.1; -.
SGD; L0002564; YTA12.
PROSTITE; PS00674; AAA; 1.
PFAM; PF01434; Peptidase_M41; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614
617
350
653
93276 1
                               east 10:1141-1155(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 63.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                          METALLOPROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
653
825 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 96158061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111 || | |
36 YRLLNRLQE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLLIRLDE 9
                  complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
YGPO_YEAST
ID YGPO_YEAST
AC P53115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
METAL
                  protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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ð g RRIENER RRIENE

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Gaps

5

Length 1489; Indels Ā

us-08-653-294-15.rsp

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AN EDULNE: 93211972.

RA DELLMAS V, STOKES D.G., PERRY R.P.;

RA DELLMAS V, STOKES D.G., PERRY R.P.;

RA DELLMAS V, STOKES D.G., PERRY R.P.;

RT SN2/5W12-11ke helicase domain.";

RT SN2/5W12-11ke helicase domain.";

RT SN2/5W12-11ke helicase domain.";

RL PAROC. Natl. Acad. Sci. U.S.A. 90:2414-2418 (1993).

CC -!- FUNCTION: SEQUENCE-SELECTIVE DNA-BINDING PROTEIN. COULD PLAY AN CC - SUBCELLULAR LOCATION: NUCLEAR.

CC -!- TISSUE SPECIFICITY: ABUNDANCE IS HIGHER IN CELLS REPRESENTING

CC -!- TISSUE SPECIFICITY: ABUNDANCE IS HIGHER IN CELLS REPRESENTING

CC -!- TISSUE SPECIFICITY: ABUNDANCE IS HIGHER IN CELLS.

CC -!- TISSUE SPECIFICITY: CONTRINE PLASMACYTES OR OTHER CELL

CC -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.

CC -!- SIMILARITY: CONTRINS 2 'CHROMO' DOMAINS.

CC -!- SIMILARITY: CONTRINS 2 'CHROMO' DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                              DNA-binding; ATP-binding; Helicase; Nuclear protein; Repeat.

DOMAIN 1 70 SER-RICH.

SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 1; Length 1709;
Pred. No. 2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             AA REPEATS OF H-S-D-H-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHROMODARIN HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).
CHD1 OR CHD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC7F932A CRC32
                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).
DEAH BOX.
3 X 5 AA REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1711 AA
                                                                                                                                                                                                                                                                                                                                        CHROMO DOMAIN.
CHROMO DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196517 MW;
                                                                                                                                                                           MIM: 00.1110,
PROSITE; PS500598; CHROMO_1; 2.
PROSITE; PS50013; CHROMO_2; 2.
PFAM: PF00177; SNPZ_N; 1.
PFAM: PF000771; helicase_C; 1.
PFAM: PF00385; Chromo; 2.
                                                                                                                               EMBL; AF006513; AAB87381.1; -. HSSP; P23197; 1AP0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       795 KLLIRLRER 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RLLIRLDER 10
                                                                                                                                                                    602118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHD1_MO
P40201;
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                           ö
                                                                                                                     Nuclear protein; Repeat
                                                                                                                                                                                                                                                                   Length 1711;
                                                                                                                                                                                             X 5 AA REPEATS OF H-S-D-H-R.
                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                      CB184D33 CRC32;
                                                                                                                                                                                                                                                                    Score 31; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
STAGE O SPORULATION REGULATORY PROTEIN.
                                                                                                                                                                         ATP (POTENTIAL).
DEAH BOX.
                                                                                                                                                                                                                                                                                                                                                                                        85 AA.
                                                                                                                                                    CHROMO DOMAIN.
                                                                                                                                                                                                                                                                                            Mismatches
send an email to license@isb-sib.ch)
                                                                                                              DNA-binding; Helicase; Nu DOMALN 1 70 SER-RICH.
                                                                                                                                                                                                                          1645
3.
196409 MW;
                                                                                   PFAM; PF00176; SNF2_N; 1.
PFAM; PF00271; helicase_C; 1.
PFAM; PF00385; chromo; 2.
                    EMBL; L10410; AAB08486.1; -.
                                                              PROSITE; PS00598; CHROMO_1;
PROSITE; PS50013; CHROMO_2;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y00526; CAA68583.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                               PIR; A47392; A47392.
HSSP; P23197; 1AP0.
MGD; MGI:88393; CHD1
                                                                                                                                                                                                                                                                                                                                    793 KLLIRLRER 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
                                                                                                                                                                                                                                                                                                               2 RLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                             SPOE_BACSU
ID SPOE_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168
                                                                                                                                                                                                                              REPEAT
SEQUENCE
                                                                                                                                                               DOMAIN
NP_BIND
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE; 92024080.
PALM P., SCHLEPER C., GRAMPP B., YEATS S., MCWILLIAM P., REITER W-.D.,
ZILLIG W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
HYPOTHETICAL 11.2 KD PROTEIN (ORF E-96).
Sulfolobus virus-like particle SSV1.
Viruses; dsDNA viruses, no RNA stage; Fuselloviridae; Fusellovirus.
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                                                                                                                                                                                                                                                Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 96;
                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of the virus SSV1 of the archaebacterium Sulfolobus shibatae."; Virology 185:242-250(1991).
                                                                                                                                                                                                                                            61.2%; Score 30; DB 1;
55.6%; Pred. No. 14;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 1;
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S03219; S03219.
Hypothetical protein.
SEQUENCE 96 AA; 11176 MW; D351EB9B CRC32;
EMBL; 299111; CAB13237.1; -.
PIR; S03746; S03746.
SUBTILIST: B010769; SPODE.
SPOTULIALID: BTANSCRIPTION requiation.
SEQUENCE 85 AA; 9791 MW; E2B23676 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 55.6 Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                      2 RLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                              |||::||:
| RLLVSIDEK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRLLIRLDE 9
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7112_SSV1
7112_SSV1
7112_SSV1
7112_SSV1
7112_SSV1
71 01-FEB
71 01-FEB
71 01-FEB
72 02 VILVES
73 NIFOLIN
74 MEDLIN
75 MEDLIN
76 MEDLIN
77 "Compl
78 AEAD
78 A
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SQ
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Search completed: February 8, 2000, 00:59:54 Job time: 3783 sec

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| AQ128909 HS_3028_B2_C12_MR (
| AQ843768 LMAJFV1_lm02c05.x3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="maxb0017Al4r"
/clone=lib="CUGI Rice Blast BAC Library"
/tlssue_type="Protoplasts"
/lab_host="E. coli DH108"
/host="E. coli DH108"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
/note="Vector: pBACWICH; Site_1: His accompacted with a haploid genome (") of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide enalysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

are available upon request."

1 others
                                                                                                                                        seq_documentation_block:
LOCUS A0324186 784 bp DNA GSS 08-JAN-1999
DEFINITION mgxb0017A14r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0017A14r, genomic survey sequence.
                                                                                                                                                                                                                                                                                                     Magnaporthe grisea.
Magnaporthe grisea
Magnaporthe grisea
Magnaporthe grisea
Magnaporthe grisea

1 (bases 1 to 784)

Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
110: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 784
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Gaps: 0
Percent Identity: 60.000
  380
390
416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
229.00
235.90
253.97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 95
High quality sequence stop: 334.
Location/Qualifiers
1.784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlaIleArgLeuAspGluArg
128.05
127.82
127.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="70-15
                                                                                                                                                                                                                                                        AQ324186.1 GI:4116038
GSS.
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US-08-653-294-13 x AQ324186/rev
34.00
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Unpublished (1998)
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dean RA
                                                                                              seq_name: gb_gss11:AQ324186
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D7550 CELKOSH2F Yuji Kohara u
D7572 CELKI06H2F Yuji Kohara u
D7572 CELKI06H2F Yuji Kohara u
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C451274 AV19322 Yuji Kohara unpul
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C458B6 C466B6 Yuji Kohara unpul
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AV1934B1 SMPCASO19SK Brugia ma
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A0331915 HS_2002_A2_D11_SP6E RF
AV199109 AV189169 Yuji Kohara u
C73120 C73120 Rice panicle at A
AV199109 AV189169 Mouse unferti
A0331915 HS_2002_A2_D11_SP6E RF
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A034280 HS_3000_B1_S000_A1
AV300501 AV390501 Chlamydomonas
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AU081869 AV201748 Wuji Kohara u
AV3021049 PRCIII-1-659:IV Rohara unpub
C63035 C63035 Yuji Kohara unpub
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                                                                                              Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Query length: 10
Database: EST:*
Database sequences: 4538634
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Shizuoka 411, Japan

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seq_documentation_block:
LOCUS D73590
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D75467 135 bp mRNA EST 18-OCT-1999
ELKIU04H2F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone ykl04h2 5', mRNA sequence. D75467
                                                                                                         Caenorhabditis elegans.
Caenorhabditis elegans
Sukaryotas, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidas
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 335)
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
                                                                                                                                                                                                    Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
Tabara,H.
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CELK051H2F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yK51h2 5', mRNA sequence.
D73508
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On Apr 14, 1993 this sequence version replaced gi:785918. Contact: Yuli Rohara Gene Library Lab National Institute of Genetics
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Percent Identity: 70.000
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Contact: Yuji Kohara
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 360) (Cohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
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Toward an expression map of the C elegans genome Unpublished (1994)
On Apr 14, 1993 this sequence version replaced gi:837454.
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                    2 others
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National Institute of Genetics
National Institute of Genetics
Tata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6855
Email: ykoharaelab.nig.ac.jp
Insert Length: 743 Std Error: 0.00
High quality sequence stop: 257.
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Yata 1111, Mishima, Shizuoka 411, J
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp
Email: ykohara@lab.nig.ac.jp
Ensert Length: 2140 Std Error: 0.
High quality sequence stop: 258.
Location/Qualifiers
                                                                                                                                                                                                                                                                         /clone="yk51h2"
/clone_lib="Yuji Kohara
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                                                                                                                                                                                                                                                                                                                       hermaphrodite embryo"/sex="hermaphrodite"
                                                                                                                                                                                                                      /strain="N2"
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88 c 83 q
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87 c 84 g
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US-08-653-294-13 x D73508
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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Elegans
Elegans
Elegans
Rhabditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Elegans 1, Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
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LOCUS

LOCUS

D75727

360 bp mRNA

DEFINITION CELKI09D2F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk109d2 5', mRNA sequence.
ACCESSION

D75727
                  D75423 360 bp mRNA EST 18-OCT-1999 CELK104C7F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone ykl04c7 5', mRNA sequence.
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
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                                                                                                                                                                                                                                                                              Tabara, H. Toward an expression map of the C.elegans genome
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Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ykohara@lab.nig.ac.jp
Insert Length: 1013 Std Error: 0.00
High quality sequence stop: 120.
Location/Qualifiers
1. 360
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hermaphrodite embryo"
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4.111 Gaps: 0
90.000 Percent Identity: 70.000
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Context: Yul Kohara
Gene Library Lab
National Institute of Genetics
Yata Ill, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Caenorhabditis elegans.
Caenorhabditis elegans
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US-08-653-294-13 x D75423
seq_documentation_block:
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Ratio:
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota: Metazoa: Nematoda: Secernentea: Rhabditia; Rhabditida;
Rhabditina: Rhabditoidea: Rhabditidae; Peloderinae; Caenorhabditis:
Caess I to 360)
Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS
D14728
360 bp mRNA
DEFINITION CELK084F3F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk84f3 5', mRNA sequence.
ACCESSION D74728.1 GI:1120512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uppublished (1994)
On Sep 21, 1992 this sequence version replaced gi:276173.
Contact: Yuji Kohara
Contact: Yuji Kohara
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp
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/organism="Caenorhabditis elegans"
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Percent Similarity: 90.000
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US-08-653-294-13 x D73590
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US-08-653-294-13 x D74728
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                                        alignment_scores:
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ACCESSION VERSION KEYWORDS

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

seq\_name: gb\_est5:D75423

BASE COUNT ORIGIN

CDNA:Strain N2

5 others

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seq_documentation_block:
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Caenorhabditis elegans
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Caenorhabditis elegans
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Rhazdaris Rhazdaris Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
1 (bases 1 to 360)
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6 
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LOCUS C40575 360 bp mRNA EST 18-OCT-1999
DEFINITION C40575 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk246c11 5', mRNA sequence.
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Gaps: 0
Percent Identity: 70.000

    .360
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Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp
Insert Length: 1157 Std Error: 0.00.
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Yata 111, Mishima, Shizuoka 411, Japan
111, 11-559-81-6854
Fax: 81-559-81-6855
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/sex="hermaphrodite"
/dev_stage="embryo"
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Location/Qualifiers
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Caenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans

Bukaryota, Metazoa, Nematoda, Secernentea, Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

(bases 1 to 360)

Roharary., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,

Sano,M., Miyata,A. and Nishigaki,A.

Expression map of the C.elegans genome

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1400867.
                                                                                                                                                                                                                                                                                                                   C42212 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo C42212 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo caenorhabditis elegans cDNA clone yk290di0 5', mRNA sequence. C42212.1 G1:2378449
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  Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. 360
/organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Library Lab
National Institute of Genetics
Yata Ill1, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Length:
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                                                                                                                                                   to: 360
                                                                                                                                                                                        /dev_stage="embryo'
90 c 82 q
                                                                                                                                              Align seg 1/1 to: C40575 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: C42212 from: 1
                         4.111
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Percent Similarity: 90.000
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US-08-653-294-13 x C40575
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US-08-653-294-13 x C42212
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LOCUS C42212
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Ratio:
Percent Similarity:
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Quality:
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alignment_scores:
                                                                                                      source
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ORIGIN
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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                                                                               FEATURES
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                                                                                                            Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rabditoidea: Rabditidae; Peloderinae; Caenorhabditis.
1 (bases I to 360)
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
On May 8, 1999 this sequence version replaced gi:801522.
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans

Bukaryota, Metazoa, Nematoda, Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

(bases 1 to 360)

Roharary. Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,

Expression map of the C.elegans genome

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1395322.
C44981 360 bp mRNA EST 18-OCT-1999 C44981 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk373f5 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS C51139
DEFINITION C51139 Yuji Kohara unpublished CDNA:Strain N2 hermaphrodite embryo
Caenorhabditis elegans CDNA clone yk491f7 5', mRNA sequence.
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hermaphrodite embryo"
/sex="hermaphrodite"
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4.111 Gaps: 0
90.000 Percent Identity: 70.000

    360
/organism="Caenorhabditis elegans"

                                                                                                                                                                                                                                                                                                                          Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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National Institute of Genetics
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95 c 79 g
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                                                             C44981
C44981.1 GI:2381218
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C51139.1 GI:2388392
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US-08-653-294-13 x C44981
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Ratio:
Percent Similarity:
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                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  LOCUS
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JOURNAL
COMMENT
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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Caenorhabditis elegans.

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa: Nematoda: Secernentea: Rhabditia; Rhabditina;

Rhabditina; Rhabditoidea; Fabditidae; Peloderinae; Caenorhabditis.

Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Nomoto,H.
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/dev_stage="embryo"
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Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unit is this sequence version replaced gi:3247424.
Contact: Yull Kohara
Gene Library Lab
National Institute of Genetics
National Institute of Genetics
Teta 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                      others
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Gaps: 0
Percent Identity: 70.000
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Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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Location/Qualifiers
                                                                     Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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4.111
90.000
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US-08-653-294-13 x C51139
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Ratio: Percent Similarity:

Align seg 1/1

Quality:

alignment\_scores:

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Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditina; Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 360)
Roharary., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Nomoto,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.
AV193922 AV11 Kohara unpublished CDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans CDNA clone yk623b7 5', mRNA sequence.
                                                                                                                   Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditoidea; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.
1 (bases 1 to 360)
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/dev_stage="embryo"
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                                                                                                                                                                                                                                                                                                         Expressed genes in C.elegans upublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948755.
Contact: Yuli Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                 General Library Lab
National Institute of Genetics
National Institute of Genetics
Tata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykoharaelab.nig.ac.jp.
Location/Qualifiers
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Caenorhabditis elegans
                                                                                AV193922.1 GI:5576074
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Ratio: 4.111
Percent Similarity: 90.000
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US-08-653-294-13 x AV193922
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                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
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    LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
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AUTHORS
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV192774 7011 Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk609e10 5', mRNA
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Unpublished (1999)
On Feb 18, 1999 this sequence version replaced gi:4299301.
Contact: Yuli Kohara
  Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
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National Institute of Genetics
Yata Ill1, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                             from: 1
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                                                                                                                                         to: AV192603
                           4.111
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US-08-653-294-13 x AV192603
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US-08-653-294-13 x AV192774
                                                                                                                                                                                                                                                                 seq_name: gb_est36:AV192774
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Quality:
Ratio:
Percent Similarity:

alignment\_scores:

107

BASE COUNT

source

FEATURES

TITLE JOURNAL COMMENT

sequence.

DEFINITION

AV19277

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT On May 9, 1996 this sequence version replaced gi:1132813.
CONTACT: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6834
Fax: 81-559-81-6834
Fax: 81-559-81-6835
FEATURES
Location/Qualifiers
Source
//Strain="N2"
//Clone="lib="Yuji Kohara unpublished cDNA:Strain N2"
//Gex="hermaphrodite embryo"
//Sex="hermaphrodite embryo"
//Sex="hermaphrodite"
//Sex="hermaphrod
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16-SEP-1993.
25-FEB-1993; U01758.
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                                                                                                                                                                                 Homo sapiens
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RESULT
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Immunomodulatory p
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Peptide B2702.75-8
Peptide B2702.75-8
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HLA *B2705. 60-84. C
Sequence of the hu
Sequence encoded b
Peptide fragment o
HLA *B2702. CTL modu
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HLA-B2702.75-84(L)
T-cell modulating
T-cell modulating
Immunomodulatory P
Peptide B2702.75-8
HLA-B2702 CTL modu
Peptide B2702.70-8
HLA-B2702 CTL modu
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HLA-B2702.75-84(D)
T-cell modulating
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Human [Phe74]-HLA-
                                                        (without alignments)
1.933 Million cell updates/sec
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                                                  ; Search time 122.56 Seconds
              Compugen Ltd
                                                                                                                                                  Total number of hits satisfying chosen parameters:
      GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                   188963 seqs, 23686106 residues
                                                                                                                                                                                                                                                          SUMMARIES
                                                 8, 2000, 01:29:38
                                   sw model
                                                                                                                                                                                                summaries
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R83075
R83094
R83096
R95423
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W47267
W33785
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Match Length DB
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                                  protein search,
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Peptide B2702.84-7
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HLA B2702 CTL modulat
HLAB38 CTL modulat
HLAB38.6084. Comps
Peptide B2702.60-8
Peptide B2702.60-8
Sequence of HLA-BW
Sequence of HLA-BW
 W33791
R41205
R48286
R83090
R83093
R95416
R95422
W33794
V058794
R031422
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779.6
779.6
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## ALIGNMENTS

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Gaps
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Claim 10; Page 36; 41pp; English.
The present requence is an immunomodulatory peptide, which
comprises a class I HiA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.
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                                                                                                                    Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1997.
23-ARR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
W47271 standard; peptide; 10
                                                                                 (first entry)
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R41212 standard; peptide; 10 AA.
R41212;
15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic I lymphocyte; modulation.

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standard; peptide; 10 AA.
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R83061-R83085, R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for alimited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CILS)
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                     mew peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 11; page 54; flpp: English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
02-MAR-1992; US-844716.
(STMD) UNIV LELAND STANFORD JUNIOR.
(STADEAGER CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R83075 standard; peptide; 10 AA.
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Best Local Similarity 90.0
Matches 9; Conservative
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WPI; 95-358582/46.
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R83061-R83085, R83090-R83096 and R82907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressent. This is administered to about the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
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R8306-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILs)
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
HIA-B2702 CTL modulating peptide (B2702.75-84(D)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graff versus host disorder; transplantation; therapy;
class I MHC; HIA-B2702.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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Matches 9; Conserv
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WPI; 95-358582/46.
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WPI, 95-358582/46.
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Gaps

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Conservative

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RESULT R83094

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RESULT R95423

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Clayberger C, Krensky AM;

WPI; 95-194027/25.

Clayberger C, Krensky AM;

WPI; 95-194027/25.

WPI; 95-194027/25.

WPI; 95-194027/25.

Comparishing lympholid surface membrane proteins - which may comparishing lympholid surface membrane of CTLs.

Example; Page 11; 29pp; English.

PT inhibit cytolytic activity and differentiation of CTLs.

R95413; and R95413-R95431 represent palindromes and fragments of R95413-R95431 represents the protein R95413-R95431 represents the protein R95413-R95431 represents and inseres can be used to isolate the protein P74 from a T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC10. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of P74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions comprising the amount of binding between the candidate compound and P74.

T-cells, by combining them with the extracellular portion of P74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mid and p74 in an amount sufficient to compete connected to a same connected to a same connected to a same connected to a same composition of P74 in an amount sufficient to compete connected to a same connected to a same and antigen presenting cells (APCS), by adding to the connected to a same connected to a same and antigen presenting cells (APCS), by adding to the connected to a same connected to same connected to a same connected to a same connected to a same connecte
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T-cell modulator; autoimmune disease; tissue destruction; alphal-domain; mammal; major histocompatability complex; MHC class I; antigen; perforin; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease; thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme; autologous target cell; cytokine release; T cell activation; therapy.
      lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Where yes 18410/51.

Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T cell mediated attack on target cells
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                                                                                                                                                                           /note= "N3D mutation"
                                                                                                                                                                                                                                 18-MAX-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                           B cell; calcium influx; cytotoxic T cytolysis; antigen presenting cell. Synthetic.
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W07513 standard; peptide; 10 AA. W07513; 04-AUG-1997 (first entry)
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05-ARY-1996. U04710.
12-MAY-1995: US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
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Matches 9; Conserv
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                                                                                                                                             misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
W07513
      δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promposes. Compprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example: Page 11: 29pp: English.

Example: Page 21: 29pp: English.

CR 89413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the fact human-leucocyte-associated antigens. This sequence represents the mannal and T-cell 19sate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunojodically cross reactive with the heat shock protein HS-70. p74 is found in a limited number of cell types, but is particularly expressed on amphoteric detergent, and then passed through an affinity column contraining a covalently bound HLA-B2702 palindromic peptide.

CC Gompositions comprising the extracellular fragment of p74 combined with the extracellular fragment of p74 combined compounds can be screened for their effect on the cytolysis. Candidate Compounds the amount of binding between the candidate compound and p74.

CC Compounds the composition of p74, induces calcium influx, and inhibits of determining the amount of binding between the candidate compound and p74.

CC Containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the containing the binding of the p74 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1996 (first entry)
HLA-B2705.75-84.
HLA-B2705.75-84.
HLA-B2705.75-84.
The pri alphal-helix; human-leucocyte-associated antigen; inhibitor; r-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell, calcium influx; cytocxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1996 (first entry) '
HLA-B2702.75-84(D).
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                               Score 44; DB 1; Length 10;
Pred. No. 0.0084;
.; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%; Score 44; DB 1; Length 10; 90.0%; Pred. No. 0.0084; ive 0; Mismatches 1; Indels
                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1993; US-150493.
(STRD) UNIV. LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                            R95423 standard; peptide; 10 AA.
R95423;
                                                                                                            89.8%;
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ID R95425 standard; peptide; 10
                                                                                                                                             Best_Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
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of the patient.
Sequence 10 AA;
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                                                                                                                  Query Match
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R95425;

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Matches

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New immunomodulating dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases

Example 1, Page 19; 41pp; English.

Peptides W33784-88 and W33778-9 were assayed for their immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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19-JUN-1998 (first entry)

Immunomodulating activity.

Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; rejection.
                                                                                                                                                                                                                                           1. .10
/note= "at least one of the amino acids is the
                                                                        22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulatory Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 1;
Pred. No. 0.0084;
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22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R, Clayberger C, Krensky AM; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1996; US-651650.
(STAD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplant rejection
Claim 10; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W33785 standard; peptide; 10 AA.
                               Ä.
                             W47269 standard; peptide; 10
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90.08;
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Best Local Similarity 90.0
Matches 9; Conservative
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23-APR-1997; U06705.
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WO9744351-A1.
                                                                                                                                                                                                                                                                                                            WO9744052-A1
                                                                                                                                                                                               Synthetic.
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claim 7; Page 20; 24pp; English.

W07512-W07518 represent T-cell modulating peptides that can be used in the w07512-W07518 represent T-cell modulating peptides that can be used in the w07512-W07518 represent T-cell modulating to residues 70-91 of the alphal-domain of the generic peptide corresponding to residues 70-91 of the alphal-domain of the major histocompatability complex (WHC) class I antigen (see W07510). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple sclerosis, rheumatoid atthitis, psoriasis, pemphigus vulgaris, sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia gravis, etc. The peptides modulate T-cell mediated attack on autologous target cells, and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an immunomodulatory peptide, which comprises a class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmarched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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Pred. No. 0.0084;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 10;
Pred. No. 0.0084;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1996; US-651650.
(STAD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W47267 standard; peptide; 10 AA.
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90.0%;
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90.0%;
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22-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
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RESULT

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RESULT

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Gaps

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1; Indels

Length 10;

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treating autoimmune diseases

Example 1; Page 19; 41pp; English.

Peptides Wa3784-98 and Wa3778-9 were assayed for their immunomodulating cetivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity.

Cctivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or cretivity and creatified forms of up to 60 amino acids, where the peptide-type compound comprises the formula A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 - E or V; aa77 - D, Sor N; aa79 - R or C; aa80 - I or N; aand aa represents amino acid; aa82 - R or L; aa83 - G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets The compounds comprise at any peptide type bond within the brackets or proteins of interest to network the can be used to inhibit cytotoxic T-lymphocytes (CTL) from the bracket or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, resed for detection and diagnosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphcoytes (CTL) from undesirably attacking cells in a host or in vitro They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, inhemmaticid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
  amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Peptide B2702.75-84D77 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI: 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alph-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1; Length 10;
Pred. No. 0.0084;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W33787 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                          89.88;
90.08;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.8
Best Local Similarity 90.0
Matches 9; Conservative
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WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rejection.
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                                                                                                                                                                                                                                                                                                                 Sequence
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PR 27-MAY-1997; U08689.

22-MAY-1997; U08689.

24-MAY-1997; U08689.

24-MAY-1997; U08689.

PR 24-MAY-1997; U08689.

PA STRD ) UNIV LELAND STANFORD JUNIOR.

Beulow R, Clayberger C, Krensky AM;

Beptide-type and W33778-9 were assayed for their immunomodulating activity, including the N-terminal acylated and/or C creminal amidated or esterified forms of up to 60 amino acids, where C c-terminal amidated or esterified forms of up to 60 amino acids, where K, B - C C R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 - E or V; aa77 - C N S or N; aa79 - R or G; aa80 - I or N; aa81, aa81 - E or V; aa77 - C N, S or N; aa79 - R or G; aa80 - I or N; aa81, aa84 - a hydrophobic or c small amino acid sequence in the brackets may optionally be absent or truncated c at any peptide type bond within the brackets. The compounds comprise c amino acid sequence in the brackets may optionally be absent or truncated c at any peptide type bond within the brackets. The compounds comprise c mino acid sequences related to a Class I HlA-B alphal domain (positions Of 9-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to arti-CD3. The peptide can be used for preventing rejection of response to anti-CD3. The peptide can be used for preventing rejection contents of theumatoid arthritis and lupus erythematosis. The products can also be used to retart the antigenic peptides of the products can also be used in condens and luminosis.
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Human HIA-B27 (62-85) antigen derived peptide; cell receptor;
interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                          19-JUN-1998 (first entry)

Peptide B3702.75-84Lb1 tested for immunomodulating activity.

Immunomodulating dimer. immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for detection and diagnosis
W33789 standard; peptide; 10 AA.
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R71442;
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12-AUG-1993; US-105416.
(REGC) UNIV CALIFORNIA.
GOLGSTEIN A, GOOGENOW RS,
WPI: 95-098577/13.
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Best Local Similarity
Matches 9; Conserv
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WO9744351-A1.
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WO9505189-A.
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                                         NAME OF THE PROPERTY OF THE PR
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Gaps

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Score 44; DB 1; Length 10; Pred. No. 0.0084; 0; Mismatches 1; Indels

89.8%;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

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Human [Phe74] HLA-B27-(62-85) antigen derived peptide.
Human [Phe74]-HLA-B27-(65-85) antigen derived peptide; cell receptor; interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                   Example 4; Page 45; 103pp; English. R71439-R71443 are human major histocompatibility complex class 1 (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides. They were used to modulate interactions between MHC 1/HLA and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
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WPI: 95-098577/13.
Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                          89.8%; Score 44; DB 1; Length 17; 90.0%; Pred. No. 0.015; Live 0; Mismatches 1; Indels
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Pred. No. 0.015;
0; Mismatches 1; Indels
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R71443;
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90.0%;
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12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
Goldstein A, Goodenow RS,
                                                                                                                                                                                                                                                                                                          Query Match 89.8
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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R71443
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Search completed: February 8, 2000, 01:29:38 Job time: 1750 sec

We'd Feb

us-08-653-294-14.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 11:54:25 Run on:

Search time 117.7 Seconds (without alignments)
4.008 Million cell updates/sec

US-08-653-294-14 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 REDLRILLRY 10 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

Database :

PIR\_62:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* pir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMM 110 111 112 113 113 113 113 113 113	SUMMARIES	Description	MHC HLA-B27-HS - 1	class I	class I	class I	엄	MHC HLA-B27d - hum	class I	MHC clas	MHC HLA-B38 chain	Н	class I	class I	class I	class I hist	MHC class	MHC class I	MHC class I	class I hist		· class I	MHC class I hi	transmembr	gene HLA B-151	lymphocyte antiq	HLA-Bw57.2 a	MHC class I	. MHC HLA-B tr	class I hist	מירני טמא
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class I histocompa	MHC class I histoc	MHC class I histoc	HLA-AW24 protein -	MHC class I histoc	MHC H-2K transplan	MHC H-2D-k protein	MHC H-2K-w28 prote	hypothetical prote	HLA-B alpha-chain	fructose-bisphosph	fructose-bisphosph			
S03537	D35997	S77963	154416	I54493	HLHU32	137515	A35997	154414	171998	168705	T15113	137516	ADMU	T05052
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36	36	36	36	36	27	362	36	32	36	36	33	35	35	35
9.62	9.62	9.62	9.6	9.64	77.6	77.6	77.6	75.5	75.5	75.5	69.4	69.4	69.4	69.4
68	36	6 8	36	6E	38	38	38	37		37			34	34
31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: 156116
C:Accession: 156116
A:Title: A novel HAA-B27 allele maps B27 allospecificity to the region around position A; Title: A novel HAA-B27 allele maps B27 allospecificity to the region around position A; Accession: 156116
A:Accession: 156116
A:Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule typ
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RESULT 1
156116
MHC HLA-B27-HS - human (fragment)
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Best Local Similarity 90.0
Matches 9; Conservative
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1 REDLRILLRY 10 ||||| |||| 75 REDLRILLRY 84 ò 셤

RESULT

HIAUDE MHC class I histocompatibility antigen HLA-B27 alpha chain precursor - human C;Species: Homo saptens (man) C;Dete: 11-Aug-1986 #sequence\_revision 28-Apr-1995 #text\_change 22-Jun-1999 C;Accession: 807441; A25092; B25092; A94087; S34180; S44942; A90493; B24741; I55965; R;Welss, E.H.; Kuon, W; Doerner, C.; Lang, M.; Riethmueller, G. Immunobiology 170, 367-380, 1985 A;Title: Organization, sequence and expression of the HLA-B27 gene: a molecular appro A;Reference number: 807441; MUID:86138405 A;Reference number: 807441 A;Accession: 807441 A;Residues: 1-362 <WEI> A;Residues: 1-362 <WEI> A;Cross-references: EMBL: 803945 A;Note: the authors translated the codon GAC for residue 61 as Ala and the codon CAG A;Note: the authors translated b\*27052 (formerly 27W) K;Seemann, G.H.A.; Reln, R.S.; Brown, C.S.; Ploegh, H.L. EMBO J. 5, 547-552, 1986 A;Title: Gene conversion-like mechanisms may generate polymorphism in human class I g

A; Accession: A25092

A;Molecule type: DNA A;Residues: 1.362 <SEE> A;Cross-references: GB:X03665; NID:g32250; PIDN:CAA27302.1; PID:g871297 A;Note: this allele is designated B\*27051 (formerly 27W) A;Accession: B25092

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Gaps

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R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A, B cDNA by using the polymerase chain reaction: freque A;Reference number: A35997; MUID:90207291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Zemmour, J.; Ennis, P.D.; Parham, P.; Dupont, B. Immunogenetics 27, 281-287, 1988
A; Title: Comparison of the structure of HLA-Bw47 to HLA-B13 and its relationship A; Reference number: 154442; MUID:88152906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC class I histocompatibility antigen HLA-B37 alpha chain precursor - human C;Species: Homo sapiens (man)
C;Dete: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 23-Jul-1999
C;Accession: C35997
R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Superfamily: class I histocompatibility antigen; immunoglobulin homology <IMM>
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M32320; NID:g187792; PIDN:AAA36233.1; PID:g307224
            F;220-285/Domain: immunoglobulin homology <IMM>
F;308-331/Domain: transmembrane #status predicted <IMM>
F;323-362/Domain: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;115-188,227-283/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                 Score 44; DB 1;
Pred. No. 0.22;
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0.22;
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Pred. No. 0.22;
0; Mismatches
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Pred. No.
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A;Cross-references: GDB:120048; OMIM:142830
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90.0%;
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90.0%;
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ilarity 90.0%;
Conservative
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Best Local Similarity 90.07
المحتادة 9, Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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99 REDLRTLLRY 108
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A;Molecule type: mRNA
A;Residues: 1-362 <ENN>
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Best Local Similarity
Matches 9; Conserv
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A; Molecule type: DNA
A; Residues: 1-100, NY, 102-103, 'IA', 106-362 <SE2>
A; Coss references: GB:X03664; NID:93236; PIDN:GA827301.1; PID:9871296
A; Residues: 1-100, NY, 102-103, 'IA', 106-362 <SE2>
A; Coss references: GB:X03664; NID:93236; PIDN:GA827301.1; PID:9871296
A; Note: this allele is designated B*2702 (formerly 27K)
Froc. Natl. Acad. Sci. U.S.A. 83, 1428-1412; 1986
A; Title: Complete sequence of HLA-B27 cDNA identified through the characterization of st A; Reference number: A94087
A; Molecule type: mRNA
A; Residues: 25-205, V', 207-362 <SZO>
A; Cross references: GB:M12678
A; Molecule type: mRNA
A; Residues: 1205, V', 207-362 <SZO>
A; Cross references: GB:M12678
A; Molecule type: mRNA
A; Reference number: S34180
A; Accession: S34180
A; Accession: S34180
A; Accession: BMBL:X73578
A; Molecule type: mRNA
A; Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A; Cross references: EMBL:X73578
A; Molecule type: mRNA
A; Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A; Cross references: EMBL:X73578
A; Molecule type: mRNA
A; Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A; Cross references: EMBL:A73578
A; Molecule type: mRNA
A; Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A; Cross references: EMBL:A73578
A; Molecule type: mRNA
A; Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A; Cross references: EMBL:A73578
A; Molecule type: mRNA
A; Residues: 1-100, 'S', 102-137, 'D', 139, 'Y', 141-175, 'E', 177-362 <VIL>
A; Cross reference number: A4942
A; Reference number: A4942
A; Accession: S44942
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Gaps

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Length 137

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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 154463
A;Title: Genetics 30, 200-207, 1989
A;Title: Genetics and serological heterogeneity of the supertypic HLA-B locus specific A;Accession: 154463; MUID:89379286
A;Reference number: 154463; MUID:89379286
A;Accession: 154463
A;Accession: 154463
A;Accession: 154463
A;Accession: 154463
A;Accession: 154463
A;Cross-references: GB:M29864; NID:q187674; PIDN:AAA36222.1; PID:g187675
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIC class I histocompatibility antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 13809
C;Accession: I3809
R;Cereb, N.; Chol, J.W.; Rlu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A;Title: HIA-B*5105, a newly identified B51 IEF variant.
A;Reference number: I38509; MUID:95176331
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-137 <RES>
A;Cross-references: EMBL:U05585; NID: 6454787; PIDN: AAA50188.1; PID: 9454788
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-273 <RES>
A;Cross-references: EMBL:U06697; NID:g469544; PIDN:AAA92997.1; PID:g469545
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                             Score 39; DB 2;
Pred. No. 0.82;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2;
Pred. No. 1.7;
1; Mismatches
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Pred. No. 1.7;
1; Mismatches
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MHC HLA-B38 chain - human (fragment)
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Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                             79.6%;
ilarity 80.0%;
Conservative
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80.0%;
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Best Local Similarity
Matches 8; Conserv
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40 RENLRILLRY 49
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74 RENLRIALRY 83
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Best Local Similarity
Matches 8; Conserv
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                                                                                                              human lymphocyte antigen HLA-B27 - human C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: 137485
R:Del Porto, P: D'Amato, M.; Fiorillo, M.T.; Tuosto, L.; Piccolella, E.; Sorrentino, R.J. Immunol. 153, 3093-3100, 1994
J. Immunol. 153, 3093-3100, 1994
A:Title: Identification of a novel HLA-B27 subtype by restriction analysis of a cytotoxi
A:Reference number: 137485; MUID:94375872
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 24 May-1996 #séquence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 180174
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I54289
C:Accession: I54289
R:Choo, S.Y.; St. John, T.; Orr, H.T.; Hansen, J.A.
Hum. Immunol. 21, 209-219, 1988
A:Title: Molecular, analysis of the variant alloantigen HLA-B27d (HLA-B*2703) identifies A:Accession: I54289; MUID:88227491
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1.362 CRES>
A;Cross-references: EMBL:233453; NID:9486652; PIDN:CAA83876.1; PID:9486653
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Pred. No. 0.22;
); Mismatches
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Pred. No. 0.22;
); Mismatches
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90.0%;
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  REDLRILLRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 REDLRILLRY 108
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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Length 274;

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us-08-653-294-14.rpr

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MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA 12.4) C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species: 16.4pr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C; Accession: A02189
R; Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. US.A. 79, 893-897, 1982
A; Fitle: Exon/Antron organization and complete nucleotide sequence of an HLA gene. A; Reference number: A02189; MUID:82151002
                                                                                                                                                                                                                                                                                                                                                                                                           A.L.; Bontrop, R.E.;
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C;Species: Pan troglodytes (chimpanzee)
C;Accession: 180169
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 189308; MuID:94286544
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C;Species: Pan troglodytes (chimpanzee)
C;Accession: 180171
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-355 <RES>
A; Cross-references: EMBL:U05580; NID:9454777; PIDN:AAA50183.1; PID:9454778
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Length 354;
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A;Molecule type: mRNA
A;Residues: 1-355 <RES>
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Pred. No. 2.2;
1; Mismatches
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1; Mismatches
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Score 39;
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R: McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. Us.S., 91, 5893-5897, 1994
A.Title: A uniquely high level of recombination at the HLA-B locus.
A. Reference number: 159308; MuID: 94286544
A. Accession: 159308
A. Accession: 159308
A. Accession: 159308
A. MuiD: 9428654
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: MRNA
A. Residues: 1-354 <- RES
A. Cross references: EMBL: U05575; NID: 9454767; PIDN: AAA50178.1; PID: 9454768
C. Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class I histocompatibility antigen - chimpanzee (fragment)
C.Species: Pan troglodytes (chimpanzee)
C.Species: Pan troglodytes (chimpanzee)
C.Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C.Accession: 180168
R.McAdam, S.N.: Boyson, J.E.; Liu, X.: Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A.Reference number: 159308; MUID: 94286544
A.Reference number: 159308; MUID: 94286544
A.Recession: 180168
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-354 cRES
A.Cocss.references: EMBL: U05579; NID: 9454775; PIDN: AAA50182.1; PID: 9454776
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 2-4 May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: 180167
R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. US.A. 91, 5893-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: 159308; MUID:94286544
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                                                                             class I histocompatibility antigen - pygmy chimpanzee (fragment)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-354 cRES>
A;Cross-references: EMBL:U05578; NID:g454773; PIDN:AAA50181.1; PID:g454774
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A:Accession: A02189
A:Molecule type: DNA
A:Residues: 1-359 cMaL>
C:Comment: The seven exons correspond approximately to the domain structure of this chain c:Genetics:
A:Map position: 6p21.3
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Reywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F:1-21/Domain: signal sequence #status predicted <EXI>
F:22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted
F:22-311/Domain: alpha-1 cEXI>
F:22-111/Domain: alpha-2 cEX2>
F:21-203/Domain: intracellular #status predicted <IMM>
F:305-329/Domain: intracellular #status predicted <IMM>
F:305-329/Domain: intracellular #status predicted <IMM>
F:307/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:224-280/Disulfide bonds: #status predicted
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KS64_CHICK
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                                     Search time 63.71 Seconds (without alignments) 4.688 Million cell updates/sec
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P30481
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P30378
P50611
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                  82229 seqs, 29864866 residues
                                      8, 2000, 00:59:53
                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                  1845_HUMAN
1801_PANTR
1801_GORGO
1802_GORGO
1803_GORGO
1815_HUMAN
1847_HUMAN
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1B29_HUMAN
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1B54_HUMAN
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1B62_HUMAN
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    protein search, using sw model

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Listing first 45
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Maximum DB seq length: 1000000
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SEQUENCE FROM N.A.
MEDLINE; 91268545.
CHOO Y.S., FAN L.A., HANSEN J.A.;
A novel HLA-B27 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain.",
J. Immunol. 147:174-180(1991).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO Gaps P30467; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-APR-1993 (Rel. 25, Last annotation update) HLA\_CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B\*2707 ALPHA CHAIN ; 0 0004472 P73851 P18654 P18653 Q15349 Q15418 P51812 P18652 Q92dx6 P14877 Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. THE IMMUNE SYSTEM. 89.8%; Score 44; DB 1; Length 338; 90.0%; Pred. No. 0.11; 1; Indels EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 33FB8134 CRC32; CYTOPLASMIC TAIL 0; Mismatches ALIGNMENTS rce\_caeel EMBL; M62852; AAA59647.1; -.
HSSP; P03989; 1HSA.
MIM: 142830; -.
PROSITE; P500290; IG\_MHC; 1.
PFAM; PF00047; 1q; 1.
PFAM; PF00129; MHC\_I; 1.
MHC\_I; Transmembrane; Glycoprotein.

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MEDLINE; 92018187.
MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
"The structure of HLA-B27 reveals nonamer self-peptides bound in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 86149317.
SCORTS H., RIETHUBELLER G., WEISS E., MEO T.,
"Complete sequence of HAA-B27 cDNA identified through the
characterization of structural markers unique to the HIA-A, -B, and
                                                                                                                       23-0CT-1986 (Rel. 02, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 85226561.
EZQUERRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
LOPEZ DE CASTRO J.A.;
"Primary structure of papain-solubilized human histocompatibility
antigen HLA-B27.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
MEDLINE; 92405152.
MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
The three-diamensional structure of HLA-B27 at 2.1-A resolution suggests a general mechanism for tight peptide binding to MHC.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        extended conformation.";
Nature 353:31-325(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 86138405.
WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.,;
"Organization, sequence and expression of the HLA-B27 gene: a
molecular approach to analyze HLA and disease associations.";
Immunobiology 170:367-380(1985).
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -C allelic series.";
Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
                                                                  361 AA
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PIR; A25128; HLHUB2.
PIR; S07441.
PDB; 1HSA; 15-OCT-92.
MIM; 142830; ---
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                                                                  STANDARD;
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                                                               1B14_HUMAN
P03989;
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1B14_HUMAN
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PROSITE; PS00290; IG_MHC; 1.

PFAM; PF00047; 19; 1.

PFAM; PF00129; MHC_I; 1.

PFAM; PF00129; MHC_I; 1.

PFAM; PF00129; MHC_I; 1.

PFAM; PF00129; MHC_I; 1.

ACTION SIGNAL 25 361 HLA CLASS I HISTOCOMPATIBILITY CHAIN CHAIN 25 361 HLA CLASS I HISTOCOMPATIBILITY CHAIN C
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Pred. No. 0.12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                          ROGNAN D., SCAPOZZA L., FOLKERS G., DASER A.;
"Rational design of nonnatural peptides as high-affinity ligands for the HIA-B*2705 human leukocyte antigen.";
Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                            SEQUENCE FROM N.A.
MEDLINE; 86220133.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human class I genes.";
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 86138405.
WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
"Organization, sequence and expression of the HLA-B27 gene: a
molecular approach to analyze HLA and disease associations.";
Immunobiology 170:367-380(1985).
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 1; Length 362;
Pred. No. 0.12;
0; Mismatches 1; Indels
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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73243566 CRC32;
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SIMILARITY.
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EMBL; X03666; CAA27302.1; JOINED.
EMBL; M12967; AAA36221.1; -.
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3D-STRUCTURE MODELING OF 115-206.
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90.08;
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Best Local Similarity 90.0
Matches 9; Conservative
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PDB; IROJ; 30-SEP-94.
PDB; IROJ; 30-SEP-94.
PDB; IROJ; 30-SEP-94.
PDB; IROL; 30-SEP-94.
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; IROH; 30-SEP-94.
; IROI; 30-SEP-94.
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362 AA;
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                                                                                                                                                                                              Gaps
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                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2703 ALPHA CHAIN
PRECURSOR (B-27D).
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P10318;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA CHAIN
HIA-B OR HLAB.
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                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          THE IMMUNE SYSTEM.
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B-27 B+2703 ALBHA CHAIN.
EXTRACELULAR ALPHA-1.
EXTRACELULAR ALPHA-2.
EXTRACELULAR ALPHA-3.
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                 362 AA
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MIM; 142830; -.

PPROSITE; PS00290; IG_MHC; 1.

PFAM; PF00129; MHC_I; 1.

PFAM; PF00129; MHC_I; 1.

PFAM; PG0129; MG_I; 1.

PFAM; PG0129; MG_I; 1.

PFAM; PG0129; MG_I; 1.
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Best Local Similarity 90.0
Matches 9; Conservative
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362
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              1B16_HUMAN
P19373;
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1B16_HUMAN
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BW-47 B*4701 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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P13750;
01-JAN-1990 (Rel. 13, Created)
01-ARN-1990 (Rel. 13, Last sequence update)
01-ARN-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
01-APR-1993 (Rel. 25, Last sequence update)
Ol-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-47 B*4701 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE, 88152906.
ZEMMOUR J., ENRIS P.D., PARHAM P., DUPONT B.;
ZEMMOUR J., ENRIS P.D., PARHAM P., DUPONT B.;
"Comparison of the structure of HLA-BW47 to HLA-B13 and its relationship to 21-hydroxylase deficiency.";
Immunogenetics 27:231-287(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMOUR SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
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MIM; 142830; -. PROSITE; PS00290; IG_MHC; 1.
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90.0%;
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SIGNAL 1 24
CHAIN 25 362
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362 AA;
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REDLRTLLRY 108
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                                                                      HLA-B OR HLAB.
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1801_PANTR
110 1801_PA
AC P13750
DT 01-JAN DT 01-JAN DT 01-ARN
DE CHLA C DE (FRAGM C E EURALY C C EURALY C C EURALY C C EURALY RN [1]
RP SEQUEN
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                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 362;
Pred. No. 0.12;
0; Mismatches 1; Indels
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-37 E
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 AA.
                                                                                       362 AA
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PFAM: PF0047; 19; 1.
PFAM: PF00129; MHC_I: 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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P30485;
01-APR-1993 (Rel. 25, Created)
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90.08;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                       STANDARD;
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 99 REDLRTLLRY 108
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HSSP; P03989; 1HSA.
MIM; 142830; -.
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227
362 AA;
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                                       1829_HUMAN
ID 1829_HUMAN
AC P18463;
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TRANSMEM
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MICROGLOBULIN).
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Best Local Similarity
Matches 8; Conserv
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                                                           MICROGLOBULIN)
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207
209
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P30380;
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MEDLINE; 89030641.

MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
KLEIN J.;
Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
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LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GOTALILB gOTILL (LOW-BATIBLE (LOW-BATILL) ELWATYOTA: Metazca: Choradata; Cranlata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                            MAYER W.; Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM. -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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5395FFC9 CRC32;
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1.2;
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Pred. No. 1.2;
1; Mismatches
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PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
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359
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106
359 AA;
                                                                                                                                                                                                                                     MICROGLOBULIN)
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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203
203
330
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P30379;
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SIGNAL
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DISULFID
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
02-APR-1993 (Rel. 25, Last annotation update)
03-111a gorilla (Lowland gorilla)
05-111a gorilla (Lowland gorilla)
05-111a gorilla (Lowland gorilla)
05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-11-05-
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CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BO101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELULAR ALPHA-2.
EXTRACELULAR ALPHA-2.
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
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0
                                        THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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; 2E33E2B8 CRC32;
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%;
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1B15_HUMAN
P10317;
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                                                         DOMAIN
                             DOMAIN
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1B15_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAXLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison
"Goriuman and chimpanzee class I.";
                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOWHAND GOTILLA)
ELVATYOTA: Metazoa: Chordata; Craniata: Vertebrata; Mammalia;
Eutheria; Primates; Catarihii; Hominidae; Gorilla.
                                                                                                                                                                                                                                                            Gaps
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PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
- r: Transmenbrane; Glycoprotein; Signal.
- C. Transmenbrane; Glycoprotein; CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                            Glycoprotein; Signal.
4 BY SIMILARITY.
2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. EXP. Med. 174:1491-1509(1991).
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                                                                                                                                                                                                                                        Score 39; DB 1; Length 362;
                                                                                                                                                                                                                                                           1; Indels
                                                                                                        GOGO-B0102 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                 CONNECTING PEPTIDE
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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or send an email to license@isb-sib.ch)
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80.0%;
                  EMBL; X60693; CAA43101.1; -. PIR; JH0540; JH0540.
                            PIR; JH0540; JH0540.
HSSP; P03989; JHSA.
PROSITE; PS00290; IG_MHC; 1.
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                                                        PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Gl
SIGNAL
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Best Local Similarity
Lase 8; Conserve
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99 RENLRIALRY 108
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P30381;
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VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
LOPEZ DE CASTRO J.A.;
Structural analysis of an HLA-B27 functional variant: identification of residues that contribute to the specificity of recognition by cytolytic T lymphocytes.";
Proc. Natl. Acad. SCI. U.S., 82:7394-7398(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
-!- SUBUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 86220133.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human
class I genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
HLA-B OR HLAB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 362;
Pred. No. 1.2;
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PARHAM P., ARNETT K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
GOGO-B0103 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                   CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FEA6A941 CRC32;
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1; Mismatches
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EMBL; X03667; CAA27301.1; JOINED.
EMBL; LSSS04; AAA69724.1; --
PIR; B25092; HLHUBK.
HSSP; P03989; 1HSA.
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80.0%;
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Matches 8; Conservative
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99 RENLRIALRY 108
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B-49(B-21) B*4901 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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Pred. No. 1.2;
; Mismatches 1; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;; E996F82F CRC32;
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
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80.0%;
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Matches 8; Conservative
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362 AA;
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99 RENLRIALRY 108
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TRANSMEM
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01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLLAMS R.C., PARHAN P.;
WILLLAMS R.C., PARHAN P.;
"Serologic cross-reactivities poorly reflect allelic relationships in the HIA-B12 and HIA-B21 groups. Dominant epitopes of the alpha 2
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Homo sapiens (Human).
ELNaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2;
1; Mismatches 1; Indels
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MEDLINE: 82235215.
PARHAM P., LAWLON., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                  CONNECTING PEPTIDE
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Y SIMILARITY.
Y SIMILARITY.
9798F0BB CRC32;
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             PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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01-FEB-1996 (Rel. 33, Last seq
01-FEB-1996 (Rel. 33, Last anno
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Best Local Similarity 80.0
Matches 8; Conservative
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362 AA;
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MEDLINE; 93056529.
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 MIM; 142830;
PROSITE; PSO(
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                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K., TAKIGUCHI M.;
HILA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha 1 domain.";
J. Immunol. 142:306-311(1989).
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 90207291.
ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HLA-A,B CDNA by using the polymerase chain reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.; "Allelic variation in HLA-B and HLA-C sequences and the evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMURE SYSTEM.
-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
362 AA
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RENLRIALRY 108
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Matches 8: Conserv
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P30490;
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DOMAIN
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DISULFID
DISULFID
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN. EXTRACELULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 357:326-329(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Mammalia;
1e; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE: 92269955.
BELICH M.P., WADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
"Unusual HLA-B alleles in two tribes of Brazilian Indians.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                Length 362;
                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4D846F30 CRC32;
                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  362 AA.
                                                                                                                                              MIM; 142830; -.
PROSITE: PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I: 1.
MHC_I: Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                 Score 39; DB
Pred. No. 1.2;
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                                   ALT_SEQ.
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80.0%;
                                                                                M22790; AAA59620.1; J
M22791; AAA59620.1; J
L41087; AAA64513.1; -
L41086; AAA64513.1; J
                                    AAA59620.1;
                                            M22786; AAA59620.1;
M22787; AAA59620.1;
                                                               M22788; AAA59620.1;
                           EMBL; M32319; AAA36232.1;
                                                                         M22789; AAA59620.1;
                                                                                                                                                                                                                                                                                                      40566
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                EMBL; M22790; AAA5962
EMBL; M22791; AAA5962
EMBL; L41008; AAA6451
EMBL; L41008; AAA6451
PIR; A30345; A30345
PIR; A30548; A30548
                                                                                                                                                                                                                                                                                                                                    Similarity 8; Conserva
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99 RENLRIALRY 108
                                                                                                                                        P30491; 1A1M.
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P30489;
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CARBOHYD
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Best Local 9
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Hel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
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J. Immunol. 142:306-311(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASS I HISTOCOMPATIBILITY ANTIGEN,
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MEDLINE: 89880265.
HAYASH H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY
B-51(B-5) B*5104 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 1; Length 362; Pred. No. 1.2;
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F22F08AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                               PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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SIMILARITY.
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EMBL; M22793; AAA59645.1; JOINED.
EMBL; M22794; AAA59645.1; JOINED.
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80.0%;
                                                                                                                                            EMBL; 215143; CAA78849.1; -. HSSP; P30491; 1A1M. MIM; 142830; -. PROSITE; PS00290; IG_MHC; 1.
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DR EMBL; M22795; AAA59645.1; JOINED.
DR BELL; M22795; AAA59645.1; JOINED.
DR BELL; M22797; AAA59645.1; JOINED.
DR BELL; M22797; AAA59645.1; JOINED.
DR BIR; B30345; B30345.
DR PIR; B30345; B30345.
DR PRSP, P30491; LALM.
DR PROSITE; P500047; 1g; 1.
DR PROSITE; P500047; 1g; 1.
DR PROSITE; P500047; 1g; 1.
DR PRAM; PF00129; MHC_I: 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT CHAIN 25 362 BW-52(B-D) B*5201 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT DOMAIN 309 332 CYTOPLASMIC TAIL.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT CARBOHYD 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULEID 125 188 BY SIMILARITY.
FT DISULEID 125 188 BY SIMILARITY.
FT DISULEID 127 283 BY SIMILARITY.
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Search completed: February 8, 2000, 00:59:5

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Query Match
Post Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels

Search completed: February 8, 2000, 00:59:53 Job time: 3782 sec THIS PAGE BLANK (USPTO)

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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BLASCZKK R., WIBER M., SALAMA A.;
SUBMILTED (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83727; CAA58698.1; -.
PFAM; PF00129; MHC_I; 1.
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019193;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
HISTOCOMPATIBILITY ANTIGEN ALPHA 1 DOMAIN (FRAGMENT).
HLA-B27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HLA-B27 VARIANT EXON 2 (ALPHAL DOWAIN) (FRAGMENT).
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Pred. No. 0.07;
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4748 MW;
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Best Local Similarity 90.0
Matches 9; Conservative
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39 AA;
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Homo sapiens (Human).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.34;
0; Mismatches 1; Indels
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Pred. No. 0.34;
0; Mismatches 1; Indels
                               SEQUENCE FROM N.A.
KOSMAN C.A., HURLEY C.K.;
KOSMAN C.A., HURLEY C.K.;
"Novel HLA Class I B Locus Alleles.";
Submitted (UNT.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF071770; AAC15939.1;
EMBL; AF071769; AAC15939.1;
HSSP; P10318; 1ROG.
FFAM; PF00129; MRC_I; 1.
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STEINER N.K., HURLEY C.K., KOESTER R.P.;
STEINER N.K., HURLEY C.K., KOESTER R.P.;
NOVEL-HLA-B alliel., Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF072764; AAC25779.1; -
EMBL; AF072764; AAC25779.1; JOINED.
HSSP; P10318; IRGG.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TIEMBLIEL. 08, Created)
01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-B27 M (FRAGMENT).
Sutheria; Primates; Catarrhini; Hominidae; Homo.
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181 AA; 21103 MW; 8CF468CF CRC32;
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21079 MW; 24949B0F CRC32;
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Matches 9; Conservative
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181 AA;
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                                                      MEDLINE; 92337445.
HIGGINS C.M., LUND T., SHIPLEY M.E., EBRINGER A.,
SADOWSKA-WROBLEWSKA M., CRAIG R.K.;
"Ankylosing spondylitis and HLA-B27: restriction fragment length
polymorphism and sequencing of an HLA-B27 allele from a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                      Score 44; DB 7; Length 90;
Pred. No. 0.17;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOSMAN C.A., HURLEY C.K.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC034012; AAC32563.1; -.
EMBL; ARC034011; AAC32563.1; JOINED.
HSSP: P10318; 1ROG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MC CLASS I ANTIGEN (FRAGMENT).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21107 MW; D8E533DD CRC32;
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90 90
90 AA; 10571 MW; F22CCB4E CRC32;
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                                                                                                                                                  ankylosing spondylitis.";
Ann. Rheum. Dis. 51:855-862(1992).
EMBL; 839758; CAB27364.1; -
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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PFAM; PF00129; MHC_I; 1.
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181 AA;
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75 REDLRTLLRY 84
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MEDLINE; 86149317.
SZOTS H., RIETHWULLER G., WEISS E., MEO T.;
"Complete sequence of HLA-B27 cDNA identified through the characterization of structural markers unique to the HLA-A, -B, and -C allelic series.";
Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
EMBL; MI2678; AAA59614.1; -.
HSSP; P10318; 1ROG.
PROSITE; PS00290; IG_MHC; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; PrImates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Score 44; DB 7; Length 359; 90.0%; Pred. No. 0.69; 1ve 0; Mismatches 1; Indels
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Pred. No. 0.7;
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BALAS A., SANTOS S., VICARIO J.L.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U31971, AAA98506.1; -.
HSSP; P10318; 1ROG.
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MHC CLASS I ANTIGEN HLA-B.
1 09C9DZ0A CRC32;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MMC CLASS I ANTICEN HLA-B PRECURSOR.
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           Eutheria; Primates; Catarrhini; Hominidae; Homo
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359 AA; 40042 MW; 069F7E64 CRC32;
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25 362 M
362 AA; 40479 MW;
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90.08;
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PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 90.0
Matches 9; Conservative
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PFAM; PF00129; MHC_I; 1.
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Best Local Similarity
Matches 9; Conserva
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96 REDLRILLRY 105
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99 REDLRTLLRY 108
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SIGNAL
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029705;
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ID Q29846
AC Q29846;
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[1]
SEQUENCE FROM N.A.
MEDLINE: 87009855.
COPPIN H.L., MCDEVITT H.O.;
"Absence of polymorphism between HLA-B27 genomic exon sequences isolated from normal donors and ankylosing spondylitis patients.";
J. Immunol. 137:2168-2172(1986).
EMBL; M14013; AAA59643.1; --
HSSP; P10318; 1ROG.
PROSITE: ASO0290; IG_MHC; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%; Score 44; DB 7; Length 274; 90.0%; Pred. No. 0.53; Live 0; Mismatches 1; Indels
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Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U11267; AAA19927.1; -.
HSSP; 930685; 1A9E.
PROSITE; PRO00309; IG_MHC; 1.
PFAM; PF00129; MHC_I; 1.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
11-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HLA-B37 (FRAGMENT).
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Last annotation update)
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Pred. No. 0.62;
); Mismatches
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274 AA; 31659 MW; 9A74A6BA CRC32;
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322 AA; 36626 MW; DF3B7744 CRC32;
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01-NOV-1996 (TrEMBLrel. 01, C)
01-NOV-1996 (TrEMBLrel. 01, Ld
01-NOV-1999 (TrEMBLrel. 12, Ld
HLA-B27 (FRAGMENT).
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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PFAM; PF00129; MHC_I; 1.
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| 99 REDLRILLRY 108
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| 75 REDLRTLLRY 84
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MEDLINE: 94375872.

DEL PORTO P., D'AMATO M., FIORILLO M.T., TUOSTO L., PICCOLELLA E., SORREWINO R.;

"Identification of a novel HLA-B27 subtype by restriction analysis a cytocoxic gamma delta T cell clone.";

J. Immunol. 153:3093-3100(1994).

BMBL: 233453; CAA83876.1:

HSSP; P10318; 1ROG.

PROSITE: PS00290; IG_MHC; 1.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEURYNCK K.L., BAXTER-LOWE L.A.;
"B27052 W4950.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF026218; AAC42275.1;
HSSP; P10318; IROG.
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019569;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
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Last annotation update)
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Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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PFAM; PF00129; MHC_I; 1.
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99 REDLRTLLRY 108
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                                                                                                                    SEQUENCE FROM N.A.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
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                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.6;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 7; Length 90; Pred. No. 1.6; 1; Mismatches 1; Indels
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF022172: AAC99794.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF017320; AAB70286.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          046697 PRELIMINARY; PRT; 90 AA. 046697; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
10606 MW; 99D11089 CRC32;
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90 90
90 AA; 10689 MW; 5E5F2495 CRC32;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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89 AA;
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74 RENLRIALRY 83
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75 RENLRIALRY 84
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SEQUENCE FROM N.A.
TISSUE=LEUKOCYTE;
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046697
AC 046697
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DT 01-JUN
DT 01-JUN
DT 01-JUN
DE MHC-CLI
GN HLA-CLI
GN HLA-CLI
COC EUKARY
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019189
AC 019189
DT 01-JAN
DT 01-JAN
DT 01-JAN
DT 01-JAN
DT 01-MC CL
GN HLA-B.
GS HOMO S
OS EUKATY
OC EUKATY
CC EUKA
8
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01-FEB-1997 (TrEMBLRel. 02, Last sequence update)
01-FEB-1997 (TrEMBLRel. 03, Last annotation update)
01-NOV-1998 (TrEMBLRel. 08, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
PLA.B. troglodytes (Chimpanzee).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=WODKA;
MEDINE: 94286544.
MEDINE: 94286544.
MCADAM S.N. HUGHES A.L.,
MCADAM S.N. WATKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
PEMBL: U05585; AASO1881;
PEMBL: U05585; AASO1881;
                                                                                                                                                                                                               Score 39; DB 7; Length 133;
Pred. No. 2.4;
1; Mismatches 1; Indels
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PETERSDORF E.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
BMBL; 161859; |AAB60357.1; -.
MIM; 142830; -.
PFAM; PF00129; MHC_I; 1.
MHC I. I.
NON_TER 133 133
SEQUENCE 133 AA; 15491 MW; 3A3BC802 CRC32;
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NON_TER 137 137
SEQUENCE 137 AA; 15922 MW; B316D3BC CRC32;
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Best Local Similarity 80.0%;
Matches 8; Conservative 1
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27 RENLRIALRY 36
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Search completed: February 8, 2000, 13:17:41 Job time: 32490 sec

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Human cell line
Human cell line
Human cell line
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2 (bases 1 to 195)
2 (bases 1 to 195)
Blasczyk, R.
Direct Submission
Submitted (16-74M-1995) R. Blasczyk, Bloodbank, Dept. of Intern. Medicine, Div of Hematol. and Oncolog., Spandauer Damm 130, Univ. Hosp. Rudolf Virchow, Freie Univ., D- 14050 Berlin, FRG
1. 195
/organism="Homo sapiens"
//solate="1235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="IEQEGPEYWDRETQICKAKAQTDREDLRTLLRYYNQSEA"
55 c 73 g 22 t
                                                                                                                                                     seq_documentation_block:
DCCUS HSLAB27V2 195 bp DNA PRI 31-JAN-1995
DEFINITION H.sapiens HLA-B27 variant gene (exon 2).
ACCESSION X83727
VERSTON X83727 GI:663002
KEYWORDS HLA-B gene; human leukocyte antigen; major histocompatability complex class I.
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HOMO Saplens MHC class I antigen HLA-B gene (HLA-B*27 variant allele), exon 2.
AF072763.1 GI:3293562
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 195)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="CaA58698.1"
/db_xref="GI:663003"
/db_xref="SPTREMBL:019688"
  U90422
U90424
U90418
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/chromosome="6"
/chi_type="EBV transformed cell line"
/map="fp21.3"
/76. '>195
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Gaps: 0
Percent Identity: 90.000
  250
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  3.20
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US-08-653-294-14 x HSLAB27V2
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                                                                                                       seq_name: gb_pr1:HSLAB27v2
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Percent Similarity:
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  gb_pr2:HSHLABI1
gb_pr2:HSHLABJ1
gb_pr2:HSHLABT1
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KEYWORDS
SEGMENT
SOURCE
ORGANISM
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ORIGIN
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DEFINITION
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AUTHORS
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1 X03665 Human Class I MHC gene I X03665 Human class I MHC gene I X03665 Human Class I MHC gene I ML2678 Human MHC class I HLA-E M54883 Human MHC class I HLA-E M54883 Human MHC class I HLA-E M539758 HLA-B27 (HLA-E*2705)-hl X03945 Human gene for HLA-E*2705)-hl X03945 Human gen
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| AC013786 Homo sapiens chromos
| AC006837 Arabidopsis thaliana
| AL021811 Arabidopsis thaliana
| AL020402 Homo sapiens clone
| AC009409 Homo sapiens clone
| AC013285 Homo sapiens clone
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i Y08693 H.sapiens HLA-B gene, ex
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U90611 Human cell line THAI
U90613 Human cell line THAI
U90615 Human cell line THAI
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                                                                                                                                                                          Command line parameters:
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-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-USTS=A.5 -DOCALIGN=20 -THR_SCORE=PCT -ALIGN=15 -MODE-LOCAL
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-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                         software, version 4.5,
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                                                                                                    About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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  GenEmbl:*
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Database length: -1518192014
Search time (sec): 11370.480000
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Query length: 10
Database: GenEmbl:*
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9b_pr3:HSMCHLBC1

9b_pr4:HS7052B1

9b_pr4:HSMLAWMBY2

9b_pr1:HUMB27052G

9b_pr1:HUMB2705CG

9b_pr1:HSU11267

9b_pr1:HSU11267
                                                   Date: Feb 8, 2000
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9b_pri: HSHLAM1
9b_pri: HSHLAM27X
9b_pri: HUMMHB27A
9b_pri: HUMMHB27B
9b_pri: HUMMHB27B
9b_pri: HUMMHB27B
9b_pri: HSHLAB27
9b_pri: HSHLAB27
9b_pri: ARO08238
9b_bri: ARO08238
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gb_pat:E01342
gb_pr1:HUMMHZUNIA
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gb_pr2:HSHLABB1
gb_pr2:HSHLABD1
gb_pr2:HSHLABF1
gb_pr2:HSHLABF1
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gb_htg5:AC013786
gb_htg3:AC006837
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gb_pr3:HSBA46E17
gb_htg3:AC009409
gb_htg7:AC013285
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gb_pr3:HSAB27HLA1
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gb_pr3:AF026218
gb_pr1:HUMHLABW4
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gb_pri:HSHLABHBB
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Percent Identity: 90.000

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Percent Similarity: 90.000
                                                                                                                                                              seq_name: gb_pr3:HSMHCHLBC1
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Homo sapiens isolate GN00211 MHC class I antigen HLA-B gene (B*1543 allele), exon 2.
AFF054011 GI:2984766
1 (bases 1 to 270)
Steiner,N.K., Hurley,C.K. and Koester,R.P.
Unpublished
Unpublished
2 (bases 1 to 270)
Steiner,N.K., Hurley,C.K. and Koester,R.P.
Direct Submission
Submitssion
Submitsted (21-JUN-1998) Microbiology and Immunology, Georgetown University Medical Center, 3970 Reservoir Road NW, Washington, DC 20007, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 270)
Kosman, C.A. and Hurley, C.K.
Direct Submission
Submitted (18-MAR-1998) Microbiology & Immunology, Georgetown
University, 3970 Reservoir Rd. NW, Washington, DC 20007, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homoo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
Kosman,C.A. and Hurley,C.K.
Novel HLA Class I B locus alleles
                                                                                                                                                                                                                                                                                                                   Length: 10 Gaps: 0 Percent Identity: 90.000
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                                                                                                                                                           1. .270
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .270
/gene="HLA-B"
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/isolate="GN00211"
/db_xref="taxon:9606"
1. .270
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87 c
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US-08-653-294-14 x HSAB27HLA1
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90 c
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Ratio: 4.889
Percent Similarity: 90.000
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LOCUS HSB1524V1
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Length: Gaps:

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HSMHCHLBC1 270 bp DNA PRI 17-SEP-1998
HOMO Saplens MHC class I antigen HLA-B gene (HLA-B*5303 allele),
exon 2.
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LOCUS HS27052B1 270 bp DNA
DEFINITION Homo sapiens MHC class I antigen HLA-B gene, HLA-B*2716 allele,
exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cosman, C.A. and Hurley, C.K.
Kosman, C.A. and Hurley, C.K.
Direct Submission
Submitted (12-JUN-1998) Microbiology & Immunology, Georgetown University, 3970 Reservoir Rd. N.W., Washington, DC 20007, USA
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
Kosman,C.A. and Hurley,C.K.
Novel HiA Class I B Locus Alleles
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Gaps: 0
Percent Identity: 90.000
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/organism="Homo sapiens"
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AF071769.1 GI:3243269
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AF102563.1 GI:4704574
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US-08-653-294-14 x HSMHCHLBC1
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alignment_block:
US-08-653-294-14 x HSB1524V1
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1 (bases 1 to 270)

Wu,J., Bassinger,S., Montoya,G.D., Yee,J., Griffith,B.B.,
Kearns,J., McKeen,M., Birkos,S., Kamoun,M. and Williams,T.M.
Identification of new HLA-B alleles in potential bone marrow donors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSHLAWMBY2 270 bp DNA PRI 06-APR-1999
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*27 allele), exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 270)
Wu,J., Bassinger,S., Montoya,G.D., Yee,J., Griffith,B.B.,
Kearns,J., McKeen,M., Birkos,S., Kamoun,M. and Williams,T.M.
Direct Submission
Submitted (30-NOV-1998) Pathology, Univ. New Mexico, 915 Camino de
Salud, NE, Albuquerque, NM 87131, USA
Location/Qualifiers
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 270)

(sosman,C.A. and Hurley,C.K.

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(comman,C.A. and Hurley,C.K.

Direct Submission

Submitted (28-ocr-1998) Microbiology and Immunology, Georgetown University, 3970 Reservoir Rd. N.W., Washington, DC 20007, USA
                                                                                                                                                                                                                                                                                                                                                                                                           44.00 Length: 10
4.889 Gaps: 0
90.000 Percent Identity: 90.000
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/organism="Homo sapiens"
/isolate="GN00246"
/db_xref="taxon:9606"
1. .270
/gene="HLA-B"
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/db_xref="taxon:9606"
/map="6p23"
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AF110257.1 GI:4566542
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US-08-653-294-14 x HS27052B1
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LOCUS HSHLAWMBY2
DEFINITION Homo sapiens
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seq_documentation_block:
Locus HuwaHBM2 822 bp DNA PRI 07-JAN-1995
DEFINITION Human MHC class I HLA-B27 M+ gene, exons 2-4 (introns unsequenced).
ACCESSION M14013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMB27052G 546 bp DNA PRI 27-FEB-1996
HOmo sapiens MHC class I HLA-B*27052 gene, exons.
L76095
L76095.1 GI:1203957
cell surface antigen; cell surface glycoprotein; class I gene; integral membrane protein; major histocompatibility complex. Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 546) Marcos; C.Y., Fernandez-Vina,M.A., Lazaro,A.M. and Stastny,P. Novel HLA-B Alleles Unpublished (1996)
Length: 10
Gaps: 0
Percent Identity: 90.000
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Gaps: 0
Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                                                       to: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .546
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                  222 CGAGAGGACCTGCGGACCTGCTCCGCTAC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
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                                                                                                                                                                                                                                                                                                                       to: HSHLAWMBY2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: HUMB27052G from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
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454
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271. .546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /replace="t"
454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M14013.1 GI:187743
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                                                                                                                                                                            alignment_block:
US-08-653-294-14 x HSHLAWMBY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-14 x HUMB27052G
44.00
4.889
90.000
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LOCUS HUMB27052G
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ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE

source

gene

CDS

JOURNAL MEDLINE FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M62852
M62852.1 GI:187760
cell surface antigen; class I gene; integral membrane protein;
major histocompatibility complex.
Homo sapiens CDNA to mRNA.
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1 (bass 1 to 1017)

Choo.S.Y., Fan, L.A. and Hansen, J.A.

A novel HiA-B27 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain

J. Immunol. 147 (1), 174-180 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-1995
                                                                                                                                                                                                                                                                                                    /function="peptide presentation; histocompatibility
      CW6, B37 / A-, CW7, B71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 90.000
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Human MHC class I HLA-B27-HS mRNA, 3' end.
   /haplotype="HLA-A2, CW6, B37
/cell_line="B lymphoblastoid"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 968
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1. .1017
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                             /product="HLA-B37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                             1. .>968
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                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HLA-B"
                                                                                                                                                                                                                                 /citation=[1]
                                                                                                                                                                                                                                                                                                                                      molecule"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: HSU11267
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US-08-653-294-14 x HSU11267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pr1:HUMMHC
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Percent Similarity:
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ACCESSION
VERSION
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ORIGIN
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TITLE
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MEDLINE
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                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUN-1994) Carolyn K. Hurley, Microbiology, Georgetown University School of Medicine, 3900 Reservoir Road, N.W., Washington, D.C. 20007 USB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQLRAYL
BGECVEWLRRYLENGKETLQRADPRYHHPISDHEATLRCWALGFYPAETTLTWY
RDGEDQTQDTDYETTERGREDTFPGWAAVVVPSGEEGRYTCHVQHEGLPKPLTLRW"
256 c 277 q 113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="GSHSMRYFHTSVSRPGRGEPRFITVGYVDDTLFVRFDSDAASPR
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Mammalia;
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

[ Dases I to 822)
Coppin.H.L. and McDevitt,H.O.

Absence of polymorphism between HIA-B27 genomic exon sequences isolated from normal donors and ankylosing spondylitis patients
J. Immunol. 137 (7), 2168-2172 (1986)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthėria; Primates; Catarrhini; Hominidae; Homo.
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Gaps: 0
Percent Identity: 90.000
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LOCUS HSU11267 968 bp mRNA
DEFINITION Human HLA-B37 (B-3701) mRNA, partial cds.
VERSION U11267 GI:511785
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/note="HLA-B27 M2+"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HLA-B"
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2 (bases 1 to 968)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 44.00
Ratio: 4.889
Percent Similarity: 90.000
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US-08-653-294-14 x HUMMHBM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: HUMMHBM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              822
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BASE COUNT

ORIGIN

source

FEATURES

ORGANISM

KEYWORDS

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS

JOURNAL

TITLE

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_pr1:HUMMHZUNIA
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US-08-653-294-14 x E01342
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FEATURES
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EEPRAPWIEQEGPEYWDRETQICKAKAGTDREDLRTLLRYYNGSEAGSHTLGSMYGCD VGPDGRLLRGHNQYAYDGKDYIALNEDLRSWTAADTAAQITQRKWEAARVAEQLRAYL SCECVEWLRYLENGKETLGRANDPKYHYHHPISDHBATLRCWALGFYPAEITHTWQ RDGEDCTQDTELVETRPAGDRTFQKWAAVVPBGEEGRYTCHVQHEGLFYPALITRWEP SSOSYVPIVGIVVAGLAVLAVVIGAVVAAVMCRRKSSGGKGGSYSQAACSDSAQGSDV SLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homoo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1026)
Szoets, H., Weiss, E., Doerner, C., Lang, M., Meo, T. and
Riethmueller, Coding therefor and its utilization
Patent: EP 0226669-A 1 24-JUN-1987;
Riethmueller, Gert, Prof. Dr
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A28264 1026 bp DNA
H.sapiens mRNA for HLA-B 27 from patent EP0226069.
A28264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 cDNA encoding C-terminal Fragment of HLA-B27.
100 control of Homo sapiens.
100 control of Homo sapiens.
                                                                                                                                                                                                   44.00 Length: 10
4.889 Gaps: 0
90.000 Percent Identity: 90.000
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4.889 Gaps: 0
90.000 Percent Identity: 90.000
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 307 c 344 g 165
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                                                                                                                                                                                                                                                                                                                                                                                                     223 CGAGAGGACCTGCGGACCTGCTCCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
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                                                                                                            343 g
                                                                                                            308 c
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US-08-653-294-14 x A28264
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LOCUS A28264
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LOCUS E01342
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...ukE AG
Human
PN JP 19872281-A 2 07-0CT-1987;

LuckE AG
Human
PN JP 19872281-A/2
PD 07-0CT-1987;

PD 07-0CT-1987
PR 28-NOV-1986 DE 85 354204, 21-DEC-1985 DE 85 3545576 PI
HANNEROORE STTSUEETSU ERIZABEETO WAISU, KURISUTA DERUNAA, PI
HANNEROORE STTSUEETSU, ERIZABEETO WAISU, KURISUTA DERUNAA, PI
MAAGOTSUTO RANGU, TOMASO MEO, GERUTO RITTOMIYURAA PC
C12N15/00,C07H21/04,C12P21/00,C12Q1/68,G01N33/577//A61K39/00, PC
C12N15/06,C12P21/00,C12R1:91);
CC Strandedness: Double;
CC Strandedness: Double;
CC Tragment_type: C-Terminal Fraor CC
C Tragment_type: C-Terminal Fraor CC
C *source: cell_type=-Eukoc...
PH Key
FT CDS
FT CDS
FT FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1084)

Matkins,D.I., McAdam,S.N., Liu,X., Strang,C.R., Milford,E.L.,
Levine,C.G., Garber,T.L., Dogon,A.L., Lord,C.I., Ghim,S.H.,
Troup,G.M., Hughes,A.L. and Letvin,N.L.
New recombinant HiA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci
Nature 357, 329-333 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS HUMMHZUNIA 1084 bp mRNA PRI
DEFINITION Human MHC class I (HLA-B 27052) mRNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
1307 c 344 g 165
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4.889
90.000
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ORIGIN

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AF026218 1089 bp mRNA PRI 23-SEP-1998
Homo sapiens MHC class I antigen HLA-B (HLA-B27052 allele) mRNA,
complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1089)
Seurynck K.L. and Baxter-Lowe, L.A.
                                                    73. .1086
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/product="MHC class I antigen HLA-B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 90.000
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1013. 1041
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                                                                                                                                                                                                                                   'note-"encodes alpha-2 domain'
                                                                                                                                                                                                                                                                                                                                'note="encodes alpha-3 domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                             note="encodes
                                                                                                                                      'note-"encodes
                                                                                                                                                                                                    343. .618
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337 c
                                     /number=1
                                                                                                                                                                                       'number-2
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US-08-653-294-14 x HSU31971
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                                                    mat_peptide
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KEYWORDS
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TITLE
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/translation="MRVTAPRTLILLIMGAVALTETWAGSHSMRYFHTSVSRPGRGEP
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RTLIRYYNGSEAGSHTLQNNYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAA
PAQOTORAWEAARVAEQNRAYLEGECVEWIRRYLENGKETLGRADPPKTHVTHPI
SDHEATLRGWALGFYPAETILTWORDGEDOTODTELVETRPAGDRTPGKWAAVVVPSG
EEGRYTCHVQHEGLPKPLILRWEPSSQSTVPIVGIVAGIAALLAVVIGAVVAAAVMGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
1 (bass 1 to 1089)
Balas,A., Santos,S. and Vicario,J.L.
Serological and molecular characterization of a novel HLA-B allele
Unpublished (1995)
2 (bases 1 to 1089)
Balas,A.
                                                                                                                                                                                                                                                                                                                                                                                                           HSU31<u>9</u>71 1089 bp mRNA PRI 27-ApR-1996
Human MHC class I antigen HLA-B precursor (HLA-B) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (20-JUL-1995) Antonio Balas, Centro de Transfusion de
Madrid, Histocompatibility, Menendez Pelayo, 65, Madrid, 28009,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /haplotype="Al Cw2 B- Bw4 DR11 DR52 DQ7"
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1. 72
/gene="HLA-B"
1. .1084
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/strain="South American Amerindian"
/db_xref="taxon:9606"
a 329 c 362 g 175 t
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Gaps: 0
Percent Identity: 90.000
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1. 1089
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US-08-653-294-14 x HUMMHZUNIA
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                                                                                                                                    alignment_scores
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REFERENCE 2 (bases 1 to 1089)
AUTHORS SILVACK Att. and Baxter-Lowe, L.A.
BITTLE SUbmitted (22.5EP-1997) Molecular Genetics, Richland Memorial
Hospital, 7 Richland Medical Park, Columbia, SC 29203, USA
LOCATION/COMPILITIES AND SPECIAL STATES AND SPECIAL STATES AND SPECIAL SPECIAL AND SPECIAL S
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Sequence of pGET2 encoding
Carcinoembryonic antigen DN
Immunogenic carcinoembryoni
SCFV-19E1 fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA, antigen or antibody
claim 2; Page 4; Spri German.
Claim 2; Page 4; Spri German.
The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, e.g. for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. He HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay.
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Sequence of genomic DNA encoding human histocompatibility antigen
Sequence of genomic should by the sequence of genomic second human histocompatibility is sequenced by the sequence of the sequence
                                                                                                                                                                                                                                            LU-APR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27.
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondylitis; ss.
Homo sapiens.
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04-JUN.1987.
28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-54576.
(BEHW ) BEHRINGWERKE AG.
RICTHMULIER G, MeO T, Weiss E, Szots H; WPI: 87-157892/23.
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ID N70225 standard; DNA; 3874 BP.
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ID N7095S standard; DNA; 1026
AC N70935;
DT 10-APR-1991 (first entry)
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N_Geneseq_36:Q71567
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18 Rattus norvegicus Class II tum
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Sequence encoding fused antibod
Enterococcus faecalis genome of
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107.6 L3 PCR primer for U7.6 var
1 2011 scFv VL PCR primer 6. Singl
1 VK3'AL2 PCR primer for U7.6 vari
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-0=Cqq1_1/USPTQ_Spool/USO8653294/runat_04022000_160701_15807/app_query.fasta.1
-0=Cqq1_1/USPTQ_Spool/USO8653294/runat_04022000_160701_15807/app_query.fasta.1
-0B=N.Geneseq_36 -QFNT=fastap -SUFFIX=rng -GAPOP=12.000
GAPOFXT=4.000 -MINAATCH=0.100 -LOOPCL=0.000 -XGAPOFXT=0.500
-GAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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-FGAPOP=6.000 -FGEEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFMT=Pf8 -NORM=ext -MINLEN=0
-MAXLEN -NORM=0.0000 -USER=USO8653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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Query: US.08 6.633-294-14
Query length: 10
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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N_Geneseq_36:N70225
N_Geneseq_36:T61639
N_Geneseq_36:029167
N_Geneseq_36:001834
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N_Geneseq_36:V19871
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N_Geneseq_36:Q69946
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N_Geneseq_36:N50356
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N_Geneseq_36:T01865
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N_Geneseq_36:076405
N_Geneseq_36:012083
N_Geneseq_36:X51732
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N_Geneseq_36:Q67406
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N_Geneseq_36:091170
N_Geneseq_36:N40062
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N_Geneseq_36:Q42561
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DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.

for diagnosis and antigen and antibody prodn.

for diagnosis and antigen and antibody prodn.

THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 lavels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ank/losing spondylitis.

Sequence 3874 BP: 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
//note= "HLA-B27 3' flanking region, downstream of
3' untranslated region"
4112. .4556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1997 (first entry)
HIA B27 consensus sequence.
HIA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d
/note= "absence of cytosine at this site is
indicative of a predisposition to SNSA"
                                                        21-DEC-1985; DE-542024.
21-DEC-1985; DE-545576.
(SEBW ) BEHRINGWERKE AG.
SZOKS H WEISE E DOTNER C, Lang M, Meo T, Riethmuller G; WPI: 87-171469/25.
DNB ACS.
                                                                                                                                                                                                                                                                              44.00 Length: 10
4.889 Gaps: 0
90.000 Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: N70225 from: 1 to: 3874
                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
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3968. .6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1995; US-522942.
(CEDA-) CEDARS SINAI MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           T61639 standard; DNA; 6553 BP.
T61639;
3009. .3041
/*tag= f
3148. .3191
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**tag= b
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/note= "3'
                                   φ
                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T61639
                                  /*tag=
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US-08-653-294-14 x N70225
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01-SEP-1995; US-5229
                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
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                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                           Ratio:
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                                            EP-226069-A
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Transgenic non-human mammalian HLA-Bw 52 gene - useful for analysis of expression of gene structure, and prodn. of analysis of expression of gene structure, and prodn. of analysis of expression of gene structure, and prodn. of anose model of human disease

Disclosure; Fig 1; Bpp; Japanese.

Disclosure; Fig 1; Bpp; Japanese.

The sequence shows the exon 2 alpha-1-domain of the human leukocyte antigen. Bw 52 gene. The complete gene may be introduced into non-human mammals, pref. rat or mouse, or their ancestors at the primary developmental biological step via transplantation into the zygote or embryo to generate transgenic non-human mammals contg. HLA-Bw 52 are useful for the analysis of expression of the gene, its structure, and prodn. of mouse models of human disease.

Chuman disease.

See also 02916672.

Sequence 270 BP; 59 A; 88 C; 86 C; 37 T;
Detecting pre-disposition to seronegative spondylarthropathies from the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele

Claim 1; Page 52-56; 68pp; Bnglish.

Claim 1; Page 52-56; 68pp; Bnglish.

Genetic predisposition to seronegative spondyloarthropathies (SNSA) is detectied by determining the absence of a cytosine nucleotide in the 3' flanking region (see also T61647-48) of an HLA-B27 consensus consition corresponding to nucleotide 4495 of the HLA-B27 consensus sequence given in T61639. Probes and primers (see also T61640-46) based on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA from B27+ normal individuals who are resistant to SNSA from B27+ normal individuals consensed to SES3 BP; 1443 A; 1619 C; 2017 G; 1474 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; transgenic; germ cells; somatic cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 90.000
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Gaps: 0
Percent Identity: 80.000
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HLA-Bw 52 exon 2 alpha-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID Q29167 standard; DNA; 270 BP.
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03-AUG-1990; 207329.
03-AUG-1990; JP-207329.
(OLYU ) OLYMPUS OPTICAL CO.
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4.889
90.000
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4.333
90.000
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US-08-653-294-14 x T61639
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US-08-653-294-14 x Q29167
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Ratio:
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Ratio:
Percent Similarity:
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J04091731-A.
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Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype blsclosure; Fig 1 A-G; 20pp; English.

The human HLA-B51 gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-B51 gene.

The transgeneic offspring were immunised with HLA antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The spleen lymphocytes were fused with myeloma cells. Hybridomas producing antibodies were selected.
                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-1991 (first entry)

HLA-B51 gene for production of monoclonal antibodies.

Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-B51 gene; ss.

Location/Qualifiers

exon 1.73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 10 Gaps: 0 Percent Identity: 80.000
  Percent Identity: 80.000
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                                                                                                                               from: 1 to: 1086
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                                                                                                                                                                                                                294 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="alpha 1-domain"
344. .619
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196. .1012
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1013. .1042
/*tag= f
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1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID 005693 standard; DNA; 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
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/*tag= b
/number=2
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/number=1
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4.333
90.000
                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:Q05693
  Percent Similarity: 90.000
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                                                                                                                               Align seg 1/1 to: Q01822
                                                 alignment_block:
US-08-653-294-14 x Q01822
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WPI; 90-255479/34.
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Ratio:
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Sequence 10
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(OLXU) Olympus Optical Co., Ltd.
Rano K, Takiquchi;
WPI: 90-046289/07.
P-PSDB; R03142.
New DNA for class I human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2; pp11-12; 23pp; English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The DNA for class I human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc. Claim 1; Page 11; 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA cyping. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells. Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;
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4.333 Gaps: 0
90.000 Percent Identity: 80.000
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Gaps:
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222 CGAGAGCTGCGGATCGCGCTCCGCTAC 251
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Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
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Sequence encoding HLA-Bw52 antigen.
Probe: HLA class I DNA; immunogen; ss.
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1. .1086
                                                                                                                                                                                                                                                                                     EP354580-A.
14-FEB-1990.
10-AUG-1989.
11-AUG-1988; JP-200758.
(OLXU) Olympus Optical Co., Ltd.
Kano K, Takiguchi;
WPI; 90-046289/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                      seq_documentation_block:
ID Q01834 standard; DNA; 1086 BP.
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ID Q01822 standard; DNA; 1086 BP.
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                                                    seq_name: N_Geneseq_36:Q01834
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US-08-653-294-14 x Q01834
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Ratio:
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Quality:
Ratio:
                                                                                                                                                                                                                                                                  Homo sapiens.
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EP-354580-A 14-FEB-1990 10-AUG-1989

alignment\_scores

Align seg 1/1

Ë 173

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N J0311240.

D 14 MAY 1991.

PR 22-SEP-1989; 247697.

PR 22-SEP-1989; 3P-247697.

PR 22-SEP-1989; JP-247697.

PR 12-SEP-1989; JP-247697.

PR 22-SEP-1989; JP-247697.

PR 22-SEP-1989; JP-247697.

PR (CLYU) OLIVENUS OPTICAL KK.

DR PP-SEDB; R12463.

PT HLA-BW53 gene, DNA probe and transformant cells - used for lumnisation, identifying specificity of antiserum etc.

PS Claim 1; Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 2; Page 1; 11pp; Japanese.

CC Claim 3; Page 1; 11pp; Japanese.

CC Claim 3; Page 1; 11pp; Japanese.

CC Claim 4: Page 1; 11pp; Japanese.

CC Claim 5; Page 1; 11pp; Japanese.

CC Claim 6: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 6: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 6: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 8: Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 1; Page 1; 11pp; Japanese.

CC Claim 6: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 6: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 7: Page 1; 11pp; Japanese.

CC Claim 8: Page 1; 11pp; Japanese.

CC Claim 9: Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid fragment encoding gene products - can be used for genetic analysis and mapping claim 1; Page 23-24; 616pp; English.

Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (076401-077613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary to (A) or (B).
                                                                                                                                                                                                                              HIA-Bw53 exon.
Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

ID 076405 standard; DNA; 213 BP.

C 076405;

DT 23-SEP-194 (first entry)

E Human genome fragment. (Preferred)

KW Brain; placenta; bone marrow; genetic analysis; gene mapping; We detection; homology; human; adrenal tissue; ds.

OS Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shaw D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.00 Length: 10
4.333 Gaps: 0
90.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-1994.
13-JUL-1993; G01467.
13-JUL-1992; GB-014857.
(MEDI-) MEDICAL RES COUNCIL.
Sibson DR, Starkey M; Howells D, Kelly M, Sibson DR, Starkey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q12114 from: 1 to: 1089
295 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                        _documentation_block:
Q12114 standard; DNA; 1089 BP
                                                                                                                                                                              Q12114;
29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q76405
                                                                             seq_name: N_Geneseq_36:Q12114
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US-08-653-294-14 x Q12114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The spieen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype blsclosure; Fig 1 A-G; 20pp; English.

The human HLA-BW52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (See Q05693).
                                                                                                                                                                                                                                                                                                                                                    03-37N-1991 (first entry)
HLA-BW52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-BW52 gene; ss.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.00 Length: 10
4.333 Gaps: 0
90.000 Percent Identity: 80.000
                                                                           Align seg 1/1 to: Q05693 from: 1 to: 1089
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896. .1012
/*tag= e
/number=5
                                                                                                                             /note="alpha 2-domain"
620. .895
/*tag= d
/number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number=2
/note="alpha 1-domain'
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                                                                                                                                                                                                                                                                         seq_documentation_block:
ID 005701 standard; DNA; 1089 BP.
AC 005701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1043. .1089
/*tag= g
/number=7
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/*tag= f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/number=1
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74. .343
                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1990.
07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
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alignment_block:
US-08-653-294-14 x Q05693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-14 x Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 90-255479/34.
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Ratio:
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intron

exon

exon

exon

exon

exon

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Outer membrane protein of Haemophilus influenzae type B - used as vectine against infections, esp. in infants and for diagnosis. Disclosure: Fig 5: 33pp; English. Plasmid pRSM793 contains only the 3' portion of the Pl gene. The plasmid pRSM793 contains only the 3' portion of the Pl gene. The sequence. The cro-lace-omppl fusion protein produced from pRSM793 was recognised by rabbit and guinea pig Pl-specific antisera in
   exhibit no more than 90% homology to a human
                                                                                                                                                                                                                                                                                                                                                                                         bacterial meningitis; vaccine; Pl gene; T-cell antigen; pRSM793; outer membrane protein; ss.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= partial cro-lac2-strain MinnA Pl
fusion protein
                                                                                                                                                                                                                                                                                                                                                 26-JUL-1991 (first entry)
H.influenzae strain MinnA (OMP subtype 1H)-cro-lacZ fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1989; GB-024473.
(CONN-) CONNAUGHT LAB LTD.
(UNIW) WASHINGTON UNIV ST LOUIS.
Munson RS, Grass S, Chong P, Yang Y, Fahlm R, McVerry P;
                               57 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
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                                                                                       Length: 9
Gaps: 0
Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                               41 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                               39 C;
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                                                                                                                                                                                         Align seg 1/1 to: Q76405 from: 1 to:
                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                     1 ArgGluAspLeuArgIleLeuLeuArg
                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID Q12083 standard; DNA; 240 BP.
                            76 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-14 x Q12083/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.00
3.778
90.000
                                                                                       34.00
4.250
88.889
                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:Q12083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:X51732
Preferred sequences exh
sequence known per se.
Sequence 213 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoblot analyses.
See also R12446-R12455
                                                                                                                                             alignment_block:
US-08-653-294-14 x Q76405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9106652-A.
16-MAY-1991.
31-OCT-1990; CA0374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein M;
WPI; 91-164201/22.
                                                                                        Quality:
                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                      012083;
   2228
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New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. neurological disorders, turbuurs, inflammation or haematological disorders tumnus flavorders, inflammation or haematological disorders Claim 1: Page 170; 215pp; English.

X51701-55 encode human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene treating or ameliorating medical conditions, e.g. by protein or gene treaty. Pathological conditions can also be diagnosed by determining the presence of mutathons in the new polynucleotides. Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autolmmune disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal cord injuries, allergy, hematopoletic disorders, asthma, immunodeficiency diseases, AIDS and transplant references.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. influenzae detection probe #2.
Detection; probe; amplification primer; bacterial pathogen; pneumonia;
Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
                                 17-JUN-1999 (first entry)
DNA encoding a human secreted protein.
Human secreted protein; anence; immune disorder; infection;
Human secreted protein; anence; immune disorder; arberosclerosis;
restenosis; autoimmune disorder; Alzheimer's disease;
restenosis; autoimmune disorder; Alzheimer's disease;
hematopoietic disorder; skeletal disorder; allergy;
arthritic disorder; skeletal disorder; neurological disorder;
transplant rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS,
Rosen GA, Ruben SM, Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: X51732 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 AGGGAGGAGCTGAGAATCCAACTGCGGTGG 70
                                                                                                                                                                                                                                                                          03-SEP-1998; U18360.
12-SEP-1997; US-058974.
05-SEP-1997; US-057625.
05-SEP-1997; US-057663.
05-SEP-1997; US-057669.
12-SEP-1997; US-058666.
12-SEP-1997; US-058677.
12-SEP-1997; US-058677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T28520 standard; DNA; 1598 BP
standard; DNA; 978 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-1997 (first entry)
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US-08-653-294-14 x X51732/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen GA, Ruben SI
WPI; 99-204988/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rejection. The p
binding partners
Sequence 978 B
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                                                                                                                                                                                                                      Homo sapiens.
WO9911293-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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Homo saplens.
                                                                                                                                                     misc_feature
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   THE SKEW KENDER OF THE SERVICE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                               With gold for the detection of bacterial species using probes and wethod for the detection and quantification of antibiotic primers - allows detection and quantification of antibiotic are statut bacteria in patients, the environment and food claim 47; Page 80-81; 216pp; English.

Contacting the method comprises using probes and/or amplification primers and detecting the contacting the probes or primers. The method comprises contacting the sample with the probes or primers. The method comprises and indication of the presence and/or amount of hybridised primers or amplification products as and indication of the presence and/or amount of the bacterial products.

Contacting the sample with the probes or primers. The method comprises as and indication of the presence and/or amount of the bacterial products.

Contacting the sample with the probes or primers or amplification products as and indication of the presence and/or amount of the bacterial products.

Contacting the sample with the probes of primers of streptococcus pneumoniae, capania, staphylococcus spiderial principles. Streptococcus symposium and products and secretial principles and moraxella catarrhalis. These bacterial and spiderial principles and secretial catarrhalis. These bacterial and spiderial principles and secretial principles and secretial principles and secretial principles and secretial principles. These bacterial and spiderial principles and secretial principles a
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyplid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus; Staphylococcus epidermidis: Enterococcus faecalis; respiratory tract; Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract; Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis; infection; intra-abdominal infection; skin infection; skin infection; bacterial resistance; beta-lactam antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections and other severe respiratory tract infections. The method may also be used to evaluate a bacterial resistance to beta-lactam
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Gaps: 0
Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1425 CGTAAAGATTTGCGTGTGCTTGAGAAGTAT 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
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541. .600
                                                                                                                                                                                                                                                                                                                                                                                                                        Roy PH;
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ID V74565 standard; DNA; 2881 BP.
AC V74565;
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                                                                                                                                                                                                                                                                                                                                                           (OUEL/) corr
(ROYP/) ROY P H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-653-294-14 x T28520/rev
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90.000
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                                                                                                                                                                                                                                                                  12-SEP-1995; CA0528.
12-SEP-1994; US-304732.
(BERG/) BERGERON M.G.
(OUEL/) OUELLETTE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.00
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                                                                                                                                                                                                                                                                                                                                                                                                                  Bergeron MG, Oue.
WPI; 96-179953/18
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                                                                                                                                                                                                                                          21-MAR-1996.
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Tati-S. aureaus vaccines

Claim 1; Page 1047-1049; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences
of the invention. The DNA sequences are recorded on a computer readable
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access
memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
that protein-encoding or regulatory regions of commercial, therapeutic or
industrial importance can be obtained. Specifically, sequences which are
likely to encode antigens have been identified and these polypeptides can
be used in a vaccine composition against S.aureus infection. The
collypeptides can also be used in a kit for the immunodatection of
S.aureus in a sample. S.aureus is implicated in numerous human diseases,
including cellulitis, eyelid infections, food poisoning, osteomyelitis,
skin and surgical wound infections, scalded skin syndrome, toxic shock
syndrome, etc. Organisms transforamed with the DNA sequences can be used
for recombinant production of the polypeptides. The new DNA sequences
can their fragments) are useful as primers or probes for isolating
computer readable medium.
/*tag= a /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                           'these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
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Neural alpha-cateain protein coding sequence.
Adhesion; neural alpha catemin; tumour; metastasis; disease; autoimmune disease; infectious disease; dermal disease;
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07-JAN-1997; 100117.
07-JAN-1996; US-009861.
(HUMA.) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 2881
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/note= "these bases
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US-08-653-294-14 x V74565/rev
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Ratio: 3.778
Percent Similarity: 100.000
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PN J06211898-A.
PD 02-AUG-1994.
PP 02-AUG-1994.
PF 25-DEC-1992; JP-358026.
PR 25-DEC-1992; JP-358026.
PR 47AKI ) TAKARA SHUZO CO LTD.
PP SDB R5778.
PP SDB R5778.
PP SDB R5778.
PR 191 adhesion, e.g., in treatment of tumour (metastasis) and pr autoimnume disease
PT autoimnume disease
PS Disclosure; Page 10-14; 14pp; Japanese.
CC The neural alpha catenin can be used for the treatmnet of diseases
CC The neural alpha catenin can be used for the treatmnet of diseases
CC Telated to intercellular adhesion such as primary tumour, tumour metastasis, autoimmune diseases, infectious diseases, dermal
CC diseases and arteriosclerosis.
Sequence 3123 BP; 920 A; 674 C; 827 G; 702 T;
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Align seg 1/1 to reverse of: Q67406 from: 1 to: 3123

alignment\_block: US-08-653-294-14 x Q67406/rev ŷ · \_

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AI055656 coau0004K01 Cotton
AW208428 uo60c03.x1 NCI_CGAP
B20285 T20J7-T7 TAMU Arabido
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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@dkf2-heidelberg.de;
sequenced by Qiaqen within the CDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
ource
//draman="Homo sapiens"
//clone="DKF2p56404043"
//clone="DKF2p56404043"
//dev_stage="fetal"
/
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LOCUS AU015838 701 bp mRNA EST 29-APR-1999
DEFINITION AU015838 Oryza sativa mature leaf Nipponbare Oryza sativa cDNA
ACCESSION AU056838
VERSION AU056838 GI-4715722
                                                                                                                                                                             AL036690 171 bp mRNA EST 27-SEP-1999 DKFZp564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564D2463_r, mRNA sequence.
AL036690 GI:5927859
                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5866258.
Contact: Duesterhoeft A
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US-08-653-294-14 x AL036690
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gb_est44:AW208428
gb_gss3:B20285
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COMMENT
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AUTHORS
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  OM of: US-08-653-294-14 to: EST:*
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Query: US-08-653-294-14
Query length: 10
Database: EST:*
Database sequences: 4538634
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                                                             Date: Feb 8, 2000 4:02 AM
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gb_est16.AA596937
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gb_est8:C03945
gb_est10:AA151891
gb_est11:AA95260
gb_est11:AA95260
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gb_est21:A1028215
gb_gss11:AQ301014
gb_est9:AA082472
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gb_est9:AA082478
gb_est37:A1946939
gb_est24:A1239094
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gb_est8:AA015279
gb_est3:A1746514
gb_est28:A1508196
gb_est11:AA239196
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gb_est39:AW119564
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human.
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

E 1 (bases 1 to 701)

S Yamamoto, K. and Sasaki, T.

Rice cDNA from mature leaf

L Unpublished (1999)

Con Jun 5, 1999 this sequence version replaced g1:3187083.

Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       am64002.s1 Barstead spleen HPLRB2 Homo saplens cDNA clone
IMAGE:1576803 3' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 402)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. Washy-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
/strain="Nipponbare"
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/clone="250919_lb"
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/ 169 c 230 g 151 t 6 others
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On Jan 19, 1998 this sequence version replaced gi:2153091.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                 Japan 305
Tel: 0298-38-7441
Eax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
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                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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US-08-653-294-14 x AU056838/rev
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LOCUS AA989542
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Percent Similarity:
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                                                                                                                   TITLE
JOURNAL
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JOURNAL
COMMENT
                                                                                REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3618
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong library availability, please contact Pieter de Jong library availability, codu, clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: -domi3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS A0440876 501 bp DNA GSS 31-MAR-1999
DEFINITION HS_5098_B2_B04_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=674 Col=8 Row=D, genomic survey sequence.
ACCESSION A0440876
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
                                                                                                                                                            1. .402

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Gaps: 0
Percent Identity: 88.889
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US-08-653-294-14 x AA989542/rev
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Percent Similarity: 100.000
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alignment_block:
US-08-653-294-14 x AA975627/rev
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Percent Similarity: 100.000
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US-08-653-294-14 x C03945
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Ratio:
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                                                                                                                         93
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                                                                                                                         BASE COUNT
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MEDLINE
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KEYWORDS
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                                                                                                                                              ORIGIN
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 505)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    og63b05.s1 NCI_CGAP_Kid6 Homo sapiens CDNA clone IMAGE:1590993 3/similar to gb:L05093 608 RIBOSOMAL PROTEIN L18A (HUMAN);, mRNA
                                                                                                                                                                                                                       /sex="male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
102 c 80 g 144 t 7 others
                                                                                                                                          /organism="Homo sapiens"
/db_xref="texon:9606"
/clone="plate=674 Col-8 Row=b"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 60.000
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High quality sequence stop: 255.
Location/Qualifiers
1. .505
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGE:1590993"
/clone="ImAGE:1590993"
/clone="ImAGE:1590993"
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2
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http://www.htsc.washington.edu
Plate: 674 row: D column: 8
Seq primer: 17
Class: BAC ends
High quality sequence stop: 501.
10.cation/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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AA975627.1 GI:3151419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-14 x AQ440876/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 bp
                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.000
Percent Similarity: 100.000
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AUTHORS
TITLE
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KEYWORDS
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/lab_host="Solk (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1:
BcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dI. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGITTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."
a 115 c 177 g 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
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/doganism="Homon sapiens"

/db_xref="taxon:9606"

/clone="3NHC2454" heart cDNA (YNakamura)"

/dev_stage="ault" heart; normalized directionally cloned cDNA

/note="Organ: heart; normalized directionally cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS
LOCUS
C03945
DEFINITION C03945 Human heart cDNA (YNakamura) Homo sapiens cDNA clone
3NHC2454, mRNA sequence.
ACCESSION C03945
VERSION C03945.1 GI:1467196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 232)
Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Oct 24, 1995 this sequence version replaced gi:1040105
Contact: Yusuke Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
12-1, 81-3-5449-5372
Fax: 81-3-5449-5433
                                                                                                                                                                                                                                                                                                 Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10 Gaps: 0 Percent Identity: 80.000
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AA975627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
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77 c 68
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AA263158 283 bp mRNA EST 02-JUL-1998
PMY0534 KG1-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 CGGGAAGAGTTGAGGCTTATTATCCGCTAC 206
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Percent Similarity: 100.000
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US-08-653-294-14 x AA952680
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                                                                    seq_name: gb_est21:AA952680
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AA263158
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                                                                                                                 seq_documentation_block:
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 255)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Worris,M., Parsons,J., Prange,C., Rikkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: colon; Vector: pBluescript SK-; Site_1:
Corn: Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGITTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                              seq_documentation_block:

LOCUS AA151891 255 bp mRNA EST 10-DEC-1996
DEFINITION zoolf06.r1 Stratagene colon (#937204) Homo saptens cDNA clone
IMAGE:566435 5' similar to gb:HI5497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97044478
On May B, 1995 this sequence version replaced gi:800234
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .255
/organism="Homo sapiens"
/db_xref="GDB14590888"
/db_xref="taxon:9606"
/clone="IMACE:566435"
/clone_lib="Stratagene colon (#937204)"
/lab_host="SOLR cells (Kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 others
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Gaps: 0
Percent Identity: 80.000
  to: 232
                                            1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                                                                         40 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 69
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from: 1
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AA151891.1 GI:1720754
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US-08-653-294-14 x AA151891
                                                                                                                                 seq_name: gb_est10:AA151891
to: C03945
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Ratio:
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Align seg 1/1
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Length: 10 Gaps: 0 Percent Identity: 60.000

from: 1

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/clone="1864" /clone_lib="T. cruzi epimastigote normalized cDNA Library"
                       epimastigote normalized cDNA Library Trypanosoma 1864 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      San Martin)
Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
Cp(1650) San Martin, Prov. de BS AS. Argentina
Tel: (54-1)752-9639 or (54-1)752-9639
Email: dsanchezelnti.gov.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="epimastigote"
/note="cDNA library constructed with oligo dr primed
epimastigote mRNA and cloned in pt7t318D phagemid with
modified polylinker (PHARMACIA)"
     29-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Instituto de Investigaciones Biotecnologicas (Univ. Nac. de
                                                                                                                                                                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jan 17, 1998 this sequence version replaced gi:1900451. Contact: Sanchez D.O.
                                                                                                                                                                                   Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
Trypanosoma; Schizotrypanum.
1 (bases 1 to 26)
Verdun, N.E., Di Paolo, N.C., Urmenyi, T.P., Rondinelli, E.,
Frasch, A.C.C. and Sanchez, D.O.
Gene discovery through expressed sequence tag sequencing
trypanosoma cruzi
Infect. Immun. 66 (11), 5393-5398 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Cl-Brenner"
/db_xref="taxon:5693"
     mRNA
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AA952680 269 bp mR
TENS1864 T cruz1 epimesti
cruz1 cDNA clone 1864 5',
AA952680 AB952680.1 GI:3115776
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90
                                                                                                                                                                       Trypanosoma cruzi.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI: Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
te the EcoRI site. cDNA was size fractionated to remove
sequences <loop by in size." 3 others
         Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
                                                                                                                                                Location/Qualifiers
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Class: shotgun
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 283) Loado, J. O. 283) Liew, C. C., Dempsey, A.A., Cukerman, E., Stewart, A.K., Na, E., Atkins, H.I., Iscove, N. N. and Hawley, R.G. Identification of sequence-tagged transcripts differentially Genomics 50 (1), 44-52 (1998)
                                                                                                                                                                                                                                                                                                                                                                                     On May 5, 1995 this sequence version replaced gi:797810.
Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley RG
Contool Wesearch Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403834
Fax: 416 3403834
Fax: 416 3403834
Fax: 416 3403836
Fax: 416 340386
Fax: 416 340386
Fax: 416 340386
Fax: 416 340386
Fax: 416 34086

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D82221 375 bp mRNA EST 09-FEB-1996 WWHBC4620, Human pancreatic islet Homo sapiens CDNA similar to
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 80.000
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D82221
D82221.1 GI:1183739
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Takeda,J.
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US-08-653-294-14:x AA263158
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San Martin)

Vo Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
CP(1650) San Martin, Prov. de BS AS. Argentina
Tel: (54-11)4752-0021
Fax: (54-11)4752-9639
Email: dsanchez@inti.gov.ar
                                                                                                                                                                                                                                                                                                                                    31-MAR-1999 cruzi genomic library Trypanosoma cruzi genomic clone G10N2 5', genomic survey sequence. AQ444169.1 G1:4555633 GSS
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Instituto de Investigaciones Biotecnologicas (Univ. Nac.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 401)
Sanchez,D.O.
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/clone=11b="Trypanosoma cruzi random
/cell_type="epimastigote"
/note="Vector: pBS(') (PHARMACIA)"
Length: 10
Gaps: 0
Percent Identity: 80.000
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93 g 65 t 3
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/strain="Cl-Brenner"
/db_xref="taxon:5693"
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LOCUS AQ44169
DEFINITION GSSTC0231 Trypanosoma
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seq_documentation_block:
LOCUS AAA47151 581 bp mRNA EST 05-DEC-1996
DEFINITION 2032406.rl Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.
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1 (bases 1 to 581)

Hillari, L. Lennon, G. Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hakkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 272.
Location/Qualiflers
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On Sep 12, 1996 this sequence version replaced gi:1393699.
Contact: Wilson RK
Washington University School of Medicine
W444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                     Length: 10
.Gaps: 0
Percent Identity: 70.000
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Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                             1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                      from: 1
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AA147151.1 GI:1716526
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4.333
90.000
                     39.00
4.333
90.000
                                                                                                                                                                                                   to: AI957215
                                                                                                                            alignment_block:
US-08-653-294-14 x AI957215
                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est10:AA147151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Ratio:
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                                                                          Percent Similarity:
                             Quality:
                                                  Ratio:
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alignment_scores
                                                                                                                                                                                                   Align seg 1/1
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ncce="Organ: Kidney; Vector: pME18S-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer |
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG); Xaite CACCATGTG, 3' site CACTGTGTG, 3' site CACCATGTG, 1stes of the pME18S-FL3 vector (5' site CACTGTGTG, 1ste CACCATGTG); Caccatage selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTCCTCTAAAAGCTGCG and 3' end primer CGACCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eckaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eckaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 424)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3187965.
Other ESTS: u177al0.yl
Mashington University School of Medicine
4444 Forest. Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fai: 314 286 1810
                                                                                                                                                                                                                                                                                                                                          seg_documentation_block:
LOCUS A1957215 424 bp mRNA EST 20-AUG-19:
DEFINITION u177a10.x1 Sugano mouse kidney mkia Mus musculus CDNA clone
IMAGE:2136570 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib-"Sugano mouse kidney mkia"
/sex-"female"
/dev_stage-"adult"
/lab_nost-"DH108"
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                    Align seg 1/1 to reverse of: AQ444169 from: 1

    .424
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: custom primer used High quality sequence stop: 263. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:2136570"
                                                                                                                                                                                                                              10
                                                                                                                                                                                                      1 ArgGluAspLeuArgIleLeuLeuArgTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI957215.
AI957215.1 GI:5749924
                                                                          alignment_block:
US-08-653-294-14 x AQ444169/rev
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Ratio: 3.900
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                     seg_name: gb_est37:A1957215
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BASE COUNT ORIGIN

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

ACCESSION VERSION

to: 618

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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/clone_lib="CpiOWANIJMpl8gDNA1"
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/lab_host="E. coli DH125"
/lab_host="E. coli DH125"
/note="Vector: MI3mpl8 Site_l: Hind III; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 1.5 and 3 kb. Adaptors (pGTGATCAA/CAAACCACTGATP) were ligated to the randomly sheared gDNA fragments and pAGCTGTTG linkers were ligated to the Hind III-cleaved MI3mpl8 vector. The adaptor-containing inserts were annealed and ligated to the vector and transformed into E. coli strain DH125. Recombinant phagemid clones from the first plating of the library were randomly selected for sequence analysis using the MI3'-21) forward primer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hyman@sequence.stanford.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seq primer: M13(-21) forward
                                                                                                                                                                                                                  Cryptosporidium parvum.
Cryptosporidium parvum.
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidildae; Cryptosporidium.
I (bases 1 to 715)
Hyman, R.W., Fung, E., (lin,F., Rowley, D. and Davis,R.W.
Cryptosporidium parvum genome sequencing demonstration project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
On Mar 23, 1999 this sequence version replaced gi:3325323.
Contact: Hyman, R. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford DNA Sequencing and Technology Center Stanford University School of Medicine, Palo Alto 855 California Avenue, Palo Alto, CA 94304, USA Tel: 650 812 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
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                              from:
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                                                                                                                            319 CGAGAGCTGCGGATCGCGCTCCGCTAC 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5807"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                              to reverse of: AI359260
                                                                              1 ArgGluAspLeuArgIleLeuLeuArgTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="IOWA
                                                                                                                                                                                                                                                                                                                                                 AQ449604.1 GI:4578741
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US-08-653-294-14 x AQ449604
                                                                                                                                                                            seq_name: gb_gss13:AQ449604
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Percent Similarity:
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                           Align seg 1/1
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ORIGIN
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 618)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS

A1359260

BEFINITION q9272007.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 3/
Similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.

ACCESSION A1359260.1 GI:4110881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homlnidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="Taxon:9606"
/clone="Taxon:0606"
/clone=11b="ncl_cGAP_Brn23"
/fissue_type="qlioblastoma (pooled)"
/lab_host="DH100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 80.000
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High quality sequence stop: 458.
Location/Qualifiers
1. 618
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                                                                                                                                                     1 ArgGluAspLeuArgIleLeuLeuArgTyr 10
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US-08-653-294-14 x AI359260/rev
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alignment_block:
US-08-653-294-14 x AA147151
                                                                            Align seg 1/1 to: AA147151
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alignment\_scores:

BASE COUNT ORIGIN

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22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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1..10
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W47268;
78883330
2444883333
24695
2666
2666
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Homo sapiens
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                     V09744052-A1
                                                                                                                                                                                                                                                                                                                                    Synthetic.
Sequence
                                                                                                                                                                                                              RESULT
 W4727;
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Immunomodulatory p
HLA-B2702 CTL modu
HLA-B2702 CTL modu
HLA-B2702 CTL modu
HLA-B2702 CTL modu
Immunomodulating d
Peptide B2702.84-7
HLA-B2702 CTL modu
HLA-B2702 CTL modu
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HLA-B2702 CTL modu
Peptide B2702.84-7
Peptide B2702.84-7
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Rice anthranilate
Rice ASA first iso
Rice anthranilate
Human calcium chan
Regulatory factor
H. pylori GHPO 121
A partial gidAl pr
Helicobacter pylor
A gidAl protein se
Human Hrs-2 partial
113 kD ISGF-3 alpha
Recognition factor
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Rat Hrs-2 polypept
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Human Nup358 prote
Immunomodulatory p
                                                                                        Search time 122.56 Seconds (without alignments)
1.933 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunomodulatory
Immunomodulatory
                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                          Compugen Ltd.
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                        188963 seqs, 23686106 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                          8, 2000, 01:29:38
                                                                 sw model
                                                                                                                                                                                                                                                                                                                                                 summaries
                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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W47270
W47266
R92909
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R92907
R95428
W33778
W33779
W33792
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R95430
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W93815
W93810
R27642
W12377
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W89446
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W89445
W79193
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R72077
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W54235
W47264
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                                                                 protein search, using
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Listing first 45
                                                                                                                                    US-08-653-294-15
49
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Match Length DB
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length: 1000000
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H. pylori GHPO 54
S. aureus gidB pro
S. aureus gidB pro
Rat FRAGI protein.
3-acylation enzyme
EHV-4 gC. Nucleic
Human TIE ligand N
Mouse Smad6 protei
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23-ARR-1997; U06705.
22-MAY-1996; U5-651550.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 98-018220/02.
NOVel immunomodulatory peptide-type compound - useful for inhibiting
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(laim 10; page 36; 41pp; English.
The present sequence is an immunomodulatory peptide, which
comprises a class HiA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.
Peptides using the D-form amino acids are more effective
immunomodulators than their diastereomers or enantiomers.
  Peptide #4
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1. .10
/note= "at least one of the amino acids is the
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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100.0%; Pred. No. 0.00025;
ive 0; Mismatches 0;
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W33783
W98580
W74405
W74406
W41592
W41592
R15428
R20796
W805397
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W805397
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Best Local Similarity 100.
Matches 10; Conservative
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1 YRLLIRLDER 10
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WO9526979-A1.
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Synthetic.
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                                     27-NOV-1997.
23-ARR-1997: U06705.
22-ARR-19997: U06705.
22-MAY-1996; US-651650.
Clayberger C, Krensky AM;
WPI; 99-018220/02.
WOVel immunomodulatory peptide-type compound - useful for inhibiting transplant rejection
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                Claim 10; Page 36; 41pp; English.

The present sequence is an immunomodulatory peptide, which comprises a Class I HIA-B alpha-1 domain sequence. It can be used comprises a Class I HIA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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The present sequence is an immunomodulatory peptide, which comprises a Class I HiA-B alpha-i domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in
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D-isomer
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Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition; Hransplant rejection; treatment; autoimmune disease.
Homo sapiens.
Synthetic.
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Pred. No. 0.0027;
1; Mismatches 0; Indels
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23-ARF-1997; U06705.
22-ARY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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90.0%;
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Best Local Similarity 90.0
اندم 9; Conservative
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WPI; 98-018220/02.
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Best Local Similarity
Matches 9; Conserv
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W47270
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1; Indels

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HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1997; U06705.
22-MAY-1996; U5-651650.
(STRD) UNIV LELAND STANFORD JUNIOR.
(STRD) UNIV LELAND STANFORD MWICE
(STRD) SP-018220/02.
WPI; 98-018220/02.
NOVEL immunomodulatory peptide-type compound - useful for inhibiting
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The present sequence is an immunomodulatory peptide, which comprises a Class I HiA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.

Peptides using the D-form anino acids are more effective immunomodulators than their diastereomers or enantiomers.
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                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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05-ARR-1995. 004349.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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R92909;
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| YRLAIRLNER 10
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| YRLAIRLDER 10
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Matches 8; Conserv
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WPI; 95-358582/46.
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                                                         The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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R83061-R83085, R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dinmer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abunish compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CLEs)
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HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
is an inverted dimer of residues 75-84 of the alpha-1 domain of the cla
I MHC HLA-B2702. These sequences can be used to extend the period of
acceptance by a recipient of a transplant from an MHC unmatched donor.
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Pred. No. 0.062;
1; Mismatches 1
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Pred. No. 0.062;
1; Mismatches 1
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R92907;
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80.0%;
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05-APR-1995; U04349
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Best Local Similarity
Matches 8; Conserv
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WPI; 95-358582/46.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                         20 AA;
                                                                                                                                                                                 of the patient.
Sequence 20 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patient.
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R92907
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Clayberger C, Krensky AM;

Clayberger C, Krensky AM;

Clayberger C, Krensky AM;

RPI: 95-194027/25.

RPI: 
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for unrent treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HIA-B2702 84-75-84 palindrome.
HIA-B2702 84-75-84 palindrome.
HIA-B2702 84-75-84 palindrome.
HIA-P74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA-P74; alphal-helix; naman-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                  Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                    Krensky AM, Parham P;
12-OCT-1995.
05-APR-1995.
05-APR-1994; UG-222851.
(S-RRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLLIRLDER 10
                                                                                                                                                                                                        Clayberger C, Kre wPI; 95-358582/46.
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| YRLAIRLNER
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(first entry)

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This sequence represents a specifically claimed immunomodulating diversity accommended a specifically claimed which has immunomodulating activity, including the N-terminal addressents a specifically claimed which has immunomodulating activity, including the N-terminal activity, where the period or esterified forms of up to 60 amno acids, where the pertide-type compound comprises the formula A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or N; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a rycophobic or small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HiLAB compounds comprise amino acid sequences related to a class I HiLAB compounds comprise amino acid sequences related to a class I HiLAB compounds comprise amino acid sequences related to a class I HiLAB compounds comprise amino acid sequences related to a class I HiLAB composites (CTL) from undesirably attacking cells in a host or in proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the class of the products of the response to anti-CD3. The peptide can be consequently activated the compound of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
                   Immunomodulating dimer peptide #2.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                  New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
                                                                                                                                                                                                       24-MAY-1996; US-653294.
(STRO) UNIY LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                      22-MAY-1997; U08689
                                                                                                                            Homo sapiens.
                                                                                                                                                                  27-NOV-1997
                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              With a compound of the peptide (s) - based on a class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autofimmune diseases a transplants or treating autofimmune diseases as the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 anino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-84) or (aa84-7) (laa37-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HiA-B aphal domain (positions 79-84). They can be used to inhibit cytocoxic alphal domain also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the products of interest to activate CTLs. They can also inhibit the used for preventing rejection of Transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
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Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Sequence 20 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulating dimer pétide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                      ö
                                                                                                                                             Score 39; DB 1; Length 20; Pred. No. 0.062;
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                                                                                                                                                                                      1; Indels
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                            79.6%; Sured
80.0%; Pred
1;
                                                                                                                                                                                                                                                                                                                                                                     W33778 standard; peptide; 20 AA
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                           Query Match 79.6
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.6
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                            1 YRLLIRLDER 10
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| YRLAIRLNER 10
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WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 - NOV - 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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20 AA;

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24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases
Example 1; Page 19, 41pp; English.
Peptides W33784-98 and W337789 were assayed for their immunomodulating
activity. A peptide-type compound or variant is claimed which has
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                      19-JUN-1998 (first entry)
Peptide B3702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer. Immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                          ö
79.6%; Score 39; DB 1; Length 20; 80.0%; Pred. No. 0.062; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                      W33792 standard; peptide; 20 AA.
                         Best Local Similarity 80.0 Matches 8; Conservative
                                                                                                            1 YRLLIRLDER 10
                                                                                                                                                WO9744351-A1.
27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
     Query Match
                                                                                                                                                                                                                                                                                                                                     W33792;
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Gaps

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1; Indels

1; Mismatches

1 YRLLIRLDER 10 

ò g W33779 standard; peptide; 20 AA. W33779;

RESULT 10

W33779

16-MX-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.

R92908 standard; peptide; 20 AA.

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I  $975-84\ \mathrm{MHC}$  antigen of the recipient

05-ARR-1993; US-222851. 05-APR-1994; US-222851. (STRD ) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Kre. wPI; 95-358582/46.

12-OCT-1995. 05-APR-1995; U04349.

Synthetic. WO9526979-A1.

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immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the perpute-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HIA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, considerating antiputs and lupus erythematosis. The products can also be accorded to a thirthing and lupus erythematosis. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHC unmatched the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length 20;
Pred. No. 0.062;
!; Mismatches 1; Indels
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Pred. No. 0.67;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extension of acceptance period of transplants from donor hosts - using Class I B75-84 MHC antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1994; US-222851.
(STRD ) UNIV-LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P
WPI; 95-338582/46.
                                                                                                                                                                                                                                                                                                                                                            used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R92910 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.4%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLLIRLDER 10
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| YRLAIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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R92910
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for unrent treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composite. 2012/2012/2012

Example: Page 12: 29pp: English.

Example: Page 12: 29pp: English.

Example: Page 12: 29pp: English.

Eystl3, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-B2702 84-757/75-84T palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein massociated with T-cell activation in manmalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1996 (first entry)
HIA-B2702 84-757/75-84r palindrome.
HIA-B2702 84-757/75-84r palindrome.
HIA-D74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 1; Length 20; Pred. No. 0.67; 1; Mismatches 2; Indels
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10-MOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytolysis; antigen presenting cell. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%; Scc.
70.0%; Pred
1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRLLIRLDER 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WÖ9513288-A1.
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Gaps

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Conservative

1 YRLLIRLDER 10 

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regitles W3374-99 and W3577-99 Were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = (B, Sor N: aa79 = R or E; aa80 = I or N: aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antiqenic peptides or proctains of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating auttoimmune diseases, e.g. diabetes, consume the seather authorities and lupus erythematosis. The products can also be consumed to the products can also be
a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolysis activity of T-cells, by combining them with the extracellular portion of p74 and determining the manut of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
Example 1; Page 19; 41pp; English.
Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1998 (first entry) Peptide B2702.84-75T/75-84 tested for immunomodulating activity. Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 69.4%; Score 34; DB 1; Length 20; Best Local Similarity 77.8%; Pred. No. 0.67; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used for detection and diagnosis. Sequence 20 AA;
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W09744351-Al.
27-NOV-1997.
22-MAY-1997; U08689.
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            8666666666666668
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Gaps

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Ouery Match 69.4%; Score 34; DB 1; Length 20; Best Local Similarity 70.0%; Pred. No. 0.67; Matches 7; Conservative 1; Mismatches 2; Indels

1 YRLLIRLDER 10

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Db 1 YRLATRINER 10
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Search completed: February 8, 2000, 01:29:38 Job time: 1750 sec

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February 7, 2000, 11:54:24; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                      142080
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 142080 seqs, 47169319 residues
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                         US-08-653-294-13
                                                                                                                                                                                                         1 YRLAIRLDER 10
                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                     Run on:
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PIR\_62:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Post-processing: Minimum Match 0% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		hypothetical prote	men		ical p		11-cis-retinol deh	nitrogen regulatio	nitrogen regulatio	probable acetate	ceni	rotei	_	sugar-phosphate al	hypothetical prote	probable seryl-tRN	glycoprotein gp13		carboxylesterase (	DNA-directed RNA p	probable membrane	ethylene receptor	efflux s	cadmium, zinc, cob	zinc-finger protei	surface layer prot	complement compone		conserved hypothet	
SUMMARIES	ΩΊ	327	327	C64941	054	111	441	A55429	I45845	RGECGL	411	290	989	129	173	229	564	250	B45343	058	408	882	452	669	383	2470	C206	55	1407	4285	7000	
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ď	Query Match	69.4	9.	67.3	7.	S.	ς.	'n.	S.	'n.	ů.	ď.	ď.	Š.	ъ.	ω.	щ.	'n.	e,	ω.	m.	æ,	m.	m.	ω.	ω.	w.	ë.	ω.	m.	<del></del> .	
	Score	, m	34	33	33	32	32	. 32	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	30	
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hypothetical prote hypothetical prote hypothetical prote probable transcrip probable transcrip probable bux adeni hypothetical prote hypothetical prote histidine acid pho RING finger proteiret finger proteiret finger proteiret probable probable prosphori puff-specific nucl conserved hypothet probable cell divi
D72544 F70457 F70457 F70459 H64759 H11237 H11537 H105369 S37583 S37589 S76869 FVHUKE S76869 TVHUKE S76869 TVHUKE S76869 H6695 H76695 H76695 H76695 H76695
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## ALIGNMENTS

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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-185 <KAN>
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RESULT 3
C64941
hypothetical protein b1803 - Escherichia coli (strain K-12)
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 29-Sep-1999
C; Accession: C64941
R; Blattner, F.R; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: C64941
A; Accession: C64941
A; Residues: 1-321 ABLAT>
A; Molecule type: DNA
A; Molecule type: DNA
A; Rosidues: 1-321 ABLAT>
A; Cross-references: GB:ABCOO0274; GB:U00096; NID:g1788089; PIDN:AAC74873.1; PID:g1788104;
A; Experimental Source: strain K-12, substrain MG1655
C; Superfamily: phthalate dioxygenase reductase: cytochrome-b5 reductase homology CER>
F; 254-309/Domain: ferredoxin [2Fe-25] homology CER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable menD protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, N.; Rutter, S.; Seeger, K.; Skelton, S.; Ramlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1554

A;Cooss-references: GB:229558; GB:AL123456; NID:93261781; PID:e316800; PID:92114017

C;Genteics:

A;Gene: menb

C;Superfamily: menD protein
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C71113
C71113
C75pecles: Pyrococcus horikoshii
C;Specles: Pyrococcus horikoshii
C;Specles: Pyrococcus horikoshii
C;Decles: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998
C;Accession: C71113
C;Accession: C71113
C;Accession: C71113
M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S; Sekin
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 321;
Pred. No. 22;
4; Mismatches 0; Indels
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Pred. No.
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55.6%;
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66.78;
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Best Local Similarity 55.6
Matches 5; Conservative
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70 YQIAVRLEE 78
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48 RLHVRIDER 56
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DNA Res. 5, 55-76, 1998
A;Tille: Complete sequence and gene organization of the genome of a hyper-thermophill
A;Reference number: A71000; MUID:98344137
A;Accession: C71113
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-151 <KRW>
A;Cross-references: GB:AP000003; NID:93236130; PID:d1030708; PID:93257082
A;Cross-references: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Bos primigenius taurus (cattle)
C; Species: Dos primigenius taurus (cattle)
C; Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 29-Sep-1999
C; Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 29-Sep-1999
R; Simon, A.; Hellman, U.; Wernstedt, C.; Eriksson, U.
J; Biol. Chem. 270, 1107-1112, 1995
A; Title: The retinal pigment epithelial-specific 11-cis retinol dehydrogenase belongs
A; Reference number: A55429; MUID:95138097
A; Accession: A55429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr. 1997 #sequence_revision 25-Apr. 1997 #text_change 21-Aug. 1998
C; Accession: S74416
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:D64001; GB:AB001339; NID:q1001102; PID:d1010985; PID:g100119
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1.518 <cim>A; Residues: 1.518 <cim>A; Cross-references: GB: X82262; NID:g663170; PIDN: CAA57715.1; PID:g663171
C; Superfamily: retinol dehydrogenase; short-chain alcohol dehydrogenase homology
C; Keywords: membrane protein; NAD; oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Synechocystis sp. (strain PCC 6803)
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Pred. No. 20;
3; Mismatches
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Pred. No. 16; 00; Mismatches
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A; Accession: S74416
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nitrogen regulation protein II (EC 2.7.3.-) ntrB - Klebsiella pneumoniae
C; Species: Klebsiella pneumoniae
C; Accession: A24114
R; MacFarlane, S.A.; Merrick, M.
R; MacFarlane, S.A.; Merrick, M.
Norleic Acids Res. 13, 7591-7607, 1985
A; Reference number: A24114; MUD:86067184
A; Accession: A24114
A; Molecule type: DNA
A; Residues: 1-349 < AAC
A; Accession: A24114
A; Molecule type: DNA
A; Residues: 1-349 < AAC
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: glnL regulatory protein II; sensor histidine kinase homology
C; Superfamily: glnL regulatory protein II; sensor histidine kinase homology
C; Superfamily: autophosphorylation; phosphohistidine; phosphotransf
F; 104-346/Domain: sensor histidine kinase homology < CSHK>
F; 139/Binding site: ATP (Lys) **status predicted
                                                                                                                                     A: Reference number: A64720; MUID: 97426617
A: Reference number: A64720; MUID: 97426617
A: Reference number: A64720; MUID: 97426617
A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-349 < RAEADOM662; GB: U00096; NID: 91790295; PIDN: AAC76866.1; PID: 917903
A: Cross references: GB: AE000462; GB: U00096; NID: 91790295; PIDN: AAC76866.1; PID: 917903
A: Rinfa, A.J.; Bennett, R.L.
J. Biol. Chem. 266, 6888-6893, 1991
A: The ference number: A39765; MUID: 91201336
A: Reference number: A39765
A: Reference number: A39765
A: Reference number: A39765
A: Residues: 2-11;136-142;158-162, 'X', 164-169 < NIN>
C: Genetics: C: Genetics: A39765
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A.Map position: 87 min
A.Map position: de-uridylylated P-II forms a complex with nitrogen regulation protein
A.Mote: phosphorylated form of P-II does not complex with ntrB; free ntrB phosphorylates ni
A.Note: phosphorylated nitrogen regulation protein I (ntrC) activates transcription o
C.Superfamily: glnL regulatory protein II; sensor histidine kinase homology
C.Keywords: ATP; autophosphorylation; phosphohistidine; phosphoprotein; phosphotransf
F:104-346/Domain: sensor histidine kinase homology ASHK>
F:139/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predited
   R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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llarity 75.0%; Pred. No. 39;
Conservative 1; Mismatches
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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277 YRLAARID 284
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277 YRLAARID 284
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Invest. Ophthalmol. Vis. Sci. 36, 1988-1996, 1995
A;Title: Cloning and expression of a CDNA encoding bovine retinal pigment epithelial 11-A;Reference number: 145845; MUID:95386398
A;Accession: I45845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrogen regulation protein II (EC 2.7.3.-) ntrB - Escherichia coli
N;Alternate names: regulatory protein glnL
C;Species: Escherichia coli
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C;Accession: A30377; S40814; B23970; H65191; A39765; Q00553
C;Accession: A.); Sanchez-Pescador, R.; Urdea, M.; Covarrubias, A.A.
Nucleic Acids Res. 15, 2757-2770, 1987
A;Itle: The complete nucleotide sequence of the glnALG operon of Escherichia coli K12.
A;Reference number: A30377; MUID:87174797
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Gene 37, 91-99, 1985
A;Title: Nucleotide sequence of the glnA-glnL intercistronic region of Escherichia coli.
A;Reference number: A91533; MUID:86031370
A;Accession: B23970
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A; Residues: 1.349 (ANIR)
A; Cross-references: EMBL: X05173; NID:941562; PIDN:CAA28807.1; PID:941564
A; Cross-references: EMBL: X05173; NID:941562; PIDN:CAA28807.1; PID:941564
A; Experimental source: K-12
R; Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic, Acids Res. 21, 3391-3398, 1993
A; Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from A; Reference number: $40802; MUID:93347969
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A;Cross-references: EMBL:L19201; NID:g304961; PIDN:AAB03003.1; PID:g304974
A;Experimental source: strain K-12, substrain MG1655
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
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A;Residues: 1-24 <ROC>
A;Cross-references: GB:KO2176; GB:M11581; NID:g146160; PIDN:AAA23881.1; PID:g146162
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                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Bos prinigenius taurus (cattle)
Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 29-Sep-1999
Accession: 145845
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Pred. No. 35;
2; Mismatches
       5;
   35;
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   Score 32;
Pred. No.
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   65.3%;
75.0%;
Query Match 65.3
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
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44 LALRLDQR 51
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LALRIDOR 52
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Length 349 Indels

DB 1; 39;

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Gaps

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Indels

Length 349;

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C;Species: Rickettsia prowazekii
C;Date: 21.NOV-1998 #sequence_revision 21-NOV-1998 #text_change 16-Jul-1999
C;Accession: H71731
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature: 364, 133-140, 1998
A;Tile: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499
                                                                                A; Accession: S61294
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-546 <12A>
A; Cross-references: EMBL: D29672; NID: 9473964; PIDN: BAA06143.1; PID: d1006705; PID: 9473
C; Superfamily: molecular chaperone t-complex-type
C; Keywords: heat shock
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C;Genetics:
C;Genetics: TM1072
A;Gene: TM1072
analysis of the heat shock protein gene from a new hyperth
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomeras
F;1-239/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T
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A;Experimental source: strain Madrid E
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: B72299
K:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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Pred. No. 61;
); Mismatches
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Pred. No. 1e+02;
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Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
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Best Local Similarity 75.0%;
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        A; Description: Cloning and A; Reference number: $61294
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A; Residues: 1-236 <ARN>
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665 KIAIRLDE 672
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418 LAIRLDE 424
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A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Cross-references: EMBL:M84911; NID:g151360; PID:g551933
A:Cross-references: EMBL:M84911; NID:g151360; PID:g551933
B:Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
B:Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
A:Title: Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding met
A:Reference number: A42902; MuID:92317087
A:Accession: D42802
A:Status: presliminary
A:Molecule type: DNA
A:Residues: 1-79 <ST2>
                                                                                                                                                                                                                                                                                 Risteele, M.I.; Lorenz, D.; Hatter, K.; Parks, A.; Sokatch, J.R.
subnitted to the EMBL Data Library, July 1992
A; Description: Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encodi
A; Reference number: $27601
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                                                                                        probable acetate--CoA ligase (EC 6.2.1.1) - Pseudomonas aeruginosa (fragment)
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: 561294 #: Takagi, M.; Imanaka, T.
Srlzawa, Y.; Kakihara, H.; Takagi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
                                                                                                        N.Alternate names: probable acetyl-CoA sythetase
C.Species: Pseudomonas aeruginosa
C.Date: 04-Mar-1993 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C.Accession: 527604; D42902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Rattus norvegicus (Norway rat)
C.Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Experimental source: PAO, ATCC 15692
A: Note: sequence extracted from NCBI backbone (NCBIN:107704, NCBIP:107709)
C: Superfamily: acetate---CoA ligase homology
C: Keywords: acid-thiol ligase
F:105-464/Domain: acetate--CoA ligase homology (fragment) <ACL>
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R:Takeuchi, F.; Tsubouchi, R.; Yoshino, M.; Shibata, Y. Biochim. Biochim
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-464 < TAK>
C; Keywords: hydrolase
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28 RVALRLDE 35
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Ouery Match (63.3%; Score 31; DB 2; Length 236; Best Local Similarity 62.5%; Pred. No. 42; Matches 5; Conservative 3; Mismatches 0; Indels
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28 ISVRLDER 35
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Search time 63.71 Seconds (without alignments) 4.688 Million cell updates/sec 8, 2000, 00:59:52; February Run on:

US-08-653-294-13

1 YRLAIRLDER 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 segs, 29864866 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	SUMMARI  ID  YEAX_ECCLI NTRB_ECOLI NTRB_ECOL	SUMMARIES	Description	ECOLI P76254 escherichi	_	_	KLEPN P06218 klebsiella	P70712		052500	024729	P41080	P22596	006220	: P18167	P32349	003824	620900	P13511	P94177	P55201	P33144	COLI P77300 escherichi	033844	P14373	062158	P39736	3 055439	P38681	003131	P27206	P39534	P42245 1	P20496	P08583	P3306
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TRYP_MOUSE LEP3_ERWCA LEP3_ERWCA RL5A_SCHPO RL5B_SCHPO RL5_BOMMO RL5_BOMMO RL5_BOMMO RL5_HELAN RUYB_THEMA CAH1_CHLRE METK_SYNY3 YUR1_YEAST
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## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTOLITY, AIRA H., BABA T., FUJITA K., HAVASHI K., INADA T., ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M., MAKINO K., MIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K., NARADES S., NARAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H., TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T., TAKEDA J., TAKEMOTO K., WADA C., TAGAMI H., TAKEDA J., TAKEMOTO K., WADA C., TAMAMOTO Y., HORIUCHI T., D., TAKEMOTO Y., HORIUCHI T., D., TAKEMOTO Y., WADA SEQUENCE OF THE ESCHELICHIA COLI K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                         RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHOO Y., "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: FMN (BY SIMILARITY).
-!- SUBGNIT: PROBABLE HETERODIMER OF YEAW AND YEAX.
-!- SIMILARITY: IN THE C-TERMINAL, BELONGS TO THE 2FE2S PLANT-TYPE
FERREDOXIN FAMILY.
-!- SIMILARITY: BELONGS TO THE PDR/VANB FAMILY.
                                                                                                                                                                                         Escherichia coll.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
RESULT 1
YEAX_ECOLI STANDARD; PRT; 321 AA.

AC 776254; 007972; 007970;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE PUTATIVE DIOXYGENASE BETA SUBUNIT YEAX (EC 1...-).
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EMBL; D90824; CAB21531.1; -.
EMBL; D90823; CAB21524.1; -.
HSSP; P31164; 2PIA.
ECGENE; EG13510; YEAX.
PROSITE; P$001017; 2FEZS_FERREDOXIN; 1.
PFAM; PF00111; fer2; 1.
PFAM; PF00175; oxidored_fad; 1.
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STRAIN-K12 / MG1655;
MEDLINE; 97426617.
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MEDLINE; 97251358.
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Gaps

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Indels

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Mismatches

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01-JAN-1988 (
01-NOV-1997 (
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NTRB_ECOLI
ID NTRB_ECOLI
AC P06712;
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MEDLINE; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARLYLES THE FILMAN U., WERNSTEDT C., ERIKSSON U.;
SIMON A., HELLMAN U., WERNSTEDT C., ERIKSSON U.;
The retinal pigment epithelial-specific 11-cis retinol dehydrogenases.";
Delongs to the family of short chain alcohol dehydrogenases.";
J. Biol. Chem. 270:1107-1112(1995).
-!- FUNCTION: STEREOSPECIFIC 11-CIS RETINOL DEHYDROGENASE, WHICH CATALYZES THE FINAL STEP IN THE BROSNIPHESIS OF 11-CIS RETINALDEHYDE, THE UNIVERSAL CHROMOPHORE OF VIGNAL PLOSEN ACTIVE IN THE PRESENCE OF NAD+ AS COFACTOR BUT NOT IN THE PRESENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: CATALYZES THE PRIMARY AND RATE-LIMITING STEP IN RETINOIC ACID SYNTHESIS.
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                                                                                                                                   SIMILARITY).
SIMILARITY).
SIMILARITY).
SIMILARITY).
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Eutheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) (P32)
   FMN; NAD;
                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 321;
Pred. No. 11;
4; Mismatches 0; Indels
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(BY
Oxidoreductase; Flavoprotein; transport.
                                                            FWN (BY SIMILARITY).
NAD (BY SIMILARITY).
IRON-SULEUR (2FE-2S) (EIRON-SULFUR (2FE-2S) (EIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADP (BY SIMILARITY).
BY SIMILARITY.
7022A583 CRC32;
                                                                                                                                                                                                                                                                       9E85CC68 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 AA.
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                                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 E
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55.6%;
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278
309
35661
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                   103
226
270
   protein; (
Electron 1
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Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; NAD
                                                                                                                                                                                                                                                                               AA;
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70 YQIAVRLEE 78
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MEDLINE; 95138097
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Hypothetical pricon-sulfur; Property Property Property NP_BIND Property NP_BIND Property Prop
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Q27979;
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                           METAL
SEQUENCE
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RDH1_BOVIN
                                                                                                                                                                       METAL
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   STTTTTT
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Score 32; DB 1; Length 318; Pred. No. 18;

65.3%; 75.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NINEA A.J., BENNET R.L.;
"Identification of the site of autophosphorylation of the bacterial
protein kinase/phosphatase NRII.;
J. Biol. Chem. 266:6888-6893(1991).
-!- FUNCTION: NTRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE
NITROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF NTRC. IN
NITROGEN LIMITATION NTRB ACTIVATES NTRC BY PHOSPHORYLATED AND CONSEQUENTLY
WHILE IN NITROGEN EXCESS NTRC IS DEPHOSPHORYLATED AND CONSEQUENTLY
INACTIVATED BY NTRB.
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                        MIRANDA-RIOS J., SANCHEZ-PESCADOR R., URDEA M., COVARRUBIAS A.A.; "The complete nucleotide sequence of the glnALG operon of Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UENO-NISHIO S., MANGO S., REITZER I.J., MAGASANIK B.;
"Identification and regulation of the glnL operator-promoter of the
complex glnaLG operon of Escherichia coli.";
J. Bacteriol. 160:379-384(1984).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE; 9334/969.
PLUNKETT G. III, BURLAND V.D., DANIELS D.L., BLATTNER F.R.;
"Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROCHA M., VAZQUEZ M., GARCIARRUBIO A., COVARRUBIAS A.A.; "Nucleotide sequence of the glnA-glnL intercistronic region of Escherichia coli.";
                                  01-NOV-1997 (Rel. 06, Last sequence update)
NITROGEN REGULATION PROTEIN NR(II) (EC 2.7.3.-).
ESCHAPIONER GLNR.
349 AA
                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 15:2757-2770(1987)
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Gaps

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Indels

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EMBL; EMBL;

EMBL;

MOD\_RES BINDING

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE AND L-3-
HYDROXYKYNURENINE INTO ANTHRANILIC AND 3-HYDROXYANTHRANILIC ACIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS FROM TRYPTOPHAN THROUGH THE KYNOTRENINE PATHWAY.
-!- SUBCELLULAR LOCATION: CYTOPLASHIC.
-!- SIMILARITY: BELONGS TO THE KYNUTENINASE FAMILY. SLIGHTLY RELATED TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
MEDIINE: 97324088.
TOMA S., NARAWURA M., TONE S., OKUNO E., KIDO R., BRETON J.,
TOMA S., NARAWURA M., TONE C., MOSTARDINI M., GATII S., BENAITI
"CLONING and recombinant expression of rat and human kynureninase."
FEBS Lett. 408:5-10(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas.
                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: L-KYNURENINE + H(2)0 = ANTHRANILATE L-ALANINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 464;
Pred. No. 26;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORFI) (FRAGMENT).
                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
KYNURENINASE (EC 3.7.1.3) (L-KYNURENINE HYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37EE19F0 CRC32;
                                                                                                                                                                                    464 AA
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2; Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
    1;
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BINDING 276 PY
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75.0%;
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Best Local Similarity 75.v.,
6; Conservative
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    Conservative
                                                                                                                                                                                    STANDARD;
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277 YRLAARID 284
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28 RVALRLDE 35
                                         1 YRLAIRLD 8
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P28812;
                                                                                                                                                                                  KYNU_RAT
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YMMS_PSEAE
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MEDLINE: 86067184.

MCFARLANE S.A., MERRICK M.J.;

MCFARLANE S.A., MERRICK M.J.;

The nucleotide sequence of the nitrogen regulation gene ntrB and the glnA-ntrBC intergenic region of Klebsiella pneumoniae.";

Nucleic Acids Res. 13:7591-7606(1985).

INTROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF NTRC. IN NITROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF NTRC. IN NITROGEN LEVEL OF CELL AND MODULATES NTRC BY PHOSPHORYLATING IT, WHILE IN NITROGEN EXCESS NTRC IS DEPHOSPHORYLATED AND CONSEQUENTLY INACTIVATED BY NTRB.

INACTIVATED BY NTRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMITTER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
ATP (BY SIMILARITY).
4 BAC1813 CRC32;
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                                                                                                                                                                                                 TRANSMITTER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-).
FOR SIMILARITY).
FOR (BY SIMILARITY).
                                                        PIR; Q00553; RCECGL.
PIR; B23970; B23970.
PIR; S40814; S40814.
ECCGENE; S19387; GLNL.
PFAM; PF00512; Signal; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Nitrogen fixation; ATP-binding.
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Sensory transduction; Transferase; Kinase; Phosphorylation;
Nitrogen fixation; ATP-binding.
                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 349;
Pred. No. 19;
; Mismatches 1; Indels
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19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-CT-1944 (Rel. 30, Last annotation update)
NITROGEN REGULATION PROTEIN NTRB (EC 2.7.3.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 AA
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No.
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K02176; AAA23881.1; -. L19201; AAB03003.1; -. AE000462; AAC76866.1; -.
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75.0%;
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
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277 YRLAARID 284
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139
329
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P06218;
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BINDING
SEQUENCE
                                                                                                                                                                                                                                                             SEQUENCE
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Gaps

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0; Indels

DOMAIN

us-08-653-294-13.rsp

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(Rel. 31, (Rel. 31, 1) (Rel. 39, 1)
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Best Local Similarity
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                                                                                                                                                                                                                                      418 LAIRLDE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LAIRLDE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LAIRLDE 9
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P41080;
01-FEB-1995
01-FEB-1995
15-DEC-1999
  Chaperone;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       THSA_THEK1
024729;
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GYRA_RICPR
ID GYRA_RI
AC P41080;
DT 01-FEB-
DT 15-DEC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                              TYPERIE W. I., LORENZ D., HATTER K., PARK A., SOKATCH J.R.;
"Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-hydroxyisobutyrate dehydrogenase.";
J. Blol. Chem. 267:13585-13592(1992).
-!-SIMILARITY: TO ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IZAWA Y., KAKIHARA H., TAKAGI M., IMANAKA T.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MOLECULAR CHAPERONE, BINDS UNFOLDED POLYPEPTIDES IN
VITRO, AND HAS A WEAK ATPASE ACTIVITY (BY SIMILARITY).
-!- SUBUNIT: FORMS AN OLIGOMERIC COMPLEX OF EIGHT-MEMBERED RINGS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 464;
Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 AA; 51208 MW; FE491D7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-DEC-1999 (Rel. 39, Last annotation update)
THERMOSOME SUBGNIT (HEAT-SHOCK PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00455; AMP_BINDING; 1. PFAM; PF00501; AMP-binding; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_2; 1.
PROSITE; PS00995; TCP1_3; 1.
PFAM: PF00118; Cph60_TCP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M84911; AAA25893.1; -.
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55.6%;
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SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.3
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P48424; 1ASX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||:|:
146 YELALRIDD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                MEDLINE; 92317087
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SEQUENCE
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THS_PYRKO
DT 01-NO'
DT 01-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermococcus sp. (strain KS-1).
Archaea; Euryarchaeota; Thermococcales; Thermococcus.
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 98022908.
YOSHIDA T., YOHDA M., IIDA T., MARUYAMA T., TAGUCHI H., YAZAKI K., ODHATA T., ODAKA M., ENDO I., KAGAMA Y.;
"Structural and functional characterization of homo-oligomeric complexes of alpha and beta chaperonin subunits from the typerthermophilic archaeum Thermococcus strain KS-1.";
J. Mol. Biol. 273:635-645(1997).
-!- FUNCTION: MOLECULAR CHARPERONE; BINDS UNFOLDED POLYPEPTIDES IN VITRO, AND HAS A WEAK ATPASE ACTIVITY (BY SIMILARITY).
-!- SUBULT: FORMS AN OLIGOMERIC COMPLEX OF EIGHT-MEMBERED RINGS (BY SIMILARITY).
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                                                                                                                 Length 546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%; Score 32; DB 1;
100.0%; Pred. No. 32;
ive 0; Mismatches
ATP-binding; Heat shock.
546 AA; 59158 MW; 5B3C9283 CRC32;
                                                                                                                    1;
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PROSITE; PS0750; TCP1_1; 1.
PROSITE; PS00750; TCP1_2; 1.
PROSITE; PS00995; TCP1_3; 1.
PFAM; PF00118; cpn60_TCP1; 1.
SEQUENCE AIP-binding; Multigene family.
SEQUENCE 548 AA; 59191 WW; 08FCFB81 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                 65.3%; Score 32; DB 1100.0%; Pred. No. 31; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 AA
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                                                                                                                    Query Match 65.3
Best Local Similarity 100.
Matches 7; Conservative
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MEDLINE: 99295997
MEDLINE: 99295997
MEDLINE: 99295997

GOLE S.T., BROSCH R., FARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GONDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNENS T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., CLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J., TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1998 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last
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                                                                                                     VIZOLOGY 179:378-387(1990).
-i- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN C.
-i- SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN GENE SUPERFAMILY.
NICOLSON L., ONIONS D.E.; The nucleotide sequence of the equine herpesvirus 4 gC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 1; Length 485;
Pred. No. 45;
2; Mismatches 2; Indels
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63F72464 CRC32;
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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PIR; B45343; B45343.
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485 AA;
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MURE_MYCTU
ID MURE_MYCTU
AC 006220;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALXZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 396:133-140(1998).

-!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
INTERCONVENSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O., SICHERITZ-PONTEN I., ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K., ERIKSSON A.-S., WINKLER H.H., KURLAND C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                               WOOD D.O., WAITE R.T.;
"Sequence analysis of the Rickettsia prowazekii gyrA gene.";
Gene 151:191-196(1994).
                                                                      Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 905; 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA CLEAVAGE (BY SIMILARITY)
V; EFBC8ADA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type 1 subtype 2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sc annotation update) (GLYCOPROTEIN 13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update
GLYCOPROTEIN.C PRECURSOR (GLYCOPROTEIN 13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB :
Pred. No. 54;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ23570; CAA14671.1; -. PFAN; PF00521; DNA_LOPOISONY; 1. TOPOISONERSES; DNA-DINGING. ACT_SITE 123 123 DNA CLEAVY SEQUENCE 905 AA: 10100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.3%;
75.0%;
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GYRASE SUBUNIT A
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=MADRID E;
MEDLINE; 95129858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 99039499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 91021040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLAIRLDE 9
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                                      RP206
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P22596;
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VGLC\_HSVE4

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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                       ACT_SITE
DISULFID
                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                             DISULFID
                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
RPC3_YEAST
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                    use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         PRECURSOR OF MUREIN (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMYL-MESO-2, 6-DIAMINOHEPTANEDIOATE + D-ALANYL-D-ALANYL-B-ADP + ORTHOPHOSPHANE + UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GAMMA-GLUTAMYL-6-CARBOXY-L-LYSYL-D-ALANYL-D-ALANINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: MAINLY IN LATE LARVAE.
SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                     -!- FUNCTION: INVOLVED IN CELL WALL FORMATION. CATALYSES THE FINAL STEP IN THE SYNTHESIS OF UDP-N-ACETYLMURAMOYL-PENTAPEPTIDE, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. Biol. Evol. 7:9-28(1990).
-!- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O - AN ALCOHOL.
+ A CARBOXYLIC ANION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CANTON-S;
MEDLINE: 90136038.
COLLET C., NIELSEN K.M., RUSSELL R.J., KARL M., OAKESHOTT J.G.,
RICHMOND R.C.;
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular analysis of duplicated esterase genes in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
ESTERASE P PRECURSOR (EC 3.1.1.1) (EST-P) (CARBOXYLIC-ESTER
                                                                                                                                                                                                                                                         PFAM; PF01225; Mur_ligase; 1.
Peptidoglycan synthesis; Cell division; Cell wall; Ligase;
ATP-binding.
                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1; Length 510;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
4F25A40A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 AA.
                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
                                                                                                                                                                                                                                                                                          142 F
51632 MW;
                                                                                                                                                                                                                                                                                                                                       63.3%;
85.7%;
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                               EMBL; 295388; CAB08670.1;
                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                      510 AA;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                |||:|||
412 RLAVRLD 418
                                                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                  2 RLAIRLD 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster.
Mol. Biol. Ev
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTP_DROME
P18167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROLASE)
                                                                                                                                                                                                                                                                                                      SEQUENCE
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(See http://www.isb-sib.ch/announce/
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Submitted (APR-1995) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAILS-288C / AB972;
STRAILS-288C / AB972;
JOHNIN-S288C / AB972;
JOHNIN-S288C / AB972;
FAVELLO A., FULTON L., GATTUNG S., GRECO I., KIRSTEN J., KUCABA T.,
FAVELLO A., FULTON L., GATTUNG S., GRECO I., KIRSTEN J., KUCABA T.,
HALLSKORTH K., HAWRINS J., HILLER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPC3_YEAST STANDARD; PRT; 654 AA.
P32349; 00(6591;
01-0CT-1993 (Rel. 27, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE III 74 KD POLYPEPTIDE (EC 2.7.7.6) (C74).
RPC3 OR RPC32 OR PSP190C OR P9677.11.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "RPC82 encodes the highly conserved, third-largest subunit of RNA polymerase C (III) from Saccharomyces cerevisiae."; Mol. Cell. Biol. 12:4433-4440(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA(N).
SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT
SUBUNITS. THIS SUBUNIT IS THE THIRD LARGEST COMPONENT OF RNA
POLYMERASE III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIANNILKULCHAI N., STALDER R., RIVA M., CARLES C., WERNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                      PFAM; PF00135; Coesterase; 1.

Hydrolase; Serine esterase; 61ycoprotein; Signal.

SIGNAL 1 19
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51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
E9F6EEDD CRC32;
                                                                                                                                                                                                                                                                                                                                                                  ESTERASE P.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                              HSSP; P21836; 1MAH.
FLYBASE; FBGHO000594; ESt-P.
FROSIE; FSOR0122; CARBOXYLESTERASE_L;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.38;
66.78;
                                                                                 EMBL; M33780; AAA28520.1; -. PIR; B34089; B34089.
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STANDARD;

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Search completed: February 8, 2000, 00:59:53
Job time: 3782 sec
                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                      15-DEC-1999
15-DEC-1999
                                                                                                   15-DEC-1999
                                         MMLB_MYCLE
006079;
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                               MMLB_MYCLE
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                ZINC-CONTAINING RNA POLYMERASES ARE
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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SUBCELLULAR LOCATION: NUCLEAR.
MISCELLANEDUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES AF
POUND IN BUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
III FOR SS AND TRNA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                          fransferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 31, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 654;
62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 705; Pred. No. 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUNT S., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAY 1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                     502 LEUCINE-ZIPPER.
537 V -> L (IN REF. 1).
74016 MW; 9E17F4F8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81466 MW; 6E07A99F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     705 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                            63.3%; Score 31; 50.0%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                 EMBL; X63500; CAA45072.1; -. EMBL; U25841; 'AAB64619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.3%;
55.6%;
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Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                           Query Match 63.3
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
HUNT S., BOWMAN S., B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I protein 705 AA; 8
                                                                                                                                                                                                                               S31298; S31298.
L0001693; RPC82
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312 YKIALRLTEQ 321
                                                                                                                                                                                                                                                                                                               654 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLAIRLDER 10
                                                                                                                                                                                                                                                                          Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
YM37_YEAST
ID YM37_YEAST
AC Q03824;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
HAMLIN N., CHURCHER C.M., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-! SIMILARITY: BELONGS TO THE MMPL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                 Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A2FC256A CRC32;
                                                                      Last sequence update)
Last annotation update)
PRT; 1014 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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POTENTIAL.
POTENTIAL.
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                                                                                                                   PUTATIVE MEMBRANE PROTEIN MMPL11
                                               Created)
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50.0%;
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                                                                                                                                               MMPL11 OR MLCL622.16C.
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117 YGVSLRLDDR 126
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530
560
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649
671
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Perfect score:

Title:

Sednence:

OM protein

Run on:

Scoring table:

Searched:

Database

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069556 mycobacteri
094830 homo sapien
082436 cucumis mel
081122 malus domes
001914 caenorhabdi
092198 aspergillus
099102 brachydinio
054436 staphylothe
04344 strongyloce
061479 mus musculu
065737 bluetongue
06527 bacillus su
06527 bacillus su
065281 escherichia
08524 escherichia
08564 escherichia
087689 aquifex aeo
027010 toxoplasma
043366 caenorhabdi
044027 toxoplasma
 O9xx98 caenorhabdi
O9yag3 aeropyrum p
O39258 equine herp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESCUENCE FROM N.A.

SECUENCE FROM N.A.

STRAIN-DSM 5908;

WEDLINE: 97449857.

WEDLINE: 97449857.

PELZER S., REICHERT W., HUPPERT M., HECKMANN D., WOHLLEBEN W.;

Cloning and analysis of a peptide synthetase gene of the balhimycin producer Amycolatopsis mediterranei DSM5908 and development of a gene of its and its system.";

J. Biotechnol. 56:115-128(1997).

REBL: X97860; CAA6644.1;

DR PROSITE: PSO0455; AMP_BINDING; 1.

PRAM: PF005501; AMP-BINDING; 1.

PRAM: PF005501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amycolatopsis mediterranei.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                           044103 PRELIMINARY; PRT; 1324 AA. 044103; OLINOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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1324 AA; 142666 MW; 2C08588E CRC32;
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80.0%; Pred. No. 20;
.ive 1; Mismatches
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099XX98
099A63
099A63
099A830
094B30
091136
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Matches 8; Conservative
                                                                                   845
11110
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YRVAGRLDER 978
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NON_TER
SEQUENCE
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 RESULT
Q19415
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Q13415 caenorhabdi
Q01375 neurospora
Q01379 neurospora
Q013734 agrobacteri
OG6421 mycobacteri
OG6407 pyrococcus
C51192 synechocyst
Q13610 schizosacch
Q28151 caenorhabdi
Q28004 bos taurus
Q28151 caenorhabdi
Q28004 bos taurus
Q2815 enterobacte
Q9xxb4 acidiphiliu
Q9x813 pyrococcus
Q00343 picnia angu
Q9xQ1 thermocoga
O5xQ1 thermocoga
O5xQ1 thermocoga
O5xQ1 thermocoga
O5xQ1 thermocoga
O5xQ1 picnia angu
                                                                                            (without alignments)
3.317 Million cell updates/sec
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                                                                                February 8, 2000, 13:17:39; Search time 209.03 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                    225878 seqs, 69334122 residues
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                                                          sw model
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0058407
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Q00943
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054045
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
                                                        - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_organelle:*
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Listing first 45
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1: sp_archea:*
2: sp_bacteria:*
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Match Length DB
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sp_human:*
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Maximum DB seq length: 1000000
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Score

Result Š. ö

Gaps

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us-08-653-294-13.rspt

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Gaps
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Agrobacterium.
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"Requirement for genes with homology to ABC transport systems attachment and virulence of Agrobacterium tumefaciens.";
J. Bacteriol. 178:5302-5308(1996).
EMBL: U59485; AABG7299.1;
PFAM; PF00005; ABC_tran; 1.
SEQUENCE 264 AA; 28745 MW; D5629761 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAMBARERI E.B., HELBER J., KINSEY J.A.;
"Tadl-1, an active LINE-like element of Neurospora crassa.";
MOI. Gen. Genet. 242:658-665(1994).
EMBL; L25663; AAA21792.1; -.
PFAM; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                         Euascomycetes; Pyrenomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2; Length 264;
Pred. No. 40;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 130.5 KD PROTEIN.
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Last sequence update)
Last annotation update)
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-LYS.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Euascom;
Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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12,
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01-JAN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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DOMAIN 1019 102
                                                    1136 YRLAVELEE 1144
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Best Local Similarity
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246 RLAVKLDRR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94203179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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  1 YRLAIRLDE
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Q01379
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032734
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                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN=J1518;
MEDLINE; 94203179.
CAMBARERI E.B., HELBER J., KINSEY J.A.;
"Tadi-1, an active LINE-like element of Neurospora crassa.";
"Office. Genet. 242:658-665(1994).
EMBL; L25662; AAA21781.1; -.
PFAM: PF00078; rvt; 1.
Hypothetical protein.
Hypothetical protein.
1019 1022
1014 POLY-LYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 229;
                                                                                                                                                                                                                                                                                                                           MCMURRAY A.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F822FE98 CRC32;
229 AA
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                                                      Created)
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
EMBL: 269383; CAA93413.1; -.
SEQUENCE 229 AA; 26620 MW;
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  PRELIMINARY;
                                                 01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
F13E9.10 PROTEIN.
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                                                                                                                                                                                    Caenorhabditis elegans.
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Best Local Similarity
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115 YEQAIRLDKR 124
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MCMURRAY A.;
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Query Match
Best Local Similarity 77.0
77.0
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Matches 6; Conserv
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                                                                                           RLLIELDER 104
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SEQUENCE FROM N.A.
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35 YRLALRILQR 44
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                                                                     2 REAIREDER 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAWANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                            COLE S.T.; 'nap of the genome of the tubercle bacillus, "An integrated map of the genome of the tubercles Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%; Score 33; DB 2; Length 554; 66.7%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                      STRAIN-H37RV;
BROWN D., CHURCHER C.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                    BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-ANN-1999 (TrEMBLrel. 09, Last annotation update)
151AA LONG HYPOTHETICAL FRXA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
EMBL; 295558; CAB08966.1; -.
SEQUENCE 554 AA; 57835 MW; C42C89FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29765.1; -.
17160 MW; 11AACD59 CRC32;
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                                                          Created)
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                                                    01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP000003; BAA29765.1;
                                                                                                                       Mycobacterium tuberculosis.
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Best Local Similarity 66...
56. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                             PRELIMINARY;
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01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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                                                                                                                                                                           SEQUENCE FROM N.A.
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48 RLHVRIDER 56
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                                           006421;
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RESULT
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KANDEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIWA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIWA I., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystls sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA'Res. 3:109-136(1996).

EMBL: D64001; BAA10334.1; -.

Hypothetical protein.

SEQUENCE 185 AA: 20830 MW; 365A078D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-PCC6803;
MEDLINE; 96127529.
MEDLINE; 96127529.
SUGIURA M., TANARA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIURA M., TABATA S.;
SUGIURA M., TABATA M., SATURA M., S
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           Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TABATA S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sacteria; Cyanobacteria; Chroococcales; Synechocystis
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
HYPOTHETICAL 22.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
Score 32; DB 1;
Pred. No. 36;
); Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-ANN-1999 (TrEMBLrel. 09, Last ann
HYPOTHETICAL 20.8 KD PROTEIN.
Synechocystis sp. (strain PCC 6803).
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65.38;
77.88;
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SEQUENCE FROM N.A.
STRAIN=57.7;
STRAIN=57.7;
DONG Y.M., IJ J.D.;
and their characterization.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF072440; AAC69221.1;
SEQUENCE 349 AA; 38412 MW; A9F4BA43 CRC32;
                                                                                                                                                                                                       MEDLINE; 95386398.
DRIESSEN C.A., JANSSEN B.P., WINKENS H.J., VAN VUGT A.H., LEBUW T.L.,
JANSSEN J.J.;
                                                                                                                                                                                                                                                          "Cloning and expression of a cDNA encoding bovine retinal pigment epithelial 11-01s retinol dehydrogenase.";
Invest. Ophthalmol. vis. Sci. 36:1988-1996(1995).
EMBL: L36533; AAA80694.1; -..
BFSP: PHO461; IPDW.
PFSP: PHO461; IPDW.
PFRM: PF00106; adh_short; 1.
PRINTS; PR00080; ALCDHDRGNASE.
                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 319;
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Pred. No. 86;
1; Mismatches 1; Indels
                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
11-CIS-RETINOL DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
WITROGEN REGULATORY PROTEIN.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                        319 AA; 34400 MW; 37A78DAA CRC32;
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           PRT; 319 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                            SEQUENCE FROM N.A.
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45 LALRLDQR 52
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                                                                                                                                                               Bovinae; Bos.
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Q92H35
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                                                                                          KUSHIDA N., YAMAZAKI S., TANAKA T., JINNO K., HAIKAWA Y., YAMAZAKI J., YAMAMOTO S., SEKINE M., OGUCHI A., NAGAI Y., SAKAI M., AOKI K., OGURA K., OTSUKA R., KUDOH Y., YANAGIDA M., MACHIDA M., ZHANG M.Q.; SUDMITTEG (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB004535; BAA21398.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MULSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DUBRIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
LIGHTONES M., KERSHAM J., KIRSTEN J., LAISTER N., LAIREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMBRE E., STADEN R., SULSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                            Gaps
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLOYD C.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                                                                                                                                                                                                                           Length 192;
                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans."; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                           Score 32; DB 3;
Pred. No. 46;
                                                                                                                                                                            .l protein.
192 AA; 22352 MW; F43F0759 CRC32;
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SEQUENCE 304 AA; 34207 MW; F9701C2D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                         304 AA
                                                                                                                                                                                                                                                                          3; Mismatches
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Pred. No. 75;
0; Mismatches
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                                                                                                                                                                                                                                           65.3%;
58.3%;
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Similarity 77.8%;
7; Conservative
                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 58.3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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                                 Schizosaccharomyces
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Best Local Similarity
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                                                              SEQUENCE FROM N.A.
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                                                                              STRAIN=972 H-
                                                                                                                                                                         Hypothetical
SEQUENCE 19
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Gaps

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RESULT

Matches

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Search completed: February 8, 2000, 13:17:41 Job time: 32490 sec
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Best Local Similarity 75.0
Matches 6; Conservative
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| 696 LAVRLEER 703
                                                       SEQUENCE FROSTRAIN=NCYC
     SORRERERROS
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MEDLINE; 99203147.

MEDLINE; 99203147.

IZUMI M., FUJIWARA S., TAKAGI M., KANAYA S., IMANAKA T.;

ISOlation and characterization of a second subunit of molecular chaperonin from pyrococous kodakaraensis KODI: analysis of an ATPase-deficient mutant enzyme."; 65:1801-1805(1999).

APPL Environ. Microbiol. (65:1801-1805(1999).

EMBL; AB018412; BAA76952.1; -

PROSITE; PS00750; TCP1_1; 1.

PROSITE: PS00751; TCP1_2; 1.

PROSITE: PS00995; TCP1_3; 1.
                                                                                                                                                                                   The metal insertion step of bacteriochlorophyll blosynthesis in an aerobic bacterium Acidiphilium rubrum, which produces zinc-containing bacteriochlorophyll as natural photosynthetic pigment."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB017351; BAA765361; -. SEQUENCE 422 AA; 45864 MW; 4248EA89 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                               SEQUENCE FROM N.A.
MASUDA T., INOÜE K., MASUDA M., NAGAYAMA M., OHTA H., SHIMADA H.,
TAKAMIYA K.;
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                                Acidiphilium rubrum.
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Acidiphilium.
                                                                                                                                                                                                                                                                                                                                    Ouery Match 65.3%; Score 32; DB 2; Length 422; Best Local Similarity 77.8%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 32; DB 1; Length 548; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
01-NOV-1999 (TrEMBLrel. 12, Last annotation update) LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CHAPERONIN LIKE PROTEIN ALPHA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Best Local Similarity
Matches 7; Conserv
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123 RAAARLDER 131
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000943
ID 000943
AC 000943:
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
DT 01-NOV.
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Q9Y8I3
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Eukaryota; Fung1; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Pichia.
                                                                                                                                         BRITO N., AVILA J., PEREZ M., GONZALEZ C., SIVERIO J.M.; J. Biochem. 317:89-95(1996).

EMBL; Z68122; CAA92206.1; -.

PFAM; PFO1077; NIES.; 1.

PFAM; PFO0357; RIES.E; 1.

PRINTS; PRO0397; SIROHAEM.

SEQUENCE 1044 AA; 116574 WW; 59F4D4B1 CRC32;
                                                                                    FROM N.A.
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Score 32; DB 3; Length 104 Pred. No. 2.7e+02; 2; Mismatches 0; Indels 65.3%; 75.0%; 3 LAIRLDER 10

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Gaps

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Length 1044;

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AC005605 Homo sapiens subt
AB015475 Arabidopsis thall
AL031032 Arabidopsis thall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submitted (30-007-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clonerquest@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
on oct 29, 1999 this sequence version replaced gi:6065875.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBLS Sw., SWISSPROT: Tr., TREMBL: Wp., WORMPEP: Information on the WORMPEP databases can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone 1106M18. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The true left end of clone 906P16 is at 142237 in this sequence. The true right end of clone dJ1193N1 is at 79367 in this sequence. This sequence has been finished according to sequence map criteria such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from part of bacterial clone contigs human chromosome 20, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 httb://www.sanger.ac.uk/HGP/Chr20 for sanger is from the library RPCI-5 constructed at the Roswell Par Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                seq_documentation_block:
LOCUS HS1106N18 142336 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from clone 1106N18 on chromosome 20q13.2-13.2,
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142336)
  37640
84325
86748
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Gaps: 0
Percent Identity: 80.000
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/clone_11b="RRCI-5"
/clone="RP5-1106NIB"
37456 a 31918 c 32886 g 40076 t
  6.9e+03
1.8e+04
1.8e+04
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1. .142336
/organism="Homo sapiens"
/db_xref="taxon:9606"
  88.18
80.84
80.58
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                                                                                                                                                                                                                                                     complete sequence.
AL035457
AL035457.13 GI:6143575
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US-08-653-294-13 x HS1106N18/rev
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Direct Submission
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  gb_pr3:AC005605
gb_pl1:AB015475
gb_pl2:ATF1715
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Len | Documentation | 14236 | AL035457 Human DNA sequence 323792 | AC004965 Homo saptens clone 3452 | AC004805 Homo saptens clone 3452 | AC0048209 Macropus eugenii inte 44887 | AC018207 Drosophila melanogas 89791 | AC018207 Drosophila melanogas 89791 | AC018208 Human DNA sequence from 129969 | 298941 Human DNA sequence from 156832 | AC010831 Homo saptens clone 166832 | AC010851 Homo saptens clone 187447 | AC010806 Homo saptens chrome 187447 | AC010819 Homo saptens chrome 187447 | AC01081 Homo saptens chrome 187447 | AC01081 Homo saptens chrome 187487 | AC010846 Drosophila melanogas 32202 | U00050 Caenorhabditis elegans 141615 | AC011071 Drosophila melanogas 155841 | AC010847 Homo saptens clone 15581 | AC010847 Homo saptens clone 15781 | AC0
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624 | ACC08274 Homo sapiens clone
881 | ACC02465 Human BAC clone RG3
541 | ACC010847 Drosophila melanoga
246 | ACC08537 Homo sapiens chromc
0 | ALLI7425 Homo sapiens mRNA, cf
9 | Y1232 D.melanogaster mRNA, for
90 | 1292817 Caenorhabditis elegans
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| AC014153 Drosophila melanogas
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i U58085 Caenorhabditis elegans
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-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04000_cAPEXT=4.000
-QAPEXT=4.000 -QAPEXT=4.000
-QAPEXT=0.000 -QAPEXT=0.000 -QAPEXT=0.000
-QAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS-Human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=-PCT -ALIGN=15 -MODE=-LOCAL
-OUTFWT=pfs -NORM=ext -MINLEN-0 -MAXLEN=100000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
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Database sequences: 821193
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Query: US-08-653-294-13
Query length: 10
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9b_in1: DWUSHAPE

9b_in1: DWUSHAPE

9b_in2: AC010400

9b_in2: AC006269

9b_in2: AC005269

9b_pr3: HSZ81HB

9b_ht91: AP000585

9b_ht96: AC008002
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9b_bal:AMPEPSYNT
9b_bal:AMPEPSYNT
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9b_bt3:AC010386
9b_htg3:AC010386
9b_htg4:AC01839
9b_htg3:AC01086
9b_htg3:AC01086
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9b_htg6:AC011071
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9b_htg1:AP000642
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9b_p12:CNSO1BRR
9b_p12:CNSO1A6K
9b_p12:AN3O1A6K
9b_p11:AN13GBNE
9b_p11:EN1230
9b_p11:EU1230
9b_p11:SCUF8
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**NOTE: This is a "working draft' sequence. It currently

**Consists of 42 contigs. The true order of the pieces

**is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                            seq_documentation_block:
LOCUS AC004965 323792 bp DNA HTG 12-JUN-1998
DEFINITION Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***, 42
UNDIGGRED PROGRESS ***, 42
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 323792)
Waterston, R.H.
                         to: 142336
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Waterston, R.H. Direct Submission
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LIGOGTRRISTPDPQNHPLGTEETEQGIETLKNGTAEENVVEKIFQNLSSLKGYITAK
EKGGGERRYEQFLDYLEEFLRTINIEWNTEWTVES"
S85 C 616 G 1205 t
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*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                   University of USA
                                                                                                                                                                                                                                                        2 (bases 1 to 3452)
Hawken,R.J., Maccarone,P., Toder,R., Marshall Graves,J.A. and
Maddox,J.F.
                                                                                                                                                                                     and
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                 05-OCT-1999
                                                                                                                 Macropus eugenii
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       join(<34. .180,406. .438,1492. .1620,1706. .>1816)
/gene="IL5"
                                                                                                                                                 Metatheria; Diprotodontia; Macropodidae; Macropus.
1 (bases 1 to 3452)
Hawken,R.J., Maccarone,P., Toder,R., Marshall Graves,J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="IL5"
join(34. .180,406. .438,1492. .1620,1706. .1816)
/gene="IL5"
                           Macropus eugenii interleukin-5 (IL5) gene, complete cds
AF064209
AF064209.1 GI:5006325
                                                                                                                                                                                                                 Isolation and characterization of marsupial IL5 genes
Immunogenetics 49 (11-12), 942-948 (1999)
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Minnesota, 1988 Fitch Avenue, St. Paul, MN 55108,
Location/Qualifiers
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Gaps: 0
Percent Identity: 70.000
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/organism="Macropus eugenii"
/db_xref="taxon:9315"
/chromosome="1"
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/protein_id="AAD37462.1"
/db_xref="G1:5006326"
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seq_documentation_block:
LOCUS AF064209
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LOCUS AC018207
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REFERENCE 1 (bases 1 to 44897)

AUTHORS MARIAN AND WORKER-1.0.

TITLE Direct Submission

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Direct Submission

Moderation of the record demanic to flyeslett.com.

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US-08-653-294-13 x AMPEPSYNT
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Pelzer,S., Reichert,W., Huppert,M., Heckmann,D. and Wohlleben,W.
Cloning and analysis of a peptide synthetase gene of the balhimycin producer Amycolatopsis mediterranei DSM5908 and development of a
Berkeley Drosophila Genome Project
Lawrence Berkeley, National Laboratory, MS 64-121
Berkeley, CA 94720
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@mhgc.lb.gov.
Library locations: 137-37, 136-25.
Location/Qualifiers
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                                                                                                                                                                                                                                                                    /clone="Pis DS03550 (D225) and DS02397 (D206)"
/note="DS03550 (d225) extends from bp 1 to bp 16,924 and
/notes"DS03550 (d205) extends from bp 13,480 to bp 89,791."
/ 20016 c 20807 g 24678 t
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Pelzer, S.
Direct Subsisted (15-MAY-1996) S. Pelzer, Universitaet Tuebingen,
Lehrstuhl Mikrobiologie-Biotechnologie, Auf der Morgenstelle 28, 72076 Tuebingen, FRG
Revised by author 14-077-97
On Oct 30, 1997 this sequence version replaced gi:1483198.
Location/Qualifiers
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LOCUS AMPEPSYNT 3975 bp DNA BCT
DEFINITION Amycolatopsis mediterranei aps gene, partial.
ACCESSION X97860
                                                                                                                                                                      1. .89791
/organism="Drosophila melanogaster"
/db_xxef="taxon:7227"
/chromosome="2R"
/map="57B6-57C1"
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Gaps: 0
Percent Identity: 88.889
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J. Biotechnol. 56 (2), 115-128 (1997)
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/db_xref="taxon:33910"
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Amycolatopsis mediterranei.
Amycolatopsis mediterranei
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/codon_start=3
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<1. .>3975
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4.875
88.889
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US-08-653-294-13 x AC005268
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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MEDLINE
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KEYWORDS
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QRDAVTEVEDGLCAVRFDLRTPPLFRVVAQRLADDVFQLTIAEHHSILDGWSFTSLLT
EILERHADPDAPPAPPPASTFRDFVAAEQAAVASAESERFWRDRLTGANGALWSSGTD
SAAATAEIPRTLERVLPDAPAQLAAIAAAAGVPVKAVGLAAHVRALARITGRDRVTTG
                                                                                          /db_xref="SPIENBL:044103"
/db_xref="SPIENBL:044103"
/translation="IPLDRGEPELTAGFDLTTGPLLRATLVDATTLVLVVHHIVWDGW
SAGYPERELAEFYTAAVEGREPVLFTTGYAGAAEAVVHDDLAYWFSQLQGAPGR
SAGYPERELAEFYTAAVEGREPVLFTGYAGAAEAVVHDDLAYWFSQLQGAPGR
SAGYPERELAEFYTAFBYFSTEPAGLAAFAALLNY
TGAADLVVGTPVTTRDRPELADLIGYFVNILPLRLKIDRAASFRDLVEHVRDTAFDAY
                                                                                                                                                                                                                                                              ACLDVPEDVVVDALALERTPRHAPLVQVVFGAHAEDPAPLRFGPLTATRRVHHNGTSK
FDFTWSTFDDGELRGEVEYRTSLFDAATVDRWTTHWRALLTAVLSEPDSPLWKIDLEP
VWPVAVTASQPRCLHESFEDSVDRFPGRPAVTFGGASVTYAELDRRANRLAHALIEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSVNGRLEERSGTEAYGLFLNTVPLVVDCTERDLVRSVHEDEVALLPHRRVPFARLAR
LMAGPRLEACFAFLRFHALGRLAGSATSIVDDRIGCEPDWRYEPTNFALGVALVQDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-AUG-1997) Chromosome 12 Project Group (http://www.sanger.ac.uk/HGP/Chr12/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk IMPORTANT; This sequence is the entire insert of clone 204E5. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
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12; ATP ligand gated ion channel; CpG island; P2X-like receptor;
QM-like; Tumour-related protein.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 80.000
/product="peptide-synthetase"
/protein_id="CAA66454.1"
/db_xref="GI:2576251"
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Kershaw,J.
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                                                                                                                            This sequence was generated from part of bacterial clone contigs of human chromosome 12, constructed by the Sanger Centre chromosome 12 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr12/
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                The true left end of clone 204E5 is at 1 in this sequence. The true right end of clone 204E5 is at 129969.
with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     586. 3607
note="clone 92N15; CAAAAAAAAAAAAAAAAAAA in this entry;
                                                                 the overlapping clone as we submit sequences with only a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="FLAM_C repeat: matches 59. .111 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319. .1383
.note="92N15 has 2 versions, both differ from 204E5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .302 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200. .4346
note="AluJo repeat: matches 282. .134 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211. 5213
note="clone 92N15; ATG in this entry; substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .295 of consensus;
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157. .6459
note="AluSx repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluSg repeat: matches 300. .3 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116. .1254
note="MIR2 repeat: matches 145. .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
Location/Qualifiers
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note="AluJo repeat: matches 118.
ncomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460. .5750
"note-"AluJb repeat: matches 302.
nocomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6761. .7142
/note="differs from 92N15"
7138. .7438
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note="22 copies of 2 mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .129969
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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/clone="XX-204E5"
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9383. 9562 / Once="MSTA repeat: matches 243. .426 of consensus" 9562. 9646 / Once="MLT2G repeat: matches 305. .387 of consensus" 9643. 9645 / Once="Clone 92N15; ACA in this entry; substitution" / replace="ata" 9686. .9688 / Once="clone 92N15; ATG in this entry; substitution" / replace="acg" / Acg in this entry; substitution" / replace="acg" / Acg in this entry; substitution" / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this acg in this entry; substitution / Acg in this in this entry / Acg 
                                                                                                                                                                                                                                                                                            8810. .8924
/note="MLT2CB repeat: matches 316. .434 of consensus"
8924. -9108
7note="MSTA repeat: matches 1. .193 of consensus"
9111. .9366
/note="Alusx repeat: matches 42. .300 of consensus;
1ncomplete repeat"
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note-"MER3 repeat: matches 200. .166 of consensus"
5274. .15452
note-"Aludo repeat: matches 123. .301 of consensus;
nocemplete_repeat"
                                                                                                               7891. .8182

7001. .8182

7001. .8183

7001. .8873

7001. .810. .8924

8810. .8924
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/note="FLAM_C repeat: matches 116. .1 of consensus"
20197. .20309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .3045. .13304 Thomatches 297. .39 of consensus;
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hote="Alusx repeat: matches 1. .301 of consensus"
1751. 18071
hote="Alusx repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715. .10013
note="AluJo repeat: matches 300. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1174. 11260 matches 146. .59 of consensus" note="MIRZ repeat: matches 146. .59 of consensus" note="MIR repeat: matches 1. .262 of consensus" note="MIR repeat: matches 302. .2 of consensus" note="MIRX repeat: matches 302. .2 of consensus" 11945. .11945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2599. .12901.
note="Alusx repeat: matches 1. .296 of consensus"
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Inote="Aluvo repeat: matches 1. .300 of consensus"
4005. .14306
Inote="Aluxa repeat: matches 1. .302 of consensus"
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note="AluJb repeat: matches 5. .291 of consensus"
5989. .16142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6463. 16765
note="AluSx repeat: matches 302. .1 of consensus"
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Moote="AluY repeat: matches 301. .1 of consensus"
19892. .20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMD2 repeat: matches 875. .582 of
16765
                                      of
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/note="AluSq repeat: matches 300.
7593. .7839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16443
                                                                            7593. .7839
/note-"PABL repeat:
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3608. .13891
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Quality:
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Submitted (22-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Louis,
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 136371)
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Waterston, R. H.
Direct Submission
Submitted (06-AUG-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Mo 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1 repeat: matches 1943. .1788 of consensus"
26469. .26770
                                                 21716. .22001
/note="AluSq repeat: matches 1. .303 of consensus"
22137. .22350
/note="AluJ repeat: matches 85. .302 of consensus;
                                 note="AluSx repeat: matches 302. .10 of consensus'
1716. .22001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJo repeat: matches 302. .1 of consensus"
26847. .27145
                                                                                                                                                                                                                                                                                                                                                        'note="AluSq repeat: matches 303. .2 of consensus"
    .43 of consensus'
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HOMO Sapiens clone NH0470K20, complete sequence.
AC009239
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MIR repeat: matches 144.
.20979
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The sequence of Homo sapiens clone Unpublished
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                                                                                                              ncomplete repeat*
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76460
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Waterston, R.H.
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With Chaptershead

Shadwin, J., Barna, N., Beckerly, R., Boqualavk, J., Boukhgalter, B.,
Baldwin, J., Barna, N., Beckerly, R., Boqualavk, J., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fiffakhy, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Locke, Y., J., McKernan, K., McLaughlin, J., Meldrim, J.,
McTwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
McTwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
McTwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
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McTwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
McTwan, P., McGurk, A., McKernan, K., McLaughlin, J., Wheeler, J.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vasalliev, H., Vo, A., Wheeler, J., Wu, X.,
Nyman, D., Ye, W.J., Zimmer, A. and Zody, M.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
http://ftp.genome.washington.edu/Rw/RepeatMasker: html.
* NOTE: This is a "working draft, sequence Iccurelly
* consists of 17 contigs. The true order of the pieces
* analystary Gang herean herean in this sequence record is
* analystary Gang herean herean herean represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC011830 166832 bp DNA HTG 20-OCT-1999 Homo sapiens chromosome 8 clone 94_A_14 map 8, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166832)
Blirren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone 94_A_14
                        n Oct 22, 1999 this sequence version replaced gi:5732147.
Location/Qualifiers
1. 136371
/organism.mom saplens"
/db.xref="taxHone saplens"
/clone="NH0470K20"
39683 a 25507 c 25721 g 45460 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 9
Gaps: 0
Percent Identity: 77.778
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AC011830.2 GI:6087976
HTG; HTGS_PHASE1.
63108, USA
Oct 22, 1999 this
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Percent Similarity: 100.000
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845: contig of 845 bp in length

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alignment_block:
US-08-653-294-13 x AC010086/rev
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Percent Similarity: 100.000
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26064
72625
72643
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Ratio:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="94_A_14"
/clone_lib="RPCI-11 Human Male BAC"
. 39419 c 39077 g 42526 t 699 others
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                                                                                                                                                                                                                                    of 12011 bp in length
unknown length
                                                                                                                                                                                                                                                                    gap of unknown length contig of 1592 bp in length gap of unknown length contig of 23896 bp in length
                                                                                                                                                                                                             of 10721 bp in length
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of 5396 bp in length
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Percent Identity: 77.778
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of 9157 bp in 1
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                               of 2802 |
unknown
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                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. 16683
7. Crganism="Mono sapiens"
/db_xref="taxon:9606"
/chromosome="8"
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gap of contig gap of contig gap of
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AC010086.2 GI:6007895
HTG; HTGS_PHASE1.
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Waterston, R.H.
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Ratio: 4.222
Percent Similarity: 100.000
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US-08-653-294-13 x AC011830
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TITLE The Sequence of Romo spiens clone

AUTROSS MALES TO 187447)

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192073 211769: contig of 1969
Location/Qualifiers
1. 211769
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                    38975:
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 296 bp in length
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of 1077 bp in length
unknown length
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g of 809 bp in length
f unknown length
g of 1575 bp in length
f unknown length
g of 243 bp in length
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of 2117 bp in length
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of 1364 bp in length
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of 1929 bp in length
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of 13451 bp in length

contig of 13015 bp in length

contig of 10529 bp in gap of unknown length

contig of 19697 bp in length

gap of unknown length contig of 14219

678 others Length: 10 Gaps: 0 Percent Identity: 70.000 /clone="CIT-HSPC\_575N7" 64860 a 39430 c 40173 g 66628 t Align seg 1/1 to reverse of: AC008591 from: 1 alignment\_block: US-08-653-294-13 x AC008591/rev 38.00 4.222 90.000

9 08:46:55 2000

Wed Feb

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J. Microbiol. Methods 28, 25-34 (1997)
2 (bases 1 to 1323)
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                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Logolitina; Liu, Y. and Robbins, P.W. Chitinases are a multi-gene family in Aedes, Anopheles, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="WAQYRQGRAKFVPEDYTPGLCTHILFAFGWMNADYTVRAYDPAD
LPNDWAGEGMYRRVNKLKVTDTQLKTLLSFGGCSFGTALFQGMAASSASRKVFIDSAT
                                         10-APR-1997
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                                                                                                                                                                                                                                                                 Insect Mol. Biol. (1997) In press
2 (bases 1 to 486)
Specht, C.A. and de la Vega, H.
Direct Submission
Submitted (19-Sip-1997) Biology, Massachusetts Institute of
Technology, 40 Ames St. E17-235, Cambridge, MA 02139, USA
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Gaps: 0
Percent Identity: 70.000
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/organism="caenorhabditis elegans"
/db_xref="taxon:6239"
join(41. .14,150. .>486)
/gene="CHT1"
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/db_xref="G1:2564715"
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/gene="CHT1"
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Hyphomicrobium sp. DNA,
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Caenorhabditis elegans strain=Bristol N2.

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;

Rhabditina; Rhabditojdea; Rhabditidae; Peloderinae; Caenorhabditis;

I (bases 1 to 2508)

Milson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,

Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,

Coulson,A., Craxton,M., Deney,S., Du,Z., Durbin,R., Favello,A.,

Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,

Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,

Latrellle,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,

Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,

Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,

Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,

Wilkinson-Sproat,J. and Wohldman,P., Weinstock,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Chases 1 to 1323)
Gliesche, C.G.
Direct Submission
Submitted (24-OCT-1996) C.G. Gliesche, CAU-Kiel, Ins
Allgemeine Mikrobiologie, Am Botanischen Garten 1-9,
(Biologiezentrum), D-24118 Kiel, FRG
Location/Qualifiers
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Gaps: 0
Percent Identity: 87.500
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Department of Genetics, Washing
St. Louis, MO 63110, USA, and
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Materston, R.
Direct Submitted (10-DEC-1995) Robert Waterston
Submitted by:
Submitted by:
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Unpublished (1995)
3 (bases 1 to 25083)

    1323
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LOCUS CELCO4F6 25083 bp DNA
DEFINITION Caenorhabditis elegans cosmid C04F6.
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94150718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: HSMOXMXU from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuAlaIleArgLeuAsp 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 25083)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U42835
U42835.1 GI:1125760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 37.00
Ratio: 4.625
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-13 x HSMOXMXU
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source

FEATURES

gene

CDS

gene

CDS

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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(1004. .1347,1404. .2716,2852. .2966, 3140. .3221))
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/note="CodF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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PADLDNWARGEGMYRRYNKLKYTDTQLCTHILFAFGGWARSASSRSVFID
SAITFVRTWEFDGIIDWEFVSGATDWAHVALVKELKAAGESEAGSTGKDRLLVTAA
VAAGPATIDAGYDIPNIAPNFDFILLMSYDFFGAWASLVGFNSPLYATTELPAEWNGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //note="coded for by C. elegans cDNA yk31e4.5; coded for by C. elegans cDNA CEMSG37F; coded for by C. elegans cDNA CEMSG37F; coded for by C. elegans cDNA for by C. elegans cDNA CEMSG37F; coded for by C. elegans cDNA CEMSE22F; coded for by C. elegans cDNA CEMSG37F; coded cEMSF39F; coded for by C. elegans cDNA CEMSG39F; coded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNTVYGOTYKWLPETAGKTPQEINRHFSPEFFGINVFLYLKHK
ASKTFALSGKPALMFISFVVQLACCIFLLDFGVNIYKNIGK"
complement(1004. .3221)
/gene="C04F6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVDSSARYWNQKGMPKEKIIVGMPTYGRGWTLNNASAINPGTSGSPAKITQYVQEAGV
GAYFEFCEMLANGATRYWDSQSQYPTIVOGNOWSYDDEESFARKMAVYREGYGGAF
WWTLDFDDFRAGSNGGOLYPLISYTAKELGGVIIPKKGGYTAPTTYVATGRP
PMTSAVTTTTAAITTTTRAATTTTASNINVCSGKSDGFYPNSNNCGLFVLCSSKSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSCPSGLQYSASLKYCTTSTASGCSVTTTRAPTTTTKSAPTVTTTRAPTTTTPAFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers
                                                                                                                                                                                                     of
of
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11313. .11448,11501. .11760)
/gene="vit-5"
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mali: rwénematode.wustl.edu and jes@sanger.ac.uk
NEIGHBORING COSMID INFORMATION:
The 5' cosmid is ZK563, 200 bp overlap; cosmid is ZK813, 200 l
overlap. Actual start of this cosmid is at base position 197 or
CELCO4F6; actual end is at 20314 of CELZK813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKDGFFGVPSDCLKFIRCVNGISYNFECPNGLSFHADTMMCDRPDFSKCAK"
5686. .11760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/map="x"
357. .673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357. .673
/gene="CO4F6.2"
join(357. .422,476. .673)
/gene="CO4F6.2"
/codon_start=1
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gene

CDS

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FREILELPFRACINGLY

FREILELPFRACINGLY

FREILELPFRACINGLY

FREILELPFRACINGLY

BUESDKISCHENGENERSTRINGLY

BUESDKISCHENGENERTHENGOOGSTURY

BUESDKISCHENGENERTHENGOOGSTURY

GSECKECEREGGFVKPOTVTYTFKNEKLOSSTUNDKCITREPTAYGLRF

GSECKECEREGGFVKPOTVTYTFKNEKLISCPYOGSTURY

VERSKINKELKKVSGPREETTYSMERKELISCPYOGOSTARPRAFALTETT

VERSKINRETKKVSGPREETTYSMERKELISCPYOGOSTARPRADLICLOLAGSPLSEK

ANGGTKNTOHLIHFEKKSITPLRADELLKKVOTHTITYTKAEKKVOTYETTL

ANGGTKNTOHLIHFEKKSITPLRADELLRKSVOGTLXPSEHTADLLICLAGSPLSEK

YEDLROSAWLAAGSVYRGTSCHOLLIRPASROTKEKYVRTHOHFRYNDSTYEKV

KNRONFPLIMAALHRMAHTIPPROPLINTSSWENSSONGHVAAFTYNVLROFYKSTN

FOYOOLAYRCSKILLFTYROPOGOMISTYSOLDLIKDSKOOPFATTFEKNAPLP

KRYQASFETVFGGNNHKYFROOFSGONFEOYILKTLEKLSLYGKGSDELKSRRVOSG

IOMLOGITKKMNINTSPROOFSGONHEOYILKTEKLSLYGKGSDELKSRRVOSG

IOMLOGITKKMNINTSPROOFSGONHEOYILKTEKLSLYGKGSDELKSRRVOSG

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IELEKLGARLVLDIYFELHRALFFYEBRERRIPTIGMPLITSGNWYNS

IELEKLGARLVLDIYPLWHTEWRFWYRYVILONGSCONHEON
for by C. elegans CDNA CEMSF59R; coded for by C. elegans CDNA CEMSH78R; coded for by C. elegans CDNA CEMSH78R; coded for by C. elegans CDNA CEMSH78R; coded for by C. elegans CDNA wyle5.5; coded for by C. elegans CDNA ykl65.5; coded for by C. elegans CDNA ykl65.5; coded for by C. elegans CDNA ykl9510.5; coded for by C. elegans CDNA ykl9510.5; coded for by C. elegans CDNA ykl16.5; coded for by C. elegans CDNA ykl565.3; coded for by C. elegans CDNA ykl565.3; coded for by C. elegans CDNA ykl588.5; coded for by C. elegans CDNA ykl588.5; coded for by C. elegans CDNA ykl588.5; coded for by C. elegans CDNA ykl189.3; coded for by C. elegans CDNA ykl189.5; CO4F6.1"
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//gene="COGFE 4"
//once="coded for by C. elegans cDNA yk21f1.5; coded for by C. elegans cDNA yk21f1.3; coded for by C. elegans cDNA yk5488.3; coded for by C. elegans cDNA yk5488.3; coded for by C. elegans cDNA yk6488.3; coded for by C. elegans cDNA yk4568.3; coded for by C. elegans cDNA yk4568.3; coded for by C. elegans cDNA yk4568.3; similar to beta transducin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSEFSOTALFPSLPRTARCTAVVLGNTPACDKIOYCNGTSVTV
PVGSLFDTEIYTEHSHQTTVAKTSPSGYYCASGDVHGNVRIWDTTQTTHILKTTIPVF
SGPVKDISWDSESKRIAAVGEGRERFGHVFLFDTGTSNGNLTGQARAMNSVDFKPSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVDGTKTGVFEDDSLKNVAHSGSVFGLTWSPDGTKIASASADKTIKIWNVATLKVEKT
IPVGTRIEDQQLGIIWTKQALVSISANGFINFVNPELGSIDQVRYGHNKAITALSSSA
DGKTLFSADAEGHINSWDISTGISNRVFPDVHATMITGIKTTSKGDLFTVSWDDHLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPAGGSGVDSSKAVANKLSSQPLGLAVSADGDIAVAACYKHIAIYSHGKLTEVPISYN
SSCVALSNDKQFVAVGGQDSKVHVYKLSGASVSEVKTIVHPAEITSVAFSNNGAFLVA
TDQSRKVIPYSVANNFELAHTNSWTFHTAKVACVSHSPDNVRLATGSLDNSVIVWNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mKSIIIASLVALAIAASPALDRTFSPKSEVVYKFDGLLLSGLPT
ASSDASQTLISCRTRLQAVDDRYIHLQLTDIQYSASHIPQSEQWPKIESLEQRELSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNTLEITHKEVVPENKKTTVSVHTRPVAFIRVPKNODSEYVEAEEKTISHSOYOMSTE
EIDROYETFGLRINAGGNVLSQWTLPMVLMTEQDFEYTLENKNRPVEFTARVTIGNLE
KTDLSEIKFDKIFEKEFDLENNESENRROYFHKMIREIQSEGGFKNLITLKLEAPQQM
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PHREVOLAFNAKWGSSKKSEITVNAQLEOSTEOKKFIRNIEREYKGIPEYELLIKAAR
LNOVNVVSEYKLIPOSEYTFSRIFDLIKAYNEWTVSEKRVQNENRRYVLOLSYEPLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVKVDGKKVNPTELEQYNIEILGDNLIVIRLPGGEVRFDGYTVKTNMPSVASONQLCG
LKGNNDGERDNEFWTADNYETEDVEEFHSYLLIKNBECCEVENDRISKKNYRNRNRE
EKGSPSESSSDYESNYDEKETEKELVKKTLIKEFSNRYCFSIEPVSEGREGLESEKTS
NKKIRFTCMPRHSKNARRFLKEAREQTVAELVDFPVSFVESVKIPTACVAY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIYRAPLTICYSLVAKDCSEQPRFAVLAKKINKNSEELLVKVVRREEEIVVKKSDDKF
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17154, 17225,17270, 17373,17416, 17649,17758, 17911,
20223, 20626,20679, 21012,21062, 21256,21312, 21497,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="C. elegans vitellogenin 5 precursor, vit-5 (Spieth et al., NAR 13:7129-7138(1985))"
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/gene="CO4F6.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="C04F6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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DNA HTG 16-NOV-1999
, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                            KIRNOMSGALMSAAQFAVTSYVČVRVLKFLYIMCKSVLVHFITPKHDLDYLKDTMTVI
TGGTDGIGKAYIEELCKTRGLKKFYLIGRNIDKLNNTKKELVEQHGCEVWCHVHDFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was identified as CDM:10210169 by the submitter. For further information on this sequence e-mail to fly@celera.com.* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly.
Drosophila melanogaster
Drosophila melanogaster
Eukarýota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M. and Venter, J.C.
Direct Submission
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
21547. .21613,21669. .21772,22130. .22204))
/gene="C04F6.5"
/note="Similar to alcohol/ribitol dehydrogenase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: CELCO4F6 from: 1 to: 25083
                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
6682 c 6750 g 6507 t
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Gaps: 0
Percent Identity: 77.778
                                                                     /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC015346
AC015346.1 GI:6435989
HTG; ḤTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-13 x CELC04F6/rev
                                                                                                                                                                                                                                                                                                                             37.00
4.111
90.000
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4.625
88.889
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US-08-653-294-13 x AC015346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_htg5:AC015346
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AUTHORS
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JOURNAL
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L5 mycobacteriophage DNA.
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ID T78508 standard; DNA; 44377
AC T78508;
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US-08-653-294-13 x T80415/rev
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     N_Geneseq_36:047357 - 3
N_Geneseq_36:V30458_0 -
N_Geneseq_36:X20248_00 -
N_Geneseq_36:V30459_0 -
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Staphylococcus aureus contig
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DNA sequence of a L5 shuttle
Mycobacteriophage L5 genome s
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-WODEL_frame+_p2n.model -DEV=xlp
-Q=/Cgnl_l/USPPO_Lppol/USO8653294/runat_04022000_160701_15807/app_query.fasta.1
-DB=/Cgnl_l/USPPO_Lppol/USO8653294/runat_04022000_160701_15807/app_query.fasta.1
-DB=/Cgnl_ganesq_36 -QFWT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPOP=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=4.500 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NOPM=ext -MINLEN=0
-MALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NOPM=ext -MINLEN=0
                                                                                                 About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 311585
Latabase length: 125096042
Search time (sec): 590.520000
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Query: US-08-653-294-13
Query length: 10
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                                                   Date: Feb 8, 2000 1:27
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N_Geneseq_36:X13037
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District PR:

WPI: 97-418047/39.

DR P-PSDB: Wa23120.

DR P-PSDB: W23120.

PT for production of spiramycin-related polyketide antibiotics

DNA encoding Streptomyces ambofaciens platenolide synthase domain -

For production of spiramycin-related polyketide antibiotics

This sequence represents the platenolide synthase gene cluster of the cinvention. This sequence is referred to as the srm6 gene, and was consolated from Streptomyces ambofaciens. This sequence encodes the nutri-functional proteins which direct the synthasis of the polyketide platenolide. Platenolide is the basic building block of the macrolide pribiting antibiotic activity based on the platenolide structure, including specifically the macrolide antibiotic spiramycin and spiramycin consumptions of the platenolide synthase DNA sequence can be made so as to change the number and type of carboxylic codes incorporated into the growing polyketide chain and to change the consumer 44377 BP; 4965 A; 15552 C; 17381 G; 6479 T;
26-FEB-1998 (first entry)
Platenolide synthase gene cluster.
Platenolide synthase gene cluster;
Platenolide synthase gene cluster; platenolide production; srmG gene;
multi-functional protein; macrolide antibiotic; spiramycin; ss.
Streptomyces ambofaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77-FBB-1998 (first entry)
Platenolide synthase gene cluster.
Tylactone synthase gene cluster; tylG gene; multifunctional protein; platenolide synthase gene cluster; platenolide production; srmG gene;
                                                                                                                                                 "ORF2 encodes protein shown in W23717" .31284
                                                                                                                                                                                     _except= (pos:20111. .20113, aa:Met) "ORF3 encodes protein shown in W23718"
                                                                                                                                                                                                                                     "ORF4 encodes protein shown in W23719"
                                                                                                  /transl_except= (pos:350. .352, aa:Met)
/note= "ORF1 encodes protein shown in W23716"
                                                                                                                                                                                                                                                                         "ORF5 encodes protein shown in W23720"
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Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                Rao RN, Richardson MA;
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                                                             Location/Qualifiers
350. 14002
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ID T80414 standard; DNA; 44377 BP.
AC T80414;
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                                                                                                                                                                                                                                                 .41830
                                                                                                                                                                                                              .36071
                                                                                                                                                                                                                                                                                                                       22-FEB-1996; US-012050.
(ELIL ) LILLY & CO ELI.
Burgett SG, Kuhstoss SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-13 x T78508/rev
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4.625
88.889
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                                                                                                                                                  /note=
20110.
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/note=
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                                                                                                                           14046.
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                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                  36155.
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                                                                                                                                                                                                                                                                                                         9-FEB-1997; 301066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
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                                                                                                                                                                                                                                                                                     EP-791656-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                               Key
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Distriction of tylosin-related polyketide compounds

Frought According Streptomyces fradiae tylactone synthase domain - for

production of tylosin-related polyketide compounds

Example 2; Pages 110-134; 200pp; English

This sequence represents the platenolide synthase gene cluster of the

This sequence is referred to as the srmd gene, and was

considered from Streptomyces ambofaciens. This sequence encodes the

multi-functional proteins which direct the synthesis of the polyketide

platenolide. Platenolide is the basic building block of the macrolide

antibiotic spiramycin. This sequence was used along with the tyld gene

(see T80413) to create a hybrid ORTS sequence (see T80415). The tyld gene

(see T80413) to create a hybrid ORTS sequence (see T80415). The tyld gene

(see T80413) to create a hybrid ORTS sequence (see T80415). The tyld gene

(see T80413) to create a hybrid ORTS sequence (see T80415). The tyld gene

(see T80413) to create a hybrid order cluster of the invention. The tyld gene

(see T80413) to create a hybrid order cluster of the invention. The tyld gene

(see T80413) to create a hybrid order cluster of the invention. The tyld gene

(see T80413) to create a hybrid direct the synthesis of the polyketide

(tylosin. The hybrid sequence can be used to transform 5. ambofaciens

(accuence, so that they can produce polyketides. The DNA sequence can be

modified so as to alter the type of carboxylic acids incorporated, the

number of carboxylic acids incorporated and/or the post-condensation

(accuence) the condensation of carboxylic acids incorporated and/or the post-condensation

(accuence) the condensation of carboxylic acids incorporated and/or the post-condensation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŧ,
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                                                                                                                                                                                                                                                                                                                                                                    /note= "ORF3 encodes protein shown in W22608" 31329. .36071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "ORF5 encodes protein shown in W22610"
                                                                                                                                                    /transl_except= (pos:350. .352, aa:Met)
/note= "ORF1 encodes protein shown in W22606"
14046. .20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "ORF4 encodes protein shown in W22609'
                                                                                                                                                                                                                                                                                       "ORF2 encodes protein shown in W22607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17381 G;
polyketide; tylactone synthesis; antibiotic; tylosin; Streptomyces ambofaciens.
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Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO ELI.
Dehoff BS, Rubstoss SA, Rosteck PR, Sutton KL;
WPI: 97-418046/39.
P-PSDB; W22606-W22610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6641
                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: T80414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrargLeuAlaileArgLeuAspGlu 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4965 A;
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ID T04154 standard; DNA; 1791 BP.
AC T04154.
DF 26-FEB-196 (first entry)
DF BCG DapB gene.
                                                                                                                                                                                                                                                                                                                     .31284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .41830
                                                                                          350. .14002
/*tag= a
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BCG DapB gene.
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4.625
88.889
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20110. .
/*tag=
/transl_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1997.
19-FEB-1997; 301056.
22-FEB-1996; US-012078.
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/*tag=
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Ratio:
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seq_name: N_Geneseq_36:T89957
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US-08-653-294-13 x T06770
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Ratio:
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01-JUN-1995; 4
20-AUG-1990; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-1992; U01-JUL-1993; U08-JUN-1994; UCIBA ) CIBA G
                                                                                                                                                                                                                                                                 alignment_scores:
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   Dihydrodipicolinate-reductase; diaminopimelate-dehydrogenase; dapB; diaminopimelic acid; peptidoglycan; mycobacteria; vaccine; Mycobacteriun tuberculosis; Mycobacteriun aviun; Mycobacteriun fortuitum; Mycobacteriun leprae; Mycobacteriun gordoneae; Mycobacteriun haemopiiliun; Mycobacteriun paratuberculosis; BCG; ss. Mycobacteriun bovis;
                                                                                                                                                                                                                                                                                Gene involved in the synthesis of di:amino:pimelic acid in mycobacteria - and methods for inhibiting its expression to treat mycobacterial infection infection.

Tale 19 3: 48pp; English.

A BCG DNA fragment (T04154) that complemented a dapB mutation in Escherichia coli was isolated. The BGC dapB gene encoded a bifunctional enzyme (R789946) capable of catalyzing the dihydrodipicolinate-reductase and diaminopimelate-dehydrogenase reactions involved in diaminopimelic acid (DAP) biosynthesis. DAP biosynthetic genes are useful as targets for anti-mycobacterial agents and for the design of in vivo selection systems. Mycobacteria having a deleted dapB gene can be used for vaccine produ.

Sequence 1791 BP; 254 A; 638 C; 640 G; 259 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: T04154 from: 1 to: 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1996 (first entry)
Pseudomonas aureofaciens phenazine gene cluster.
Antipathogenic substance; phenazine; antibiotic;
fungloide; pesticide; ss.
                                                                                                                                                                                 /product- unidentified
                                                                                                                                                                                                                                     (YESH) UNIV, YESHIYA EINSTEIN COLLEGE.
Cirillo JD, Jacobs WR;
WPI: 95-311535/40.
P-PSDB: R79946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "phz2 (ORF2)"
2764. .3600
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aureofaciens.

Key
Location/Qualifiers
cds
230. 1597
/*tag a
/note= "phz1 (ORF1)"
cds
1598. .2761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlalleArgLeuAspGlu 9
                                                                             297. .303

/*tag= a

312. .1127

/*tag= b

/product= DapB

1136. .1140

/*tag= c

1151. .1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID T06770 standard; DNA; 4602 BP.
AC T06770;
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US-08-653-294-13 x T04154/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:T06770
                                                                                                                                                                                                                  27-FEB-1995; UO2455.
28-FEB-1994; US-203190.
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                                                                                                                                                             cds
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DON KEEL THE SELL THE
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Pyrrolnitrin; biosynthetic pathway; pathogen protection; phenazine;

Pyrrolnitrin; biosynthetic pathway; pathogen protection; phenazine;

plant antipathogenic substance production; anti-fungal antibiotic;

fungal respiratory electron transport inhibitor; lipoprotein damage; ss.
                                                                                   brotecting plants against pathogens with genetically transformed biological control agent - which expresses all polypeptide(s) involved in pyrrolnitrin biosynthetic pathway bxample 18: Column 135-144; 8Bpp; English.

Example 18: Column 135-144; 8Bpp; English.

This genomic DNA sequence encodes a cluster of genes involved in phenazine biosynthesis. Phenazines are nitrogen-containing heterocyclic compounds with a common planar aromatic tricyclic structure. It has been proposed that phenazine antibiotic function arrises from the formation of intercalative complexes with DNA interfering with DNA metabolism. Transgenic plants containing such antipathogenic genes should have enhanced resistance to attack by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Pee K;
WPS 198-556391/47.
P-PSDB: W69401, W69402, W69403, W69404.
Cenes encoding enzymes of the biosynthetic pathway of pyrrolnitrin useful for producing transgenic plants which can produce pyrrolnitrin as an anti-pathogenic agent Example 18; Column 147-156; 109pp; English.
This sequence represents the phenazine gene cluster, isolated from
                                                                                                                                                                                                                                                                                                                                                                        818 T;
  Lam ST;
                                                                                                                                                                                                                                                                                                                                                                        1342 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 70.000
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09-0cT-1996; 729214.

09-0cT-1996; US-729214.

08-JUN-1994; US-258261.

30-MXY-1995; WO-IB0414.

30-MXY-1995; WO-IB0414.

Hammer PE, Hill DS, Kirner S, Lam ST, Ligon JM,
Hammer PE, Hill DS, Schupp T, Uknes SJ;
                                                                                                                                                                                                                                                                                                                                                                        1516 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T89957 from: 1 to: 4603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beck JJ, Gaffney TD, Hammer PE, Hill
Ligon JM, Ryals JA, Schupp T, Uknes
WPI: 97-447901/41.
P-PSDB, W31304; W31305; W31306; W31307.
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1598. 2761
/*tag= b
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2764. .3600
/*tag= c
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3597. .4265
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                        925 A;
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aureofaciens.
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3.778
90.000
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US-08-653-294-13 x T89957
                                                                                                                                                                                                                                                                                                                                                                        4603 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                          phytopathogens
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                                                                                                                                                                                                                                                                                                                                                                             Sequence
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pseudomonas aureofaciens. This sequence was used to isolate the pyrrolnitrin gene region of the invention, that encodes at least one enzyme required in the biosynthetic pathway of pyrrolnitrin. The DNA and host cells transformed with it are useful for the production of transgenic plants with protection against phytopathogens. The enzymes substances (APS). The compound ulfimately plant antipathogenic fungal respiratory electron transport and causes general lipoprotein damage. The transformed cells can additionally be used in compositions to be applied to plants to provide resistance, as can purified APS produced by them Transgene dependent resistance eliminates the need to spray crops with chemical based pesticides and antibiotics, which is expensive and time consuming, and in addition, especially in the case of antibiotics, their over use leads to resistance. In addition, transgenic production of these enzymes overcomes problems of applying micro-organisms which can be slow growing and isolated in their growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas fluorescens phenazine gene cluster.
Pseudomonas; genetic engineering; biocontrol; plant; pathogenic;
Rhizoctonia; Pythium; antifungal; pyrrolnitrin; crop protection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1342 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 70.000
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Gaffney TD, Hill DS, Lam ST, Ligon JM, Stafford JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1516 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 4603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994 TAICGACTIGCCIGCCACCICGAICGGCGC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrArgLeuAlaIleArgLeuAspGluArg 10
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105. 1307
/*trag= a /product= "phzF"
note= "ORFI"
1323. 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "phzC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product "phzB'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: V58732 from: 1
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ID V39844 standard; DNA; 5698 BP.
AC V39844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   925 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ORF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /hote= "ORF2
1943. .3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:V39844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1998.
05-DEC-1997; E06815.
09-SEP-1997; US-058304.
06-DEC-1996; US-761258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-13 x V58732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4603 BP;
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9824919-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 areas.
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misc_feature
                                                                                                                                                                                                                                 alignment_scores:
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88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agenetically engineered biocontrol strain of Pseudomonas has been developed that can control attacks on crop plants by pathogenic fungi, developed that can control attacks on crop plants by pathogenic fungi, developed that can control attacks on crop plants by pathogenic fungi, acteria and microflora in the plant rhizosphere. The strains can be acterial and microflora in the plant rhizosphere. The strains can be included with agronomically acceptable carriers or chemical fungicides (e.g. metalaxyl compounds) in biocontrol compositions. The strains or compositions can be applied to a plant/plant part to protect it from a plant pathogenic fungus, by controlling or inhibiting fungal growth. They can also be applied to the environment in which a plant pathogenic fungus will grow (e.g. soil) to similarly control or inhibit pathogenic fungus. They are especially effective against plant pathogenic fungus. They are especially effective against conton. Rhizoctonia also infects many other crop species (e.g. beans and wheat), and no effective chemical fungicides are available. The present sequence represents the Pseudomonas fluorescens phenazine gene cluster used in an example from the present libé A; 1855 C; 1677 G; 1000 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125-JUN-1999 (first entry)
Human secreted protein 5' EST SEQ ID NO: 109.
Human secreted protein EST: expressed sequence tag; diagnosis;
forensic, gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
differentiation; haematopoiesis regulation; tissue growth regulation;
reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
thrombolytic, anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which may have cytokine, immune, regulatory, haematopolesis regulating, anti-inflammatory or tumour inhibition activity claim 1; Page 256; 577pp; English.

X51787 to X52019 represent 5° expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in Y12987 to Y13219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated brain-derived nucleic acids - used to develop products
             WPI; 98-33337/29.
Genetically modified Pseudomonas strains - useful to protect crop plants by controlling or inhibiting plant pathogen growth, e.g. growth of Rhizoctonia species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.00 Length: 10
3.778 Gaps: 0
90.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A, Dumas Milne Edwards J, Lacroix B; WPI; 99-153782/13.
P-PSDB; Y13095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 5698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2089 TATCGACTTGCCTGCCACCTCGATCGGCGC 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrArgLeuAlaIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: V39844 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID X51895 standard; DNA; 278 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:X51895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-1998; IB1236.
01-AUG-1997; US-905223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-13 x V39844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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WO9906552-A2.
11-FEB-1999.
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POLYMUCLEOLIGE(S) and proteins derived from Staphylococcus aureus - stored on computer readable medium and used in the production of anti-S.aureus vaccines

POLYMUCLEOLIGE(S) and proteins derived from staphylococcus aureus PT stored on computer readable anti-S.aureus vaccines

PR Claim 1; Page 1230-1231; 3271pp; English.

Claim 1; Page 1230-1231; 3271pp; English.

Colaim 2; Page 1230-1231; 3271pp; English.

Colaim 2; Page 1230-1231; 3271pp; English.

Colaim 2; Page 1230-1231; 3271pp; English.

Colaim 3; Page 1230-1231; 3271pp; English.

Colaim 3; Page 1230-1231; 3271pp; English.

Colaim 4; Page 1230-1231; 3271pp; English.

Colaim 5; Page 1230-1231; 3271pp; English.

Colaim 5; Page 1230-1231; 3271pp; English.

Colaim 5; Page 1230-1231; 3271pp; English.

Colaim 6; Page 1231; 3271pp; English.

Colaim 7; Page 1231; 3271pp; Page 1231pp; Antens 1231pp; Page 1231pp; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241. .300
/*tag= a
/note= "these bases represent a line of missing text in
/note= "the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemotactic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or or or cher activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or sequence 278 BP; 95 A; 56 C; 58 G; 67 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus config SEQ ID #351.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1997,
07-JAN-1997; 100117,
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 9
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TACAGACTAGCTCTGCGCATCACAGAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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ID V74662 standard; DNA; 1816 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.125
88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V74662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: X51895
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US-08-653-294-13 x X51895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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Ratio:
Percent Similarity:
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                                                        intron
                                                                                                                                   intron
                                                                                                                                                                      exon
                                                                                                exon
 (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.

Sequence 1816 BP; 539 A; 307 C; 240 G; 667 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laccase-LCC2; Polyporus pinsitus; Trametes villosa; primer; polymerase chain reaction; PCR; signal peptide; cellulase; polymerase chain reaction; PCR; signal peptide; cellulase; lignilus oryzae; cDNA probe; Escherichia coli; plasmid pDSY19; lignin; lignosulphonete; polymerisation; Kraft pulp; depolymerisation; oxidation; hair dye; phenol; aniline; vector; coloning; basidiomycetes; ss.
                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: V74662 from: 1 to: 1816
                                                                                                                               33.00 Length: 9
4.714 Gaps: 0
77.778 Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
364. .2492
/*tag= a
/roduct= Laccase-LCC2
/note= "EC-1.10.3.2"
364. .423
                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuAlaIleArgLeuAspGlu 9
                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID T15599 standard; DNA; 2880 BP.
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1188. .1283
/*tag= m
1284. .1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= n
1344. .1498
/*tag= o
1499. .1553
/*tag= p
1554. .1751
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836. .899
/*tag= h
900. .1013
/*tag= i
1014. .1066
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.067. .1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-1996 (first entry)
Laccase-LCC2 gene.
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364. .543
/*tag= c
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544. .592
/*tag= d
593. .661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
662. 715
/*tag= f
716. .835
/*tag= g
836. .899
                                                                                                                                                                                                          alignment_block:
US-08-653-294-13 x V74662/rev
                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T15599
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1752. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polyporus pinsitus.
Trametes villosa.
                                                                                                                                 Quality:
Ratio:
Percent Similarity:
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                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
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15-JUN-1995; U07556.

PR 24-JUN-1995; U07-180534.

PR 15-MAY-1995; U0-441147.

PR 15-MAY-1995; US-441147.

PA (NOVO) NOVO-NORDISK BIOTECH INC.

PA (NOVO) NOVO-NORDISK AS.

PA ASSIYNG DA, Dalboge H, Schneider P, Xu F, Yaver DS;

MPI; 96-068874/07.

DR P-PSDB; 890722.

DR P-PSDB; 890722.

DR P-PSDB; R90722.

DR P-PSDB; R90722.

PT In e.g. lighth manipulation, juice mfr., phenol polymerisation and phenol resin prodm

PT The sequence encodes laccase-LCC2 (pI 5.95) from Polyporus pinsitus

CLaim 5; Page 62-65; 137pp; English.

CC The sequence encodes laccase-LCC2 (pI 5.95) from Polyporus pinsitus

CC Trametes villosa). Polymerase chain reaction (PCR) amplification of princes villosa). Polymerase chain reaction (PCR) amplification of CC (Trametes villosa). Polymerase chain reaction (PCR) amplification of CC (Tow a 43-kDa cellulase using primer pHD433 (T15605) and a pUC (Tow a 43-kDa cellulase using primer pHD433 (T15605) and a pUC (Tow a 43-kDa cellulase using primer pHD433 (T15605) and a puc convarion planer in percentage of schema of the convarion of LCC1 (T15504) gives and a cDNA probe is obtained and used to screen a P. pinsutus convening also results in isolation of LCC1 (T15509) and LCC3 (T15600-T15602), which encode different laccases produced by P. CC (T15600-T15602), which encode different laccases produced by P. CC (T15600-T15602), which encode different laccases produced by P. CC (T15600-T15602), which encode different laccases produced by P. CC (T15600-T15602), which encode different laccases are well-expressed in Aspergillus spp. (with vector integration in the genome), in Aspergillus spp. (with vector integration in the genome), in contrast to previous basidiomycet laccases are well-expressed of the recombinant encode integration in the genome), in the produced page of the produced produced produced page of the produced produced page of the produced page of the produced produced page of the produced page of the produced page of the produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-1999 (first entry)
Bacterial artificial chromosome (BAC)-F2 contig 3.
Yeast artificial chromosome; YAC; probe; eukaryotic chromosome;
neccentromere; replication; extra-chromosomal element; segregation;
cell division; artificial chromosome; gene therapy; BAC; transgenic;
human artificial chromosome; bacterial artificial chromosome; ss.
WO9851790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 66.667
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ID V83943 standard; DNA; 11811 BP.

AC V83943.

DT 03-MAR-1999 (first entry)

DE Bacterial artificial chromosome; YRO;

KW Yeast artificial chromosome; YRO;

KW neocentromere; replication; extra-

KW numan artificial chromosom

KW human artificial chromosom

KW Numan artificial chromosome; Dacter

OS Synthetic.

PN W09851790-A1.
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2196. 2492
/*tag- w
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US-08-653-294-13 x T15599/rev
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1929. .2
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2136. .2
/*tag=
1873. ..
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The present sequence represents a bacterial artificial chromosome (BAC) contig, and exemplifies the invention. The specification describes nucleic acid sequences derived from a eukaryotic chromosome, including a nucleic acid sequences derived from a eukaryotic chromosome, including a compatible cell, of replicating, acting as extra-chromosome lelement a compatible cell, of replicating, acting as extra-chromosome lelement and segregating during cell division. The sequences can be used to construct artificial chromosomes for use in gene therapy comprising a replicable, segregating nucleic acid that confers a specific phenotype on cells. Human artificial chromosomes can propagate in human cells and carry large amounts of DNA (e.g. therapeutic genes), and, being extra-chromosomal, they are not mutagenic. The artificial chromosomes can production of proteins and to make diagnostic reagents, e.g. for expression of cytokines, receptors and growth factors, or to increase the copy number of a gene in a cell. The constructs may also be used for functional and structural analysis of chromosomes.
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                                                                                                                                                                New isolated nucleic acid comprising neocentromere sequences from eukaryotic chromosome - used to produce replicable, segregating artificial chromosomes that can carry large amounts of DNA for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-1996 (first entry)
Immunogen DNA from n-(ABCDE) hepatitis virus.
non-A, non-B, non-C, non-D, non-E hepatitis virus; n-(ABCDE);
immunogen; antibody; vaccine; phage library; ds.
Non-A, non-B, non-C, non-D, non-E hepatitis virus JFA clone 4B11.
W09532290-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: V83943 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4851 TACAGAATTTCAGTCAGGGAGGATGAAAA 4822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrArgLeuAlalleArgLeuAspGluArg 10
19-NOV-1998.
13-MAY-1998. AU0352.
26-AUG-1997; AU-008791.
13-MAY-1997: AU-006784.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Cancilla MR. Choo K, Du Sart D;
WPI: 99-009773/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID T07040 standard; DNA; 612 BP.
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3.667
90.000
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/*tag- a /note- "Residue not given in the specification, included to maintain open reading frame and to encode the amino acid given in the specification at this
immunoreactive with n-(ABCDE) serum. Inserted sequences in gtll
c are expressed as beta-galactosidase fusion proteins. Clone 4B11
has 3 multiple insert sequences; each insert can be fractionated
into discrete sequences by restriction enzymes, or portions of the
inserts can be PCR amplified by sequence specific primers. Each
resulting individual region can be subcloned and immunostreened.
This allows identification of specific regions responsible for
immunoreactivity. n-(ABCDE) hepatitis virus polypeptides can be
used for the production or detection of antibodies, and in
vaccines. The antibodies can be used for detection, diagnosis and
in passive immunotherapy. The DNA can be used in detection and
diagnosis, and as hybridisation probes for identification of
further n-(ABCDE) hepatitis virus coding sequences. Culture systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure: Columns 61-64; 52pp; English.
The sequences given in T34189-90 encode proteins from the pentachlorophenol (Pcp) breaddown pathway, designated Pcpb and Pcpt. The Pcpb gene was found to code for a 323 amino acid polypeptide, mol. wt. 35942 daltons. Based on multiple sequence alignments, Pcpb belongs to the family of class I dioxygenase electron transport proteins. Pcpb was predicted to have three structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PcpD coding sequence.
Pentachlorophenol breakdown pathway; PcpC; PcpA; PcpB; environment;
Pentachlorophenol breakdown pathway; PcpC; PcpA; pcpB; environment;
Pctrachloro-p-hydroquinone reductase; PCP-degrading enzyme complex;
Flavobacterium; PCP; 2,3,5,6-tetrachloro-p-hydroquinone; TeCH;
glutathione; 2,3,6-trichloro-p-hydroquinone; TrCH; food chain;
2,6-dichloro-p-hydroquinone; wood preserving industry; fungicide;
Pesticide; herbloide; disinfectant; ds.
Flavobacterium sp. Strain AfCC 39723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flavobacterium sp. penta:chloro:phenol breakdown pathway genes enzymes - useful in the bio-remediation and dechlorination of F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 9
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ArgLeuAlaIleArgLeuAspGluArg
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23-MAR-1992; 856015.
23-MAR-1992; 0S-86015.
13-JUL-1992; US-914282.
18-JUL-1994; US-276887.
(IDAH-) IDAHO RES FOUND INC.
Lange CC, Orser CS, Xun L;
WPI; 96-229872/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID T34189 standard; DNA; 972 BP.
AC T34189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 A;
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US-08-653-294-13 x T07040/rev
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Ratio: 3.556
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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comains, one involved in binding flavin mononucleotide (FMN), the second responsible for binding reduced NADPH and the third forming a plant-flaved contrype (ZPE-ZS) centre. PcpD is classified as an iron sulphur flavoprotein-oxidoreductase, and has been designated the PCP 4-monooxygenase reductase. It is transcribed as a dicistronic message with PcpB (see also T14184). The pcpR open reading frame encodes a 303 amino acid protein with a mol. Wt. of 33549 daltons, which possesses a helix turn helix motif in its N-terminal portion. PcpR is thought to activate the transcription of pcpBD and pcpA. In combination with pcpA, pcpB and pcpC, these enzymes catalyse the initial steps of PCP breakdown. These enzymes can specifically be used in the breakdown of PCP containing matter which persists in the environment and in food chains pesticide, and in products such as herbicides and disinfectants. Sequence 972 BP, 181 A; 310 C; 313 G; 168 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restricted P. aeruginosa waaC, waaG, waaF and waaP gene cluster vesful in the diagnosis or treatment of P. aeruginosa infections claim 2; Fig 6; 6ipp; English.

This is the nucleotide sequence of the waaF gene (rfaF gene) of the waa gene cluster of Pseudomonas aeruginosa PAO1. It codes for WasZell), a heptosyl transferase II that adds the second heptose residue onto the core oligosaccharide in the biosynthesis of the propolysaccharide inner core. The four waa genes of P. aeruginosa (see V84116-19) are arranged contiguously in an operon with the gene order waaF, waaC, waaG and waaP. The functions of the encoded proteins (see W82210-13) were tested by complementation of specific Salmonella typhimurium mutants, and knockout mutations of the genes in P. aeruginosa. The waa nucleic acids or proteins can be used to diagnose a bacterial, especially a P. aeruginosa. Infection in an animal. They can further be used to screen for compounds that affect core lippopolysaccharide biosynthesis or assembly. A claimed method of treating or preventing a bacterial infection in comprises administering an agent that inhibits a waa gene to naminal. A claimed wack, waaG, waaG, as a seambly. WaaC, WaaF and WaaG. 364 G; 178 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeuginosa héptosyl transferase II waaf gene.
Waaf gene; rfaf gene; lipopolysaccharide; infection; therapy;
diagnosis; vaccine; heptosyl transferase II; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burrows LL, De Kievit TR, Lam JS, Matewish M, Walsh A; WPI: 99-034725/03.
P-PSDB; W88211.
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Quality: 32.00 Length: 8
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 75.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LeualaileargLeuaspGluarg 10
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ID V84117 standard; DNA; 1038 BP
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US-08-653-294-13 x T34189/rev
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09-MAY-1997; US-046149.
02-MAY-1997; US-045418.
(UXGU-) UNIV GUELPH.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 13:17:45; Search time 209.03 Seconds (without alignments) 3.980 Million cell updates/sec Run on:

US-08-653-294-18 58 Title: Perfect score: Sequence:

1 YRLAIRRILLRY 12

Scoring table:

225878 seqs, 69334122 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

225878 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SPTREMBL\_12:\* Database :

sp\_archea:\*
sp\_bacteria:\*
sp\_fungl:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_mhc:\* Sp\_organelle:\* Sp\_organelle:\* Sp\_plant:\* Sp\_plant:\* Sp\_vorus:\* Sp\_vorus:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

## SUMMARIES

	Description	060503 cricetulus	045795 caenorhabdi		085853 sphingomona	086347 mycobacteri	016382 caenorhabdi			Q9xeq1 qossypium h	09z7s9 chlamydia p	Q9xb05 myxococcus	045803 caenorhabdi	Q9y136 drosophila		096446 vairimorpha	Q9whv4 squash yell	P70780 anabaena sp	09wym7 thermotoga		035043 bacillus su
· •	ID	060503	045795	084514	085853	086347	016382	022063	P91495	Q9XEG1	681260	Q9XB05	045803	Q9Y136	024393	096446	Q9WHV4	P70780	O9WYM7	092671	035043
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	Query Màtch Length DB	259	321	141	243	309	725	795	1847	1899	142	325	350	683	1283	1605	61	111	152	261	280
æ	Query Match	63.8	63.8	62.1	62.1	62.1	62.1	62.1	62.1	62.1	60.3	60.3	60.3	60.3	60.3	60.3	58.6	58.6	58.6	58.6	58.6
	Score	37	37	36	36	36	36	36	36	36	35	35	35	35	35	35	34	34	34	34	34
	Result No.		7	m	4	S	Q	7	œ	6	10	11	12	13	14	15	16	17	18	19	20

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## ALIGNMENTS

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RESULT 2
045795
1D 045795
AC 045795;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

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01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

X MEDLINE, 9415018.

A REDILINE, 9415018.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

A CRAXTON M., DERR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A CREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,

A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

A THIERRY-MIEG J., THOMAS K., VADDIN M., VAUGHAN K., WATERSTON J.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

Elegans.,

T elegans.,

T elegans.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
Science 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAVIS R.W.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS
EMBL; AE001323; AAC68107.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 5; Length 321;
Pred. No. 22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                           Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
50S RIBOSOMAL PROTEIN L17.
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
T19C9.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL: 292972: CAB074891; -.
PAM: PF01604; 7tm_5; 1.
SEQUENCE 321 AA; 36504 WW; 70031B52 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2570FFF7 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AA; 16152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.8%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.8
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                              Caenorhabditis elegans.
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298 YRAAIRRIL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIRRIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAVIS R.W.;
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084514
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                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENSEN C.W., GASTERLAND T., SAFFER J.D., FREDRICKSON J.K.; Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans strain F199."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AFO79317, AAD03868.1, ... Hypothetical protein; Jasmid 40CDFBF4 CRC32; SEQUENCE 243 AA; 26455 MW; 40CDFBF4 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; 2ymomonas group;
Sphingomonas.
  Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 33.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
Score 36; DB 2;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2;
Pred. No. 26;
2; Mismatches
                                                                                                                                                                                                                                                                      243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 AA
                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL 26.5 KD PROTEIN. Sphingomonas aromaticivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 08, (TrEMBLrel. 08,
                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence
Nature 393:537-544(1998)
[2]
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                              |||: |:::||
64 RLAVGRLMVRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLAIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| ||::||
5 RLAQRRVTIRY 15
                                                                                               2 RLAIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-H37RV;
MEDLINE; 98295987
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WILLSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEEKS M.,
WILLSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEEKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., PERCY C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., SOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VADUIN M., VAUGHAN R., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SIMILARITY TO RAT INTEGRAL MEMBRANE GLYCOPROTEIN GP120 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
WAMSLEY P., BRADSHAW H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U80033; AAC48199.1; -.
SEQUENCE 1847 AA; 199637 MW; BOA25E0F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WILD A.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r00060; 11g_chan; 1.
: 795 AA; 89703 MW; DD722166 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1847 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 281061; CAB02939.1; -.
EMBL; 278413; CAB02939.1; JOINED.
EMBL; 278413; CAB01667.1; -.
EMBL; 281061; CAB01667.1; JOINED.
HSSP; P19491; IGR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.1%;
50.0%;
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10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel. 03, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                   PRELIMINARY;
                                                                                                                                      01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
TOLC3.10 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994).
                                                                                                                                                                                                                                                        T01C3.10.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLAIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || ::||: ||
6 YRTSLRRLATRY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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MEDLINE; 9415071B

A RISCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

A RILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A.,

CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CLLLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RAALDON N., SMITH A., SONNHAMMER E., STRADEN R., SULSTON J.,

ANATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                       Length 309;
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                                               PARKHILL J.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL AL008967; CAA15591.1;
HSSP; P33164; 2PIA.
HSSP; P800197; ZFPZS_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JÚL-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF016442; AAB65917.1; -. SEQUENCE 725 AA; 84926 MW; A4847D75 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2;
Pred. No. 33;
1; Mismatches (
                                                                                                                                                                                               PFAM; PF00111; fer2; 1.
PFAM; PF00115; oxidored_fad; 1.
Hypothetical protein; Iron-sulfur.
SEQUENCE 309 AA; 33517 WW; B152B590 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 5
Pred. No. 77;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                       62.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 62.1
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
JONES K., WOHLDMANN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLAIRRILLRY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                             STRAIN-H37RV
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STARIN-ER-15;
PAITAN Y., ORR E., RON E.2., ROSENBERG E.;
Genetic and functional analysis of genes required for the post-
"Genetic and functional analysis of genes raquired for the post-
modification of the polyketide antibiotic Ta of Myxococcus xanthus.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132503; CAB46503.1; -.
SEQUENCE 325 AA; 35985 MW; 4CC64E85 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94150718.

MILSON R., AINSCOUGH'R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., AINSCOUGH'R., ANDERSON K., BAYNES C., BERKS M.,
MILSON M., DEAR S., DU Z., CONNELL M., COPERT T., COOPER J., COLLSON A.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KRRSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KRRSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFREN L., ROOPRA A., SAUNDERS D., SHOWNEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULISTON J.,
THIERRY-MIEG J., THOMAS R., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Rhabditida, Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
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LLOYD C., WILKINSON J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                U1-NOV-1999 (TIEMBLEEL. 12, Created)
01-NOV-1999 (TIEMBLEEL. 12, Last sequence update)
01-NOV-1999 (TIEMBLEEL. 12, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB
Pred. No. 54;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                   PRT;
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58.38;
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EMBL: Z82051; CAB04815.1; -.
PFAM: PF01461; 7tm_4; 1.
SEQUENCE 350 AA; 40291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                       PRELIMINARY;
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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 YRLTVDRFPLRY 213
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   64 RIAIGRLMVRY 74
                                                                                                                                                                                                                                                                                                                                                                                                    Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T23D5.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                              09XB05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elegans
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                                                                                               RESULT 11
Q9XB05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. TEXAS MARKER-1; TISSUE-PRIMARY-STAGE COTTON FIBER;
CUI X., SHIN H., BROWN R.M.;
"Cotton CFL1 gene shows homology to the yeast beta-1,3-glucan synthase subunit FKS1.";
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L., GRIMWOOD J., DAYIS R.W., STEPHENS R.S.;
"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
Submitted (DEC-1998) to the EMEL/Genbank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
EMBL; AE001647; AAD18764.1;
-- PROSITE; PS01167; RIBOSOMAL_L17; 1.
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Pred. No. 2e+02;
2; Mismatches 2; Indels
Score 36; DB 5; Length 1847;
Pred. No. 1.9e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 60.3%; Score 35; DB 2; Length 142; Best Local Similarity 54.5%; Pred. No. 24; Matches 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF085717; AAD25952.1; -
SEQUENCE 1899 AA; 218627 MW; E695145F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TIEMBLREL. 12, Created)
01-NOV-1999 (TIEMBLREL. 12, Last sequence update)
01-NOV-1999 (TIEMBLREL. 12, Last annotation update)
PUTATIVE CALLOSE SYNTHASE CATALITIC SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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SEQUENCE 142 AA; 16400 MW; 4839EC84 CRC32;
                                                                                                                                                                                                                                                                                                                                                               PRT; 1899 AA
                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
   62.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12, 508 RIBOSOMAL PROTEIN 1.77.
Query Match 62.1
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                 1 YRLAIRRILLRY 12
                                                                                                                                                                                              19 YRLNVPRVLLPY 30
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                                                                                                                                                                                                                                                                                                                                                                                                 Q9XEG1;
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Length 325;

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DB 54;

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DB 5;
Score 35;
60.3%;
Query Match
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Search completed: February
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096446
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"Full length Drosophila melanogaster cDNA sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF145636; AAD138611.1;
SEQUENCE 683 AA; 79171 MW; 72C620E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          Ogy136;

01-NOV-1999 (TrEMBLrel. 12, Created)

01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

BCDNA.GH07188.

BCDNA.G
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                              Gaps
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MEDILE: 94010914.
GERRARD B., STEWART C., DEAN M.;
"Analysis of Mdr50: a Drosophila P-glycoprotein/multidrug resistance
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TIEMBLEEL. 01, Created)
01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-NOV-1999 (TIEMBLEEL. 12, Last annotation update)
P-GLYCOPROTEIN/MULTIDRUG RESISTANCE PROTEIN.
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SEQUENCE 1283 AA; 142538 MW; 65012909 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1283 AA
       Pred. No. 58;
3; Mismatches
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EMBL; L07065; AAA16186.1; -.

FLYBASE; FEBGO010241; MdrS0.

PROSITE; PS00211; ABC_TRANSPORTER; 1.

PFAM; PF00664; ABC_membrane; 2.

PFAM; PF00005; ABC_tran; 2.
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   66.78;
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Best Local Similarity
Matches 6; Conserv
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MEDLINE; 99110933.
HIRTR R.P., LOGSDON J.M. JR., HEALY B., DOREY M.W., DOOLITTLE W.F.,
EMBLEY T.M.;
"Microsporidia are related to Fungi: evidence from the largest subunit
of RNA polymerase II and other proteins.";
Proc. Natl. Acad. Sci. U.S.A. 96:580-585(1999).
EMBL; AF060234; AAD12604.1; ...
SEQUENCE 1605 AA; 180946 MW; 2D013184 CRC32;
                                              Gaps
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  Length 1283;
Score 35; DB 5; Length 128
Pred. No. 2.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Vairimorpha necatrix.
Eukaryota; Microsporidia; Burenellidae; Vairimorpha.
                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
LARGEST SUBUNIT OF RNA POLYMERASE II.
                                                                                                                                                                                                                                                          1605 AA.
                                                                                                                                                                                                                                                             PRT;
60.3%;
70.0%;
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Best Local Similarity 58.3
Matches 7; Conservative
Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
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547 RIAIRRALIR 556
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AJ006381 Platythyrea punctat AF130141 Fusarium solani f. AJ131275 uncultured euryarch
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Baldwin, J., Barnaa, N., Beckerly, R., Boqualavkiy, L., Boukhgaiter, B.,

Baldwin, J., Barnaa, N., Beckerly, R., Boqualavkiy, L., Boukhgaiter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreitar, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, K., McLaughlin, J., Meldrim, J.,

Norrow, J., Naylor, J., Norman, K., McLaughlin, J., Meldrim, J.,

Reterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vasalilev, H., Vo, A., Wheeler, J., Wu, X.,

Direct Submission

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Dec 10, 1999 this sequence version replaced gi:6425750.

All repeats were identified using Repeathasker:

Conter, Whitehead Institute/ MIT Center for Genome Center

Center: Whitehead Institute/ MIT Center for Genome Center:

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                  AC013772 142796 bp DNA HTG 09-DEC-1999
Homo sapiens clone RP11-7024, WORKING DRAFT SEQUENCE, 6 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142796)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
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Center clone name: 7_024

Center clone name: 7_024

Center clone name: 7_024

Sequencing vector: M13, M7815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 13712 bases at least 040

Consensus quality: 13712 bases at least 030

Consensus quality: 14075% bases at least 020

Insert size: 138000; agarose-fp
Insert size: 142796; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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     17.95
48.54
83.80
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HTG; HTGS_PHASE1; HTGS_DRAFT
  134.56
126.81
122.55
  38.00
38.00
                                                                                                            seg_name: gb_htg7:AC013772
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LOCUS AC013772 1
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  gb_in1:PPU6381
gb_pl2:AF130141
gb_ba1:UEU131275
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
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1692 1AF026541 Mycobacterium tubercu
7150 1AB007931 Homo sapiens mRNA for
3600 1AC009605 Leishmania major chr
38122 1U28732 Caenorhabditis elegans
38631 1296072 Mycobacterium tubercul
40890 1AC012873 Drosophila melanogas
56237 1AC012873 Drosophila melanogas
86130 1AC005365 Homo sapiens chromos
97906 1AL109912 Homo sapiens chromos
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AL080317 Human DNA sequence
AC011957 Homo sapiens chronc
AC011702 Drosophila melanoga
AC005286 Drosophila melanoga
AL121767 Human chromosome 14
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                                                                                                       About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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8.2e+03
8.5e+03
1.2e+04
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1.5e+03
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2.6e+03
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1.8e+03
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Database length: -1518192014
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OM of: US-08-653-294-18 to:
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Database: GenEmbl:*
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9b_htgs AC00564

9b_htg1 AC005647

9b_htg1 HSA392M18

9b_htg1 AC008835

9b_htg3 AC008835

9b_htg3 AC008835

9b_htg3 AC008835

9b_htg3 AC008835

9b_htg3 AC015746

9b_htg5 AC015746

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9b_htg:.RC009605
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9b_htg:.RS1141E20
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gb_htg7:AC013772
gb_htg2:HSDJ655C5
gb_htg5:AC011145
gb_htg4:AC012150
                                                  Date: Feb 8, 2000
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gb_htg7:AC017966
gb_htg5:AC013927
gb_ba1:MLCB2533
gb_ba1:000017
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gb_htg4:AC011957
gb_htg5:AC011702
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2606bp 1648bp 4175bp 1781bp 10365bp

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Simms, S.

Direct Submission

Laboratted (26 Nov-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Nov 27, 1999 plis sequence version replaced g1:6066017.

IMPORTARY: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Contig_ID: 00008 Length: 1036bp
Contig_ID: 00019 Length: 9963bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS HSDAC55C5 306999 bp DNA HTG 26-NOV-1999
DEFINITION Homo sapiens chromosome 6 clone RP4-655C5, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 306999)
                  gap of unknown length
contig of 4377 bp in length
gap of unknown length
contig of 15946 bp in length
gap of unknown length
contig of 41051 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                   1 others
                                                                                                                                                                                                contig of 76588 bp in length
  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AC013772 from: 1 to: 142796
                                                                                                                                                                                             209 142796: contig of 76588 bp in leng Location/Qualiflers
1. 142796: downward of 76588 bp in leng 1. 142796. downward of 76588 bp in leng 1. 142796. downward of 76588 bp in leng 1. 14280 c. 24540 g 45686 t. 1 oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13521 TATAGACTAGCAGTCAGAAGACATTTACTTAAATAT 13486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuAlaIleArgArgIleLeuLeuArgTyr 12
of 2692
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Length: 1518bp
Length: 1518bp
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1083bp
1408bp
1477bp
3742bp
4834: contig
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AL121956.2 GI:6469398
HTG; HTGS_PHASE1.
human.
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US-08-653-294-18 x AC013772/rev
                                                9211:
                                                                                                  25157:
                                                                                                                                                66208:
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Contig_ID: 00031
Contig_ID: 00039
Contig_ID: 00059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00059
00062
00088
00092
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Contig_ID:
Contig_ID:
2143
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Percent Similarity:
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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Homo sapiens chromosome 12p13 clone RPCIII-946L16, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                        Center project name: 12522
Center clone name: 2.A.8
Center clone name: 2.A.8
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 116065 bases at least Q40
Consensus quality: 136485 bases at least Q30
Consensus quality: 148288 bases at least Q30
Insert size: 164000; agarose-fp
Insert size: 156243; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4018: contig of 4018 bp in length gap of unknown length 18534: contig of 14516 bp in length 29198: contig of 10664 bp in length gap of unknown length 44793: contig of 15595 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length 103069: contig of 37711 bp in length gap of unknown length gap of unknown length gap of unknown length 156243: contig of 53174 bp in length
          /clone_lib="RPCI-11 Human Male BAC"
32079 c 31296 g 46894 t 26 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 156243
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Gaps: 0
Percent Identity: 72.727
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1. 156243
Corganism="Homo sapiens"
Ab xref="taxon:9606"
/clone="RP11-2A8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ArgLeuAlaIleArgArgIleLeuLeuArgTyr 12
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HTG: HTGS_PHASE1.
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US-08-653-294-18 x AC011145/rev
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Ratio: 4.000
Percent Similarity: 100.000
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LOCUS AC012150
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AC011145 156243 bp DNA HTG 19-NOV-1999
DEFINITION Homo sapiens clone RP11-2A8, WORKING DRAFT SEQUENCE, 7 unordered
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156243)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-2AB
Contig_ID: 01937 Length: 1573bp
Contig_ID: 01944 Length: 1865bp
Contig_ID: 01965 Length: 1096bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                    /clone="RP4-655C5"
/clone_lib="RPCI-4"
48318 c 46393 g 68867 t 71293 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 75.000
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                                                                                                                                                                                                              1. :306999
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                         Location/Qualifiers
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AC011145.2 GI:6454030
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US-08-653-294-18 x HSDJ655C5
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4.091
91.667
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JOURNAL
REFERENCE
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SOURCE
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fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.

1 (bases 1 to 1650)
Hosbach,H.A., Silberklang,M. and McCarthy,B.J.
Evolution of a D. melanogaster glutamate tRNA gene cluster
611 21 (1), 169-178 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMRNA3 1050 bp DNA INV 31-MAR-19
Three Drosophila melanogaster genes for transfer RNAs (Glu
                                                                                             30 others
                                                                                                                                                                                                                                                                                                                             to: 37459
                                                                                                                                                                                        Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1050
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FlyBase:FBgn0011851"
190 c 213 g 323 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="transfer RNA:glu4:62Aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"FlyBase:FBgn0011851"
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262. .333
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                                                                                                                                                                                                                                                                                                                         to reverse of: AC012150 from: 1
           /organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12p13"
/clone="RPCHI-946116"
a 7909 c 7207 g 11198 t
                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuAlaIleArgArgIleLeuLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V00238 J01146
V00238.1 GI:8458
transfer RNA; transfer RNA-Glu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="tRNA:E4:62Aa"
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/note="tRNA Glu"
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US-08-653-294-18 x AC012150/rev
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         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Burdota, B., Bouck, J., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Buarco, J., Bovid, R., Deshazo, D., Ding, Y., Domah-Rashid, N., Duyan Rocha, S., Durbin, K.J., Ferrandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, J. H., Gorrell, J. H., Gorrell, J. H., Gorrell, S., Kondejewski, N., Kong, Y., Medigson, L., Jackson, L., Jackson, L., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Luier, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Stampel, S., Scher, H., Simon, M., Sparks, A., Stamps, A., Scher, S., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Wensford, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, R., Wrens, C., Wrens, Stone, J., Marson, D. and Gibbs, R., Direct Submission

Li Oppublished

Li Charage, L., Simon, M., Nelson, D. and Gibbs, R., Mero, J., Meros, I., Shon, M., Morris, S., Mrens, Stone, J., Wall, J., Milliamson, D. and Gibbs, R., Wen, S., Chere, J., Marson, D. and Gibbs, R., Direct Submission

Li Dipublished
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Direct Submission

Submitted (21-0CT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

* NOTE: This is a "working draft" sequence. It currently

* Consists of 34 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            840 bp in length
808 bp in length
350 bp in length
350 bp in length
358 bp in length
817 bp in length
818 bp in length
818 bp in length
818 bp in length
819 bp in length
810 bp in length
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1115 bp in 1
1350 bp in 1
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1489 bp in 1
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COMMENT

FEATURES

31-MAR-1992

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

REFERENCE AUTHORS

JOURNAL

JOURNAL

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DNA HTG 09-DEC-1999
*** SEQUENCING IN PROGRESS ***, in ordered
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                        Lular Liura melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Petrygota; Neopera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 8849)

S Adams, M. and Venter, J.C.

Direct Submission

L Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, USA

This sequence was identified as CDM:10212817 by the submitter.

For more information on this record e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Mooptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 12771)
Adams, M. and Venter, J.C.
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Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, 198A
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/db_xref="taxon:7227"
1735 c 1884 g 2626 t
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/db_xref-"taxon:7227"
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Gaps: 0
Percent Identity: 58.333
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AC017966.1 GI:6553224
HTG; HTGS_PHASE2.
fruit fly.
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AC013927.1 GI:6437408
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/translation="MAPRTLLLVLSGALALTETWAGSHSLRYFSTAVSRPGRGEPQYR
XIAVSYVDDTOFLREDSDAAIPRWEDRAPWYEQEGPOYWERTIGYAKANARTDRVALR
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TVARITQRFYEAEFYAEFRTYLEGECLELLRRYLENGKETLQRADPPKAHLAHHPVS
DREATLRCWALGFYPDEITLIWQRDGEEQTQDTELVETRPAGDGTFOKWAAVVVPSGE
EQRYTCHVQHEGLPQPLTLRWESSSQPTIPIVGIVAGLAVLAVVTGAVVAAVWWRKK
SSDRNRGSYSQAAM"
76. 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of the rhesus macaque (Macaca mulatta) equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-FEB-1993) Ronald R.E. Bontrop Ph.D, chronic and infectious diseases, ITRI-TNO, Lange Kleiweg 151, Rijswijk, 2280 HV, The netherlands
                                                                                                                                                                                                                                                                          221819
221819.1 GI:38568
FILA-F gene...
rhesus monkey.
Macaca mulattes mulattes.
Eukaryota; Metazoa: Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Cararrhini; Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 1056)
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Gaps: 0
Percent Identity: 63.636
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/product="HLA-F like protein"
/protein_id="Ca77985.1"
/db_xref="G1:38569"
                                                                                /product="HLA-F like protein'
318 c 349 g 175 t
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/organism="Macaca mulatta"
/isolate="1km"
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Bontrop.R.R.
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M.mulatta HLA-F like mRNA.
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US-08-653-294-18 x MMHLAFHOM
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Percent Similarity: 100.000
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US-08-653-294-18 x DMRNA3
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LOCUS MMHLAFHOM
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                                          Align seg 1/1
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source

FEATURES

mRNA CDS

BASE COUNT

ORIGIN

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Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae
Mol. Microbiol. 7 (2), 197-206 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for
CDS which show significant similarity to other CDS in the database.
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Details of M. Leprae sequencing at the Sanger Centre are available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/)
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Work in Paris is supported by the Heiser Trust, the Association Francaise Raoul Follereau and the Groupement de Recherches et des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS are numbered using the following system eg MLCB33.01c. ML (M. leprae), cB33 (cosmid name), .01 (first CDS), c (complementary
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James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (26-JAN-1998) Mycobacterium leprae sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Dr.
Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne,
Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15,
France Requests for cosmids should be sent to Karin Eiglmeier
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Mycobacterium leprae cosmid B2533.
AL035310
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Mycobacterium leprae.
Mycobacterium leprae
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Hamlin, N. and Churcher, C.M.
2497
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US-08-653-294-18 x AC013927/rev
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2428
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SOURCE

COMMENT

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/gene="ansp"
//gene="ansp"
//g
The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position G + C. CAUTION: We may not have predicted the correct initiation G + C. CAUTION: We may not have predicted the correct initiation odon. Where possible we choose an initiation codon (aty, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a incation/qualifiers
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GERAAYVVGMLYFLDWAMTAIVDTAIATYLHRWTIFTALPOWTLALLALAVVLVMNL
ISVEWFGELEFWAALIKVCALMAFLVVGTIFLGGRYPVDGHVTGLSLWTSHGGLFPTG
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protein_id="CAA22915.1"
/db_xref="G1200259"
/translation-"MATLAESPEPKSGASRAGVLGEEAGYHKGLKPROLQMIGIGGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAQLIVVSSGVMFAYAAVELVGTAAGETVEPKKIMPRAINSVIARIAIFYVGSVILLA
LLLPYSAFKASESPFVTFFSKVGFYGAGDLMNIVVLTAALSSLNAGLYATGRVMHSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"overlap with EMBL:ML017 cosmid B2126 from 1 to 31682. There are 16 conflicts between this sequence and ours. In each case our sequence has been checked and is thought to be correct"
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/gene="ansp2"
/note="MLCB2533.02c, ansp2, probable L-asparagine
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complement(2, .991)
/gene="ansp"
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/clone="cosmid B2533"
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permease, len: 505 aa; highly similar to many amino-acid permeases e.g. ANSP_SALTY (EMBL:004831) S.typhimurium AnsP, L-asparagine permease (L-asparagine transport protein) (497 aa), fasta scores: 1891 z-score: 2218.9 E(): 0, 58.9% identity in 477 aa overlap. Equivalent to M.tuberculosis Rv2127 (MTCY261.26, 83.7% identity in 485 aa overlap). Also similar to M.tuberculosis permease Rv0446c (MTCY18E10.06c, 69.8% identity in 473 aa overlap). Probable integral membrane protein, contains PS00218 Amino acid permeases signature. Pfam match to entry PF00324 aa_permeases, amino acid permease. Annotated as ORF 7R:049802, designated lysp in M.leprae cosmid EMBL:00017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2903. .3856)
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complement(2903. .3856)
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HYVSHPPNPKATVALLRRVEDVLDVEVPLADLPTQAEDWEQALTEIAAEDDELAEYVH
SLEQRGDAEVDVNDALGKIDGDALAAEFERYLRRRRPGFGR"
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VAPLIVVSSGVMFAYAAVELVGTAAGETVEPKKIMPRAINSVIARIAIFYVGSVILLA
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/gene="ansp2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00324 aa_permeases, Amino acid permease, score 501.80, E-value 5.1e-147" 1668. .2835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="conflict: C is CT in EMBL:ML017"
complement(2500. .2592)
/gene="ansP2"
/note="PS00218 Amino acid permeases signature"
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/gene="metH"
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/gene="metH"
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GGTVLAYLVLSKALGFLLIVGSGVQVTALSGDRYFGFLLNLLVVFGVSFEFPLLIVML
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On Mar 31, 1994 this sequence version replaced gi:414223.
This sequence data was produced by the Genome Sequencing Center located at Collaborative Research Incorporated (1365 Main St., Waltham MA, 02159). [617-487-7979). Please contact Doug Smith (smith@cr.cric.com). The annotation should be considered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-NOV-1993) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
3 (bases 1 to 42157)
(MTCY261.20c, 88.7% identity in 1183 aa overlap).
Annotated as METH_MYCLE, designated metH2 in M.leprae
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                                                                                                      Length: 12
Gaps: 0
Percent Identity: 75.000
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Mycobacterium leprae cosmid B2126.
U00017
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Location/Qualifiers
1. .42157
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Smith, D.R.
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Mycobacterium leprae
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75.000
                                                                                                                                                                                                                                                                                                     to: MLCB2533
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US-08-653-294-18 x MLCB2533
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Complement(12950. .13234)
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f unknown length
of 1181 bp in length
g unknown length
g of 806 bp in length
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Drosophila melanogaster chromosome 3 clone BACR01E04 (D714) RPCI-98
01.E.4 map 89E-89E strain y; cn bw sp, *** SEQUENCING IN PROGRESS
***, 99 unordered pieces.
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Bukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
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Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:
Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.

E 1 (bases 1 to 130336)
S (Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Champe,M., Chawez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hinkle,A., Hoskins,R.A., Humasati,S.R.A., Harris,N.L., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfelffer,B., Richards,S., Sethi,H., Syirskas,R.R., Wan,K.H., Webster,D., Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-JUN-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA on Nov 23, 1999 this sequence version replaced gi:5670524. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu All contigs in this submission meet the following cutoffs: length >= 200 bases. It currently * consists of 99 contigs. The true order of the pleces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.K., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Rubin, G.M.
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8 Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

**NOTE: This is a 'working draft' sequence. It currently consists of 89 contigs. The true order of the pleces

** is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as ** runs of N, but the exact sizes of the gaps are unknown.

** This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
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ACO10564 143914 bp DNA
LOCUS
DEFINITION Drosophila melanogaster chromosome 3L/62A1 clone RPC198-2701,
SEQUENCING IN PROGRESS ***, 89 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     831: contig of 831 bp in length 1645: contig of 814 bp in length 2519: contig of 874 bp in length 3350: contig of 835 bp in length 4206: contig of 836 bp in length 5469: contig of 1263 bp in length 5413: contig of 844 bp in length 7273: contig of 960 bp in length
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Gaps: 0
Percent Identity: 81.818
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                                                                                                                                                                                                                                                                                                                                                               2 ArgleuAlaIleArgArgIleLeuLeuArgTyr 12
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ACO10564.4 GI:5917942
HTG; HTGS_PHASE1.
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Direct Submission
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Humian,
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HOMO Sapiens clone RG014E15, *** SEQUENCING IN PROGRESS ***, 2
unordered pieces.
ACOO5047
ACOO5047.1 GI:3212944
HTG: PHASE1.
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    /clone="RG014E15"

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318 121885: contig of 3:
886 12521: contig of 4:
222 129338: contig of 4:
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812 137892: contig of 5:
893 143914: contig of 5:
Location/Qualifiers
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Eutheria; Primates; Catarrhin; Hominidae; Homo.

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Weinstock, I.R., Williamson, A., Worley, K., Wrensford, G.,

Yu, W., Zhou, X., Naylor, S.L., Nelson, D. and Glbbs, R.
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Submission (28-07-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 28, 1999 this sequence version replaced g1:6087894.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS ACO07687 164655 bp DNA PRI 28-OCT-1999
DEFINITION Homo sapiens 3q26.2-27 BAC RPCI11-419414 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-JUN-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 164655)
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Percent Identity: 72.727
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Worley, K.C.
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                                                                             Percent Similarity:
                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC007687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
alignment_scores:
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TITLE
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AUTHORS
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JOURNAL
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
           STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                              QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases.

Standards of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
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Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus:
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cctaataact(t)cgtatagcat
ctaataactt(c)gtatagcata
taataacttc(g)tatagcatac
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cgagggacct(a)ataacttcgt
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ANNOTATION OF FEATURES:
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22
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nnnnnnnnn (n)nnntatata nnnnnnnnn (n)nntatataa

acattatacg(a)agttnnnnta cattatacga(a)gttnnnntaa

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

Overlapping clone Features listing.

Length: 11 Gaps: 0 Percent Identity: 72.727

41.00 4.100 90.909

Ratio: Quality:

alignment\_scores:

Percent Similarity:

from: 1 to: 164655

to: AC007687

Align seg 1/1

alignment\_block: US-08-653-294-18 x AC007687

11

25920 TACTCTATGGCCATCAGGAGGATAATACTGAGA 25952

seq\_name: gb\_htg1:HSA392M18

1 TyrArgLeuAlalleArgArglleLeuLeuArg

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tggtgatgca(g)attgctttca
tatttatctg(t)ctataatctg
ctcatggtga(t)acagatagtc
                                                                                                                                                      aaaaaaaac(t)tttataaag
aaaaaaactt(t)ttataaagta
                  nnnnnnnnt(a)tataagggtt
                                                                                                                                                                                                  cagcagcagg(c)tagaaggcag
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                                                          nnnnnnntat(a)taagggttcc
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tacgaagttn(n)nntaagggtt
                                       acgaagttnn(n)ntaagggttc
                                                                               aaaaacaaaa(n)acaaaaatgg
                                                                                               tggtgatgca(n)attgctttca
tatttatctg(n)ctataatctg
                                                                                                                                         ctcatggtga(n)acagatagtc
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aaaaaaacnt(n)ttataaagta
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ttttcttttc(n)tttttttttt
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cnaaagcagi(n)tingcactag
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18268
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33217
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32
--- Distribution of Quality < 40 Bases
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Phrap Value Range
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                                                    #
bases
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Length:

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Direct Submission.

Direct Submission.

Direct Submission.

Submitted (10-NOV-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires:

Cambridgeshire, CB10 15A, UK. E-mail enquires:

Numquery@sanger.ac.uk

ON Nov 15, 1999 this sequence version replaced gi:605524.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence as in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coll, yeast, vector, phage etc. Order of sequence is not known; 800 n's separate sequences. Duffinished: ba392M18 Contig_ID: 00029 acc=AL121897 Length: 1432 bp Unfinished: ba392M18 Contig_ID: 00029 acc=AL121897 Length: 1577 bp Unfinished: ba392M18 Contig_ID: 0014 acc=AL121897 Length: 1677 bp Unfinished: ba392M18 Contig_ID: 00289 acc=AL121897 Length: 1677 bp Unfinished: ba392M18 Contig_ID: 00289 acc=AL121897 Length: 10037 acc=AL121897 Length: 10033 acc=AL121897 Length: 100419 acc=AL121897 Length: 10055 acc=AL121897 Length: 10055 acc=AL121897 Length: 10055 acc=AL121897 Length: 100550 acc=AL121897 Length: 1005
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1873 bp Unfinished: ba392M18 Contig_ID: 00817 acc=AL121897 Length: 1940 bp Unfinished: ba392M18 Contig_ID: 00829 acc=AL121897 Length: 5357 bp Unfinished: ba392M18 Contig_ID: 00809 acc=AL121897 Length: 1064 bp Unfinished: ba392M18 Contig_ID: 00008 acc=AL121897 Length: 1064 bp Unfinished: ba392M18 Contig_ID: 01023 acc=AL121897 Length: 1331 bp Unfinished: ba392M18 contig_ID: 01166 acc=AL121897 Length: 1386 bp Unfinished: ba392M18 Contig_ID: 01166 acc=AL121897 Length: 4 bp Unfinished: ba392M18 Contig_ID: 01201 acc=AL121897 Length: 4
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216149)
                                                                                                                                                                                  AL121897
AL121897.2 GI:6433871
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                 human.
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AUTHORS
TITLE
JOURNAL
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Langth: 6619 bp Unfinished: ba392M18 Contig_ID: 01203
acc=AL121897 Length: 1468 bp Unfinished: ba392M18 Contig_ID: 01205
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alignment\_block: US-08-653-294-18 x HSA392M18

Gaps: 0 Percent Identity: 66.667

41.00 3.727 91.667

alignment\_scores: Quality: Ratio: Percent Similarity:

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Encodes Babesia bovis 60kD
Babesia merozite surface p
Human Rab3-GAP gene. GTP hy
Hamster HMG-COA reductase c
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The synthetic immunoglobulin binding proteins derived from protein L comprise repeated sequences from protein L which bind immunoglobulin Kappa light chains. They can be used in protein analysis, purification procedures and other biochemical processes e.g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell wall binding (The repeat regions commencing at nucleotide numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- b hone-"Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347, 2345 and 2731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 757" 1044
                                                                                                                                                                                                                                                                                                                                                     Sequence encoding protein L. Peptide; purification; ELISA; enzyme linked immunoabsorbant assay; ss.
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/note= "Repeat units are adjacent, repetitions
/fotte= "Repeat en ent 100% homologous and
begin at nucleotide positions 2935, 2953,
2968, 2986, 3001, 3019 and 3034"
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07-MAY-1993; G00950,
24-DEC-1992; GB-026928,
(PUBL-) PUBLIC HEALTH LAB SERVICE BOARD,
AKTAINSON A, DUGGLEDY CJ, MURPHY JP, Trowern AR;
P-PSDB; R42203.
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Q50946;
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   N_Geneseq_36:033064
N_Geneseq_36:T18995
N_Geneseq_36:V34005
N_Geneseq_36:Q70609
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Sequence encoding protein L. N. Sequence encoding protein L. I. Mutated BRCAI genomic sequence BRCAI genomic sequence BRCAI genomic sequence BRCAI genomic sequence Mutated BRCAI genomic sequence BRCAI genomic sequence Mutated BRCAI genomic sequence SECAI genomi
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                                                                                                                                                                                                                                              -MODEL-frame-pon-model -DEV-x1p
-OG-GGM1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-DB-N_GGM06seq_36 -OFMT-fastap -SUFFIX-ring -GADODE-12.000
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-GAPRXT-4.000 -MINMATCH=0.100 -KGAPDE-10.000 -KGAPEXT=0.000
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-DELOP-6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT-0.500
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-MAXLEN-10000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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                                                                                                                          Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
      out_format : pfs
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Database length: 125096042
Search time (sec): 590.520000
OM of: US-08-653-294-18 to:
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Query: US-08-653-294-18
Query length: 12
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N_Geneseq_36:T17515
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N_Geneseq_36:T17514
N_Geneseq_36:T17516
N_Geneseq_36:T17517
                                                                                                                          About: Results were
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_Geneseq_36:Q51556
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N_Geneseq_36:T17518
N_Geneseq_36:T17519
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N_Geneseq_36:T17522
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N_Geneseq_36:X04340
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N_Geneseq_36:T68162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score_list:
Sequence
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intron
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A PLANTER LANDER PROPERTY ELL PERTY 
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/*tag= b
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 673 and 856"
574. .672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c //note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1045. .1158
//tag= e
//octe= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1261, 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and legin at nucleotide positions 2347 and 2545" 1939. .2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7335. .2094

/*tag* h

/note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 2209"

2055. .2208

/*tag* "Repeat units are not adjacent, repetitions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375 and 1597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= g
/note= "Repeat units are not adjacent, repetitions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding protein'L. Protein; immobilisation; light chains; antibodies; diagnosis; pharmaceutical; ss. Peptococcus anginus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of this sequence are not 100% homologous and
begin at nucleotide positions 2479, 2665
                                899
                                                                                                                                                                                                                                                                                                                                                                         3279
                                                                                                                                                     Length: 12
Gaps: 0
Percent Identity: 50.000
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                             625
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                                ΰ
                                481
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103. .3185
/*tag= a
/product= Protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID Q51556 standard; cDNA; 3279 BP.
AC Q51556;
1045, 1261, 1483 and 1705).
Sequence 3279 BP; 1505 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1822. .1938
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                              US-08-653-294-18 x Q50946/rev
                                                                                                                                                     Ouality: 37.00
Ratio: 3.083
Percent Similarity: 100.000
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                                                                                                                           alignment_scores:
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07-ocr-1996 (first entry)
Mutated BRCAl genomic sequence from sample set MSKCC family 19921.
Cancer therapy, breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasis; human; gene therapy; protein replacement therapy; protein mimetic; BRCAl; ds.
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                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin binding polypeptide, protein L - used for prodn. of pharmaceuticals and for immobilising antibodies e.g. on columns, in diagnostic tests and in assays
bisclosure; Figure 1: 29pp; English.
Protein L forms a complex with immunoglobulin Kappa light chain. Purified protein can be used as a reagent for immobilising antibodies e.g. on columns, in diagnostic tests and in assays.
may also be used in the production of pharmaceuticals. Sequence 3279 BP; 1505 A; 480 C; 626 G; 668 T;
                                                                     /*tag- j
/note= "Repeat units are adjacent, repetitions
of this sequence are not 100% homologous and
of this sequence are not 100% to 2035, 2953,
2968, 2986, 3001, 3019 and 3034"
of this sequence are not 100% homologous and
begin at nucleotide positions 2269"
2914. .2934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 12
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                    11-NOV-1993.
07-MAX-1993.
07-MAX-1993.
07-MAX-1993.
08-009804.
(PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
Atthinson A. Duggleby CJ, Murphy JP, Trowern AR;
WPI; 93-368797/46.
P-PSDB; R43699.
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/note= "known polymorphic site"
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/note= "intron 1"
1295
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/note= "intron 2"
1925. .1937
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/*tag= a
/note= "exon 1"
356. .1512
/*tag= b
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ID T17455 standard; cDNA; 24025 BP.
AC T17455;
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/note= "exon 2"
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US-08-653-294-18 x Q51556/rev
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Ratio: 3.083
Percent Similarity: 100.000
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                                                   repeat_unit
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us-08-653-294-18.rng

91649209 /*tag= af	exon 9		=			/*tag= ak /note= "intron 10" 1138411396		/rdg= am //rote= "exon 11" 11908	/*tag= an /note= "known polymorphic site" 11994	/*tag= ao /note= "known polymorphic site"	12932 /*tag= ap /nota= "known polymorphic site"	aq	-		/*tag= as /note= "known polymorphic site" 13238	<pre>/*tag= at /*tag= at //ote= "known polymorphic site" //ote= "known polymorphic site"</pre>		ВV	/note= "known polymorphic site"   13951   13852   13953   13955   13955   13955   13955   1395	/~cay= aw /note= "known polymorphic site" 14041	/*tag= ax /*tag= ax /note= "known polymorphic site"	14046 /*tag= ay /note= "known bolymorphic site"	az	=	/"tag= ba /note= "known polymorphic site" 14891	-	/*tag- bc /note- "known polymorphic site" 1502415424
exon	misc_feature	intron	misc_feature	exon	intron	misc_feature	exon	misc_feature	misc_feature		mrsc_reacute	misc_feature	misc_feature	misc_feature	misc_feature	4	יייי ביייי בייייי בייייי	misc_feature	misc_feature	misc_feature		misc_reature	misc_feature	misc_feature	misc feature	misc_feature	intron
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														-													
/note= "known polymorphic site" /227, .2260 /****	- 7	/*tag= 1 /note= "intron 3" 2569. 2581	/*tag= 1 /note= "indefinite interval within intron 3" 2678. 2788	/*tag= k /note= "exon 4"	//2/29 1 /*tag= 1 /note= "known polymorphic site"	27893328 /*tag= m //ote= "intron 4"	<pre>/*teap n /*teap n /*cope 'indefinite interval within intron 4"</pre>	. 50 0	34073813 /*tag=	3610	a within third	/note= "known polymorphic site" 38143902	<b>B</b>	. 50 00	4223 /*tag* u /note= "site of 1 nucleotide deletion"	40764088 /*tag= v /*nto= indafinite internet		<b>*</b> 9.	/*tag= x //octe= "intron 7"	/*154: "352. /*tag= y /note= "known polymorphic site"	4614	/notes Thosinite interval Within intron /" /*tag= aa	= 6	/*tag= ab		Ω.	ae "known polymorphic
exon	intron	misc_feature	exon	400	misc_reature	intron	mrsc_reacure		ıntron	misc_feature	misc_feature	exon	4		mutation	misc_feature	exon	intron			misc_feature	misc_feature	exon	1	11111111	misc_feature	misc_feature
7 F F	EE		FT FT	FT	FI	FI	- E E E	1 E E E	r r r	FT	FF	FT	FF	FI	FI	FI	FT	FT	FT	FI	FI	T L L	FF	FI	- E- E-	FT FT	FT FT

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us-08-653-294-18.rng

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/*tag= ad
/note= "site of 1 nucleotide deletion at known
polymorphic site"
9163. .9208
                                                                                     *tag- j
note- "indefinite interval within intron 3"
678. .2788
                                                                                                                                                                                                                                                                                                                                                       *tag= q
note= "indefinite interval within intron 5"
653
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                                                                                                                                                                                                                                          *tag* n
note= "indefinite interval within intron 4"
329. .3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "indefinite interval within intron 6" .4364
                                                                                                                                                              /*tag- 1
/note- "known polymorphic site"
2789. .3328
/*tag- m
/note- "intron 4"
3063. .3075
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note= "known polymorphic site"
572. .6677
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note= "known polymorphic site"
814. .3902
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502. .4614
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"known polymorphic site"
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/note= "intron 5"
3598. .3610
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                                                             note- "intron 3"
569. .2581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "intron 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "intron 7"
                                                                                                                           /*tag= k
/note= "exon 4"
2725
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exon 6"
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hote= "exon 8"
                         note= "exon 3"
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note=
106
                                                   *tag=
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                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-1996 (first entry)
Mutated BRCA1 genomic sequence from PM15.
Mutated BRCA1 genomic sequence from PM15.
Ender therapy; breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
                                                                                                                                                   "indefinite interval within intron 12".16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **tag- e
|note= "inron 2"
|25. .1937
|*tag- f
|note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                to: 24025
                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 63.636
                                   "known polymorphic site".
15511
                                                                                                                                                                                                                             bj
"known polymorphic site"
.16565
bk
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"known polymorphic site"
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/note= "known polymorphic site"
                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: T17455 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
256. 355
/*tag= a
566. 1512
/*tag= b
/*tag= b
/*tag= "intron 1"
                                                                                                                          "intron 12"
.15659
                                                                                                                                                                                                                                                                             "intron 13"
bd
"intron 11"
                                                                                     "exon 12"
.15952
                                                                                                                                                                                                      "exon 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID T17515 standard; cDNA; 24025 BP.
AC T17515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "exon 2"
                                                                                                                                                                                                                                                                                                                                         37.00
3.700
90.909
                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-18 x 117455/rev
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/note= '
16243
/*tag=
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note= '
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note= '
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Quality:
Ratio:
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1. .55

/*tag- a

56. .153

/*tag- b

156. .1512

/*tag- d

/*tag- d

1612. .206

/*tag- d

1612. .206

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2261. .267

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278. .278

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2789. .338

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2789. .338

/*tag- n at 3063-3075 represent an indefinite
                                                                                                                  **tag= bg
note= "indefinite interval within intron 12"
| http://withia.com/read= bg. 16125
| http://withia.com/read= bh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSCAL, human breast and ovarian cancer predisposing gene. BRCAL, human breast and ovarian cancer, predisposing gene. BRCAL; breast cancer; ovary cancer; predisposing gene; susceptibility gene; diagnosis; prognosis; gene therapy; ds. Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 24025
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3.700 Gaps: 0
90.909 Percent Identity: 63.636
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bd
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ID T18325 standard; DNA; 24026 BP.
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US-08-653-294-18 x T17515/rev
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9206
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3047
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15423
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"known polymorphic site"
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14873 az
/note= "known polymorphic si
14890
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11383. 11395
/*tag= ak
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1907
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10530.
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11993
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'note=
2951
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3003
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3950
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					*		
interv 3329. /*tag= /*tag= /*tag= /nterv interv /*tag+	39034.	/note- " interval 65726 65789 /*tag- 92081	/*tag** 10608. /*tag** /*tag** /note** interva	/*tag- 15024. /*tag- 15425. /*tag- /*tag- /*tag-	/note- interva interva ispss./ tag- /atag- /note- interva	/*tag- 16693. /*tag- /note- interval 17536. /*tag-	/rage as in at 1829-18312 represent an indefinite interval within the intron" 18417. 18787 /*tag at 18787   /*tag ag //rag ah //rag ah //rag ah //rag ah //rag ah //rag ai //rag within the intron"
exon intron exon	intron exon intron	exon intron exon intron	intron	intron exon intron	exon	intron exon intron	exon intron exon intron
FT F	FT F		FT F				

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/*tag- s
/note= "exon 6"
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/*tag- t
/note= "intron 6"
/*tag- u
/note= "indefinite interval within intron 6"
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/*tag= ab
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note= "known polymorphic site"
106
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"known polymorphic site"
.9209
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9207
/*tag= af
/note= "known pc
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'note=
164.
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D T17512 standard; cDNA; 24026 BP.

AC T17512.

DT 04-OCT-1996 (first entry)

DE Mutated BRCA1 genomic sequence from PM04.

KW antibody production; germline alteration; probe; lesion neoplasia; human; KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

Seq_documentation mimetic; BRCA1; ds.

Seq_documentation mimetic; BRCA1; ds.
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/note= "intron 2"
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Gaps: 0
Percent Identity: 63.636
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356. .1512
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3.700
90.909
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US-08-653-294-18 x T18325/rev
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Ratio:
Percent Similarity:
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us-08-653-294-18.rng

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seq_documentation_block:

ID T1513 standard; CDNA; 24026 BP.

AC T17513 standard; CDNA; 24026 BP.

T17513 standard; CDNA; 24026 BP.

T17513 standard; CDNA; 24026 BP.

T17513 standard; CDNA; CONA; CO
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Gaps: 0
Percent Identity: 63.636
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.15659
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/*tag= b
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"exon 12"
.15952
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note= "exon 13"
6077
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3.700
90.909
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US-08-653-294-18 x T17512/rev
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Ratio:
Percent Similarity:
                                                                                                              misc_feature
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intron	misc_feature	exon misc feature	intron	misc_feature	exon	intron	mich foaturo	misc_teacuire	misc_reachie	exon	intron	misc_feature	exon		THETOH	misc_feature	misc_feature	misc_feature		יי יי יי	intron	misc_feature	misc_feature			misc_feature intron

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note= "indefinite interval within intron 4"
329. .3406
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hote- "indefinite interval within intron 5"
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//ote= "indefinite interval within intron 7"
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note= "indefinite interval within intron 3"
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1D 717514 standard; cDNA; 24026 BP.

AC 717514.

DT 04-OCT-1996 (first entry)

E Mutated BRCA1 genomic sequence from PM11.

KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

KW antibody production; germline alteration; probe; lesion neoplasia; human;

KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

CS Homo sapiens.
                                                                  bg
"indefinite interval within intron 12"
.16126
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**tag= e
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*tag= f
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3.700 Gaps: 0
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/note= "known polymorphic site"
2207. .2560
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2261. .2677
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seq\_documentation\_block:

ID T17516 standard; cDNA; 24026 BP.

AC T17516,

IT 7516,

O4-00T-1996 (first entry)

DE Mutated BRCAl genomic sequence from PM16.

WY cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

WY antibody production; germline alteration; probe; lesion neoplasia; human;

WY gene therapy; protein replacement therapy; protein mimetic; BRCAl; ds.

OS Homo sapiens. /\*tag- c
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1925. .1937
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misc_fe	exon	intron	misc_feature	exon	mico fosture		misc_feature	misc_feature	misc_feature	nico form	1	misc_feature	misc_feature		misc_feature	misc_feature		misc_reature	misc_feature	misc_feature		misc_feature	misc_feature		misc_reature	misc_feature	to the		misc_feature	exon		intron
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	"indefinite interval within intron 3" .2788		"known polymorphic site"		3075 "indefinite interval within intron 4"				ooro g "indefinite interval within intron 5"	I Process and resorable of the					"indefinite interval within intron 6"				X Xoown polymorphic site" ארזא	y y y "indefinite interval within intron 7"		morphic site"				morphic site"		מונים מונים		af "known polymorphic site"		
/note- "intron 3" 25692581	/*tag= ] /note= "indefinite 26782788	/*tag= k /note= "exon 4"	/*tag= 1 /note= "known poly	//tag= m //tag= m /note= "intron 4"	30633075 /*tag= n /note= "indefinite		/note= "exon 5" 34073813	/*tag= p /note= "intron 5" 3598 3510	/*tag= q /note= "indefinite	3653 /*tag= r /noto= "tnoim nol:	38143902 /*tag= s	/note= "exon 6"	/*tag= t /note= "intron 6"	40764088 /*tag= u	/note= "indefinite	/*tag= v //note= "exon 7"	5571 w	/note= "intron 7" 43914392	/*tag= x /note= "known poly	/*tag= y /note= "indefinite	6538	/rcay= "known polymorphic site" $65726677$	/*tag= aa /note= "exon 8"	66789163 /*tag= ab	/note= "intron 8" 6823	/*tag= ac /note= "known polymorphic	/*tag= ad	91649209	/rey ac	920/ /*tag= af /note= "known poly	921010530 /*tag= ag	
misc_feature	exon	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	misc_leature	THELOH	misc_feature	exon	intron	mico foaturo	שוזאר <sup>-</sup> ופסרתופ	misc_feature	exon	intron		misc_feature	exon		intron	misc_feature	mico fosturo		misc_feature	exon		intron	misc_feature	,	misc_leature	exon		misc_teature	intron	

us-08-653-294-18.rng

PT FTT FTT FTT FTT FTT FTT FTT

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3407. 3813
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3598. 3610
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*1814. 3902

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9210. .10330
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106
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note= "known polymorphic site"
572. .6677
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0572. 6677
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/*tag= "intron 8"
6823
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/note= "exon 4"
2725
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207
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ID 717517 standard; CDNA; 24026 BP.

AC 717517

C17517 standard; CDNA; 24026 BP.

DT 04-0CT-1996 (first entry)

E Mutated BRCA1 genomic sequence from PWA02.1.

W Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

KW antibody production; germline alteration; probe; lesion neoplasia; human;

KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

OS Homo sapiens.
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note= "indefinite interval within intron 2"
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Gaps: 0
Percent Identity: 63.636
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16370. .16382
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2011 - 2260
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256. .355
7.429= "exon 1"
356. .1512
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7.429= c To A mutati
1533. .1611
7.429= e Recon 2"
1513. .1611
7.429= e Recon 2"
1612. .2206
7.429= e To A mutati
7.429= e Recon 2"
1612. .2206
7.429= e Recon 2"
1612. .2206
7.429= e Recon 2"
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.15659
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.6243
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2261. .2677
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/note= "intron 3"
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3.700
90.909
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US-08-653-294-18 x T17516/rev
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15953. .1
/*tag= b
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3004
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"known polymorphic site"
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note= "known polymorphic site"
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note= "known polymorphic site"
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ote= "known polymorphic site"
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note= "known polymorphic site"
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note= "known polymorphic site"
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note= "known polymorphic site"
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ote= "known polymorphic site"
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note= "known polymorphic site"
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11384. 11396
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1908
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seq_documentation_block:

ID 717518 standard: cDNA; 24026 BP.

AC 717518.

DT 04-OCT-1996 (first entry)

DE Mutated BRCA1 genomic sequence from PMA03.1.

KW antibody production; germline alteration; probe; lesion neoplasia; human;

KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag- g
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//note- "exon 3"
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2569. .2581
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Gaps: 0
Percent Identity: 63.636
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[1513. .161]
/*tag- d
/*tag- d
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[1612. .2206
/*tag- e
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/*tag- bk
/note-"known polymorphic site"
16370..16382
/*tag- bl
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//note= "known polymorphic site"
//stag- bj/*tag- bj
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256. 355
/*tag a
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356. 1512
/*tag b
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295
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90.909
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US-08-653-294-18 x r17517/rev
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Standard Co.

//oce= //ocymposymorphic sice= 10531 . 10607 //oce=			/130c 11396   11384 , 11396  *tag** ak			/*tag= am /note= "known polymorphic site" 11904	/*tag= an /*tag= //note= "known polymorphic site"	ao	/note= "known polymorphic site" /#1304 /#1304	E	/*tag= aq /note="known polymorphic site" 13048.	/*tag= ar /*note= "known polymorphic site"	13438 /*tag= as /note= "known polymorphic site" 13448	/*tag- at /*tag- at //facte- "known polymorphic site"	13339   /*teg= au /note= "known polymorphic site"		ANOWII POLYMOLPHIC SE	=	/*tag= ax /note= "known polymorphic site"	144/3 /*tag= ay /note= "known nolymorphic site"	Anothin Postymosphisc	=	/*tag= ba /note= "known polymorphic site" 1466	/*tag= bb //morphic site" /note= "known polymorphic site"	)	=	/*tag= bd /note= known polymorphic site" 5425. 15511	
exou	introp		misc_feature	exon	misc_feature	misc feature		misc_feature	misc_feature	misc_feature	misc_feature	1 00 10	misc_reature misc feature		misc_reacute	misc_feature	misc_feature	misc_feature		misc_leature	misc_feature	misc_feature	miso foature		intron	misc_feature	exon	intron
T EL S		FT	- E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E	FF	- :-		TH H	FT	FT	4 TH TH	. E. E.	F.T.	4 E4 E4 E4		T.S.	FT	TH TH	FT	H H H			FT	14 F	4 EL EL	4 E4 E4	THE THE	FT **	THE THE
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/note= "intron 4"
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.10530
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note- "known polymorphic site"
106

    ad
    "known polymorphic site"
    .9209

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/note= "known polymorphic site"
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note= "intron 2"
1925. 1937
*tag= f
note= "indefinite interval within intron 2"
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/note- "known polymorphic site"
/*tag- h
/note- "exon 3"
2261. .2677
/*tag- "intron 3"
2569. .2581
/*tag- j
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16370. .16382
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513. 1611
ttag= d
note= "exon 2"
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.16565
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256. 355
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/*tag= a
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/*tag= b
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                                                        /note= "indefinite
15953. .16126
/*tag= bh
/note= "exon 13"
16077
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3.700
90.909
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US-08-653-294-18 x T17518/rev
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6127.
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Ratio: 3
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seq_documentation_block:

ID 717521 standard; CDNA; 24026 BP.

AC 717521

T17521 standard; CDNA; 24026 BP.

DT 04-0CT-1996 (first entry)

DE Mutated BRCAl genomic sequence from PMA08.1.

KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

KW antibody production; germline alteration; probe; lesion neoplasia; human;

KW gene therapy; protein replacement therapy; protein mimetic; BRCAl; ds.

OS Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- g
//note- "known polymorphic site"
2207. .2260
/*tag- h
/note- "exon 3"
2261 .2677
//tag- intron 3"
2569 .2581
//note- "indefinite interval within intron 3"
bg
"Indefinite interval within intron 12"
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note= "1937
*tag= f
note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                                                      to: 24026
                                                                                                                                                                                                      Length: 11
Gaps: 0
Percent Identity: 63.636

bk
"known polymorphic site"
16382
bl

                                                                bi
"known polymorphic site"
.16565
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note= "known polymorphic site"
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356. .1512
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'note= "exon 2"
612. .2206
                     .16126
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US-08-653-294-18 x Il7519/rev
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.15659
                    "exon 10".11597
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'note='
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exon 2678. 2788 FT	/*tag= 1 /note= "known polymorphic site" 2789. 3328	/*tag= m /note= "intron 4" FT misc_feature 3063. 3075 FT	"indefinite interval within intron 4" 3406 "exon 5"	3813 P "intro	/*tag= q /note= "indefinite interval within intron 5" 3653	"known polymorphic site" 3902 s	1017on 6 4088 u u	"indefinite interval within intron 6" 4364	"exon 7" 6571 w	"intron 7" 4392	"known polymorphic site" 4614 y	"indefinite interval within intron 7" z	"C to T mutation at known polymorphic site" 6677 aa	9163 8"	"intron 8" ac	"known polymorphic site" ad	"known polymorphic site" 9209 ae e	exou y af "known polymorphic site"	10530 ag "intron 9"	/*tag= ah /note= "known polymorphic site" 10531. 10607

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"tig= ac
note= "A to T mutation at known polymorphic site"
106
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/*tag- m
/*tag- m
/*tag- n
/*tag- n
/*tag- n
/*tag- o
/*ote- "excn 5"
/*tag- o
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/*note- "intron 5"
/*tag- p
/*ote- "intron 5"
/*tag- g
/*ote- "indefinite interval within intron 5"
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789. .3328
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note= "known polymorphic site"
210. .10530
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10531. 10607
/*tag= al
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note= "known polymorphic site"
572. .6677
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note= "intron 8"
823
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note= "intron 9"
376
k
exon 4"
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/note= "exon 8"
6678. .9163
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                                         misc_feature
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10 T17522 standard; cDNA; 24026 BP.

AC T17522.

DT 04-0CT-1996 (first entry)

E Mutated BRCA1 genomic sequence from PMA08.2.

KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

KW gene therapy; production; germine alteration; probe; lesion neoplasia; human;

KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

Solution sapiens.
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//ote= "known polymorphic site"
2207. .2260
//tag= h
/note= "exon 3"
2261. .2677
//tag= intron 3"
2569. .2581
//tag= j
/note= "indefinite interval within intron 3"
2678. .278
"indefinite interval within intron 12".16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= e
note= "intron 2"
925. .1937
note= "indefinite interval within intron 2"
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Gaps: 0
Percent Identity: 63.636
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/note= "known polymorphic site"
1513. 1611
/*tag= d
/note= "exon 2"
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/note= "known polymorphic site"
16370. 16382
/*tag= bl
                                                                                                                           "known polymorphic site".
16565
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256. .355
/*tag= a
note= exon 1"
356. .1512
/*tag= b
/note= "intron 1"
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/note= "known polym
16127. 16565
/*tag= bj
/note= "intron 13"
                                                              "exon 13"
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US-08-653-294-18 x T17521/rev
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    /note=
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.6077
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"indefinite interval within intron 12"
                                                        "indefinite interval within intron 10".15023
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.11396
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"exon 12"
.15952
"exon 10"
.11597
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/note=
15647.
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/note- "indefinite interval within intron 3"
2678. .2788
/*tag- k
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*tag- f
note- "indefinite interval within intron 2"
                                                                                                                                                                                                                                           to: 24026
                                                                                                                                                                  Length: 11
Gaps: 0
Percent Identity: 63.636
                                                 "known polymorphic site"
.16565
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note= "known polymorphic site"
513. .1611
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/note= "known polymorphic site"
16370. .16382
/*tag= bl
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note= "known polymorphic site"
207, .2260
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256. .355
/*tag= a
//note= exon 1"
356. .1512
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.6243
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/note= "intron 2"
1925. .1937
                    "exon 13"
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note= "exon 2"
.16126
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3.700
90.909
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US-08-653-294-18 x T17522/rev
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                     note-
6077
                                         *tag=
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Ratio:
Percent Similarity:
                               misc_feature
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_	intron 10608. "Exon 10" /*tag= a1				am Transfer contracts	misc_feature 11994 an /*tag= an	E	/*tag= ao. /note= "known polymorphic site" misc feature 1304	` ` \ ' '	` ``		'	at	/note= "known polymorphic site" misc_feature 13539 /*tag= au	=	`	Wa	/note= "known polymorphic site" misc_feature 14046 /*tag= ax	=	/*tag= ay //tag= a/note= "known polymorphic site"	misc_reature 148/4 /*tag= az //n/tag= "tanvan nolumownkin site"	ba	/note= "known polymorphic site" misc_feature 14966 /*+*ar= hh	/note- "known polymorphic site" 1502415424	/*tag= /note=	pq	.15511 be	/note= "exon 12" intron 15512. /*tag= bf	
exon 4"	"known polymorphic site" 3328	/*tag= m /*tag= m /*tote= intron 4"	_reature	3406	"exn 5" 3813 :	"intron 5"	/*tag= q /*tag= q /*tag= nterval within intron 5"	r "known polymorphic site"	3814. /*tag¤ /note	4224 "intron 6"	4088 "Independent intervent intervent intervent in		"exon 7" 6571	ron 7"	/*tag= x /note= "known polymorphic site"	4614 Y	"indefinite interval within intron 7"	/*teg= z /*teg= FT /*teg= FT //note= "known polymorphic site" FT exon 65726677 FT	/*tag= aa /note= "exon 8"	.9163 ab	Intron 8"	"known polymorphic site"	ad known polymorphic site"	/*tag= ae /note= "exon 9"	af	Thom polymorphic side:	ag "intron 9"	/*tag= ah //note= "known polymorphic site" FT FT FT FT FT FT FT	/*tag- ah /note- "T to C mutation at known polymorphic site"

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AV117866 AV117866 Mus muscul
AU022889 AU022889 Mouse unfe
AQ366741 HS_5038_B2_D09_SP6E
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 461)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Heller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                        å
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LOCUS A0869567 438 bp DNA GSS 03-NOV-1999
DEFINITION nbeb0035D05f cUGI Rice BAC Library (EcoRI) Oryza sativa genomic
clone nbeb0035D05f, genomic survey sequence.

ACCESSION A0869567
KERXION A0869567.1 GI:6220018
KEYWORDS GSS.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_bref="taxon:9606"
/clone="late=3058 Col=18 Row=F"
/clone=lib="CIT Approved Human Genomic Sperm Library
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scanning the human genome scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
Tol. (206) 616-3618
Fans: (206) 616-3818
Fans: (206) 616-388
Fans: (206) 616-388
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Gaps: 0
Percent Identity: 75.000
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Class: BAC ends
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130.33
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AQ137850.1 GI:3528503
38.00
38.00
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US-08-653-294-18 x AQ137850
                                                                                                                    seq_name: gb_gss9:AQ137850
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                        human.
gb_est33:AV117866
gb_est23:AU022889
gb_gss12:AQ366741
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VERSION
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AQ869567 nbeb00135005f CUGI Rice
AQ8662871 nbeb0019113f CUGI Rice
AV120004 AV120004 Mus musculus
AV182651 AV182651 Yuji Kohara u
AQ864125 nbeb0025799f CUGI Rice
AQ460667 HS_5135_B2_B07_SP6
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AA119739 mn14602.r1 Beddington
AA414705 vc69C04.s1 Knowles Sol
AA62200 vt19h09.r1 Barstead mc
AQ863678 nbeb0021F21f CUGI Rice
AA839058 vw47all.r1 Scares mous
AA012276 TgESTZZ16cll.r1 TgM849
AA012276 TGESTZZ16cll.r1 TgM849
AA168371 mr28a04.r1 Soares mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H72837 9506001.51 Soares fetal
AA289553 vb17b05.r1 Soares mous
AA239656 mx80f12.r1 Soares mous
AA139305 mo21d11.r1 Life Tech m
AR891896 u160c04.x1 Sugano mous
AA174998 ms88h04.r1 Soares mous
AA869826 vq1c07.r1 Barstead st
AA869826 vq1c07.r1 Barstead st
AA8699645 HS.5344.A1.F08_T7A RPG
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9 EST231943 Normalized r

9 HS_2130_BB_DAR CIT

1 nbeb0067L07f CUGI Rice

9 nbeb0004H21f CUGI Rice
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AA748739 ny06e12.s1 NCI_CGAP_GC
AA389896 vb30f04.r1 Soares mous
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AQ649156 Sheared DNA-5K21.TF Sh
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AA571878 vm04e12.rl Knowles Sol
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AW124405 UT-W-BH2.1-ape-d 08-C
AV135435 AV135435 MNS mNSCONTIN
                                                                                                                                                                                                                               - MODEL-frame_p2n.model - DEV-xlp

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                                                                                                                       About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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/note="vector: pBaCIndigo; Site_1: ECORI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.
/monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from oryza sativa. Nipponbare variety using EcorI as the cloning enzyme. The equivalents: The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the Whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                             Wing, R.A. and Dean, R.A. and Sequencing Framework to Sequence the Rice Genome Unpublished (1988)
On Mar 23, 1999 this sequence version replaced g1:3324665. Contact: Wing RA Clemson University Genomics Institute Clemson University Genomics Institute Clemson University Tolemson University Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@lemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 24
High quality sequence stop: 397.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Japonica"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LeuAlaileArgArgileLeuLeuArgTyr 12
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Percent Similarity: 100.000
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US-08-653-294-18 x AQ869567
                                                                                                              Poaceae; Oryza
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                                Oryza sativa
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SOURCE
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                    COMMENT
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seq\_documentation\_block:

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Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones than particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
AQ862871 483 bp DNA GSS 03-NOV-1999
nbeb0019L13f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic
clone nbeb0019L13f, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                     Poaceae; Oryza.
1 (bases 1 to 483)
Migy.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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Gaps: 0
Percent Identity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
Fax: 864 656 4293
Seq brimer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
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High quality sequence stop: 411.
Location/Qualifiers
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                                                                                                                                                                       AQ862871.1 GI:6213328
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US-08-653-294-18 x AQ862871
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Oryza sativa
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AGACTCTCTATACGGCGAATTCTTTTAGCCTAT 54

seq\_name: gb\_est34:AV120004

AV120004.1 GI:5302155

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
                                                                                                                                                                                                                         Kohara, Y., Shin-1, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishiqaki, A., Motchashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.
Caenorhabditis elegans cDNA clone yk640g7 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Osceae; Oryza.

1 (bases 1 to 411)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University Genomics C 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

LOCUS
LOCUS
DEFINITION hobo0022F09f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic
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ACCESSION AQ864125
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Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189500.
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
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Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. 300
/organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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68 c 54 g
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                                                                                               Caenorhabditis elegans. Caenorhabditis elegans
                                               AV182651.1 GI:5562552
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4.000
83.333
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US-08-653-294-18 x AV182651
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Oryza sativa
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Ratio:
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  embryo Ca
AV182651
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KEYWORDS
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TITLE
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                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                           Carninoi, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niltsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Tominaga, N., Watanabe, S., Yaqame, M., Tamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. RIKEN Mouse ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Themostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Flease visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                          seq_documentation_block:
LOCUS AV120004 259 bp mRNA EST 30-JUN-1999
DEFINITION AV120004 Mus musculus C57BL/6J 10-day embryo Mus musculus CDNA
ACCESSION AV120004
                                                                                                                                                                                                                                                                         house mouse.
Mus musculus musculus Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota: Metazoa; Chordata; Craniata; Wuridae; Murinae; Mus.

1 (bases 1 to 259)
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LOCUS AV182651 300 bp mRNA EST 21-JUL-1999
DEFINITION AV182651 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jun 5, 1998 this sequence version replaced gi:3188908
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 259
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Gaps: 0
Percent Identity: 63.636
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Location/Qualifiers

FEATURES

/sex="mixed"

Genome Science Laboratory

RIKEN

TITLE JOURNAL

COMMENT

241 AAGTTAGCCCTTAAAAGGATCCTATTAAAATAT 209

seq\_name: gb\_est36:AV182651

2 ArgLeuAlaIleArgArgIleLeuLeuArgTyr 12

alignment\_block: US-08-653-294-18 x AV120004/rev

Quality: 40.00
Ratio: 3.636
Percent Similarity: 100.000

alignment\_scores

BASE COUNT ORIGIN

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AUTHORS
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         TITLE
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//note="Vector: pBACIndigo; Site_l: EcoRI; Site_2: EcoRI;
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//db_host="E. lDH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A0460667 443 bp DNA GSS 23-APR-1999 HS_5135_B2_B07_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=711 Col=14 Row=D, genomic survey sequence. A0460667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC/EST Resource Center (www.genome.clemson.edu). 54 c 47 g 156 t 1 others
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Gaps: 0
Percent Identity: 90.000
Tel: 864 656 7288
Fax: 864 656 4293
Fax: 864 656 4293
Faz: 864 656 4293
Seq priner: TAATACGACTACACTATAGGG
Class: BAC ends
High quality sequence start: 26
High quality sequence stop: 385.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ArgLeuAlaIleArgArgIleLeuLeuArg 11
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Ratio: 4.000
Percent Similarity: 100.000
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US-08-653-294-18 x AQ864125
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LOCUS AQ460667
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ORGANISM
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KEYWORDS
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3887
Email: jWallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejonjmed.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 95~{\rm c} 83 g 130~{\rm t} 1 others
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poaceae; Oryza.
1 (bases 1 to 460)
Midy.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                           Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 12
Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuAlaIleArgArgIleLeuLeuArgTyr 12
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Location/Qualifiers
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Seg primer: SP6
Class: BAC ends
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AQ857430.1 GI:6207887
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Percent Similarity: 100.000
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US-08-653-294-18 x AQ460667
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Contact: Lee,
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Rattus sp.
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Ratio:
Percent Similarity:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                 /cultivar="Nipponase"
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/clone="bb="Coli BH10B"
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/tlssue_type="Leaf
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LOCUS
AI235399
DEFINITION EST231961 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVCR36 3' end, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 502)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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Impublished (1998)
On Jan 19, 1998 this sequence version replaced gi:2151609.
Other_ESTs: TC63429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 11
Gaps: 0
Percent Identity: 72.727
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                                                                                                                                                     /organism="Oryza sativa"
/strain="Japonica"
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High quality sequence start: 82
High quality sequence stop: 353.
Location/Qualiflers
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AI235399.1 GI:3828905
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Ratio: 3.636
Percent Similarity: 100.000
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US-08-653-294-18 x AQ857430
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ORIGIN
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VERSION
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AUTHORS
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SOURCE
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                                                                                                FEATURES
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seq_documentation_block:
LOCUS A1407553 511 bp mRNA EST 09-FEB-1999
DEFINITION EST235843 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
RCVDZ17 3' end, mRNA sequence.
ACCESSION A1407553
VERSION A1407553.1 GI:4251057
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1 (Dases I to 511)

Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index

Unpublished (1998)

On Feb 17, 1998 this sequence version replaced gi:2889619.
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/clone="RovCR36"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib-"Normalized rat ovary, Bento Soares"
/note-"Organ: ovary, Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: Not1"
108 c 108 g 144 t
                                                                                The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3329 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhiee@tigr.org
Seq primer: M13-21
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Percent Identity: 75.000
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/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="ROVDZ17"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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US-08-653-294-18 x AI235399/rev
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/GD xref="texon:4530"
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//Lab_host="codi Rice BAC Library (ECORI); Site_2: ECORI;
//Lab_host="codi DH10B"
//Lab_host="codi H10B"
//Lab_host="codi DH10B"
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//Lab_host="codi H10B"
//Lab_host="codi H10B"
//Lab_host="codi H10B"
//Lab_host="codi DH10B"
//Lab_host="codi DH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
Oryza sativa
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                   seq_documentation_block: 522 bp DNA GSS 02-DEC-1999
LOCUS A0917001 522 bp DNA GSS 02-DEC-1999
DEFINITION nbeb0067L07f cuGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0067L07f, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poaceae; Oryza.
1 (bases 1 to 522)
Migy.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Octaban Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 34
High quality sequence stop: 383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .522
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Japonica"
/cultivar="Nipponbare"
                                                                                                                                    1 TyrArgLeuAlaIleArgArgIleLeuLeu 10
to reverse of: AQ661929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ917001.1 GI:6513517
                                                                                                                                                                                                                                           seq_name: gb_gss7:AQ917001
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Align seg 1/1
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AUTHORS
TITLE
JOURNAL
COMMENT
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 519)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:

LOCUS AG61529 519 bp DNA GSS 23-JUN-1999

LOCUS AG61529 519 bp DNA Human Genomic Sperm Library D Homo
DEFINITION HS_2130_B2_H03_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2130 Col=6 Row=P, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Discourses
On Sep 10, 1998 this sequence version replaced g1:3556096.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
11 (206) 616-3618
Fax: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                      511
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Gaps: 0
Percent Identity: 70.000
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Percent Identity: 75.000
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to:
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/db_xref="taxon:9606"
/clone="Plate=2130 Col=6 Row=P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AI407553 from: 1
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Location/Qualifiers
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AQ661929.1 GI:5169697
                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-18 x AI407553/rev
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US-08-653-294-18 x AQ661929/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 c
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Ratio: 4.000
Percent Similarity: 100.000
                                                                                                                                                                      4.444
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                                                                                         alignment_scores:
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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BASE COUNT ORIGIN

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/cultivar="Nipponica"
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/note="Vector: pB4CIndigo; Site_1: EcoRI;
/note as their primary source of carbohydrate.
/note as their primary for farabilitate positional contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones high density filters, each containing 18,432 clones high density filters, each containing and can be requested from the Clemson University BAC/EST Resource Center: (www.genome.clemson.edu)."
/note as their propresent twe whole library for colony source clemson (whole income.clemson.edu)."
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1 (bases 1 to 801)

Midy. R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

LOCUS A0857059 801 bp DNA GSS 03-NOV-1999

DEFINITION nbeb0004H21f CUGI Rice BAC Library (ECORI) Oryza sativa genomic

Clone nbeb0004H21f, genomic survey sequence.

ACCESSION A0857059

VERSION A0857059 GI:6207425

KEYWORDS GSS.
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Percent Identity: 90.000
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
Clemson University
                                                                                                                                     to: 522
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/organism="Oryza sativa"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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158 c 162 g 23
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High quality sequence stop: 360.
Location/Qualifiers
                                                                                                                                                                                        2 ArgleuAlalleArgArglleLeuLeuArg 11
                                                                                                                                                                                                                 /strain="Japonica"
                                                                                                                                       from: 1
                                                                                                                               Align seg 1/1 to: AQ917001
Percent Similarity: 100.000
                                                  alignment_block:
US-08-653-294-18 x AQ917001
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Oryza sativa
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Vence. To see of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Otherss: CTTB1-E1-2513B14.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3 Reverse
Class: BAC ends.
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/clone=11b="CITBI-E1"
/cs=1 type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;

CalTech Human BAC Library D"
a 76 c 55 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,

Butharia, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 308)

1 (bases 1 to 308)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and

Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AQ279730 308 bp DNA GSS 22-NOV-1998
DEFINITION CITBI-E1-2513B14.TR CITBI-E1 Homo sapiens genomic clone 2513B14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 58.333
                                               Percent Identity: 80.000
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/organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                                                                                                   3 LeuAlaIleArgArgIleLeuLeuArgTyr 12
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AQ279730 from: 1
                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ279730.1 GI:3905634
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Quality: 40.00
Ratio: 4.000
Percent Similarity: 100.000
                                                                                                                                                                   Align seg 1/1 to: AQ857059
                                                                                             alignment_block:
US-08-653-294-18 x AQ857059
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US-08-653-294-18 x AQ279730
                                                                                                                                                                                                                                                                                                           seq_name: gb_gss11:AQ279730
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Tumor Gene Index

Unpublished (1997)

On Jan 14, 1998 this sequence version replaced gi:1797612.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@fih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CoAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note...vorcor: pr713D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI: 1st strand cDNA was prepared from human tonosillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was primed with a Not I - Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                               seq_documentation_block:
LOCUS AA748739 309 bp mRNA EST 22-JAN-1998
DEFINITION ny06e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270990 3',
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 309)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="INAGE:1270990"
/clone="INAGE:NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
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Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 674 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 256.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnī.gov/bbrp/image/image.html
Align seg 1/1 to reverse of: AA748739 from: 1
                                                                                                                                                                                                                              mRNA sequence.
AA748739
AA748739.1 GI:2788697
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US-08-653-294-18 x AA748739/rev
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75.000
                                                                                                   seq_name: gb_est19:AA748739
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ORIGIN
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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Wed Feb

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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein 8, 2000, 01:29:40; Search time 122.56 Seconds (without alignments) 2.319 Million cell updates/sec February Run on:

US-08-653-294-19 54

1 YRLAIXRIALRY 12 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	10 To 44 TO 20 C	702 84-7	02.84-	Immunomodulating d	TLE	HLA-B2702 84-75-84	Immunomodulating d	HLA-B2702 CTL modu	HLA-B2702 CTL modu	de B2702.84	Peptide B2702.84-7	Hepatitis GB virus	84-	odulatory	#1 used	Peptide fragment o	HLA-B2702 CTL modu	CIL mo	helix	02.75-6	<pre>-cell modula</pre>	modulat	>	odulator	B2702.75-	e B2702.	02 CTL mod	e B27	H 단	Ψï	Peptide fragment o	ď	8 CEJ 8	32702.	HLAB38.6084. Comps
SUMMAKIES	er er		542	3379	3379	9290	9542	377	9290	9290	3379	3379	144	543	726	378	120	90	309	541	542	21	0751	4726	4726	3378	3378	291	3379	142	4120	28	8309	8309	R95416	9542
	E C	3	7	Н		-	Н	٦.	-	Н	-	Н	Н	٦	-	-	٦	~	Н	٦	П	П	П	Н	-	~1	Н	п	Н	Н	Н	Н	Н	<del>, ,</del>	Н	~
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	Score	) !	52	52	52	38	38	38	33	33	33	33	32	31	29	29	53	29	58	53	58	29	29	29	29	29	53	53	29	29	29	29	58	58	29	29
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Peptide B2702.60-8 Peptide Seq ID No:	Flea cysteine prot Flea cysteine prot	Flea cysteine prot	Sequence of HLA-BS	HLA-Bw53 exon. HLA	Recombinant cold-r	E. histolytica pyr
W33794 Y06801	W41965 W41993	W41994	R03144	R12463	R76710	R90926
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25 184	191	327	362	362	882	882
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53	53.7	53	53.5	533	23	23
7 7 7 7	7 7 7 8	500	53	500	5 6	58
36 36	37 38	30	41	4 4 2 6	44	45

### ALIGNMENTS

Composes. Comportsing lymphoid surface membrane proteins - which may promibit cytolytic activity and differentiation of CTLS.

Frample: Page 12; 29pp; English.

Example: Page 12; 29pp; English.

R95413, and R95413-R9541 represent palindromes and fragments of chuman-leucocyte-associated antigens. This sequences can be used to isolate the protein p74 from a T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSc70.

CC protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSc70.

CC protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSc70.

CC protein associated with T-cell activation in mammalian T-cells and is also immunologically cross reactive with the heat shock protein HSc70.

CC plum containing a covalently bound HLA-B2702 palindromic peptide.

CC column containing a covalently bound HLA-B2702 palindromic peptide.

CC column containing a covalently bound HLA-B2702 palindromic peptide.

CC compounds can be screened for their effect on the cytolysis. Candidate compounds them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. 12-NOV-1996 (first entry)
HIA-B3702 84-79-84 palindrome.
HIA-B3702 84-79-84 palindrome.
HIA-B774: plyal-helix; human-leucocyte-associated antigen; inhibitor;
HIA- p74: alphal-helix; membrane protein; mammal: heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell. 10-NOV-1993; US-150493. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger C, Krensky AM; WPI; 95-194027,725. ¥ R95429 standard; peptide; 12 .0-NOV-1994; U12985. 

Gaps ö 96.3%; Score 52; DB 1; Length 12; 91.7%; Pred. No. 0.00017; 1ve 0; Mismatches 1; Indels Conservative Query Match Best Local Similarity Matches II; Conserv

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1 YRLAIRRIALRY 12 1 YRLAIXRIALRY 12 à 셤

Fn.

N RESULT W33798 ID W33 AC W33

W33798 standard; peptide; 12 AA. W33798;

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                                                                                                                                                                                                                                                                                           PR 24*MAY-1996; UGB689.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

Bellow R, Clayberger C, Krensky AM;
WPI: 98.086530/08

New immunomodulating dimer peptide(s) - based on a Class I HIA-B

Replace Wajs78-98 and Wajs778-9 were assayed for their immunomodulating activity. Including the N-terminal acylated and/or creminal and/adted or esterified forms of up to 60 anino acids, where care the peptide-type compound comprises the formula; A-B, where A, B = creminal amidated or esterified forms of up to 60 anino acids, where the peptide-type compound comprises the formula; A-B, where A, B = cc * terminal amidated comprises the formula; A-B, where A, B = cc * terminal amidated comprises the formula; A-B, where A, B = cc * transplant amino acid; aa82 = R or E, aa89 = G or R; and as represents amino acid; aa99-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = C * small amino acid; aa82 = R or E, aa83 = G or R; and as represents amino acid sequences related to a Class I HLA-B alphal domain (positions or small amino acid sequences related to a Class I HLA-B alphal domain (positions or undestrably attacking cells in a host or In Vitro. They can also be used to inhibit the proliferation of relis in cresponse to anti-CD3. The peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of relis in resed in combination with antigenic peptides or proteins of interest consorse to anti-CD3. The peptide can be used for preventing rejection of remained arthritis and lupus erthemetosis. The products can also be conneced or remained arthritis and lupus erthemetosis. The products can also be conneced or co
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Claim 17: Page 35: 41pp; English.
This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1998 (first entry)
Immunomodulating dimer peptide #3.
Immunomodulating dimer: immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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Pred. No. 0.00017;
0; Mismatches 1; Indels
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(STRD) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
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Best Local Similarity 91.7
Matches 11; Conservative
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| YRLAIRRIALRY 12
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WO9744351-Al.
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WO9744351-Al.
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                                                                                                                                                                      Synthetic
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claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a rycresents amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid; sequences related to a class I HLAP alphal domain (positions 79-84). They can be used to inhibit cyctoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the profleration of relativate CTLs. They can also inhibit the cyclosic used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus errythematosis.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MRC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate for almited period of time (compared to the lifetime modulate (or inibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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12-OCT-1995.
05-APR-1995, U04349.
05-APR-1995, ULAZ2851.
05-APR-1995, UNIV LELAZUS STANFOND JUNIOR.
Clayberger C, Krensky AM, Parham P;
WIL; 95-358582/46.
WIL; 95-358582/46.
Extension of exceptance period of transplants from MHC unmatched strension of a cospinate strong Class I B75-84 MHC antigen of the recipient works.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 1; I
Pred. No. 0.00017;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R92907 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%;
91.7%;
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Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
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WO9526979-A1.
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treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
claimed which has immunomodulating activity, including the N-terminal
acylated and/or C-terminal amidated or esterified forms of up to 60.

Claimed which has immunomodulating activity, including the N-terminal
acylated and/or C-terminal amidated or esterified forms of up to 60.

Claimed which has immunomodulating activity, including the N-terminal
activity including the N-terminal
activity including the N-terminal as 10.

Vi and 7 = D, Sor N; and 9 = R or (a) and 8 = T or N; and 8 = E or N;
vi and 7 = D, Sor N; and) = R or G; and 0 = I or N; and 2 = R or C;
vi and 7 = D, Sor N; and 9 = R or G; and 0 = I or N; and 3 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit the compounds of interest to activate cTLS. They can also be used in combination with antigenic peptides or proteins of interest to activate cTLS. They can also inhibit the used for producing of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid atthritts and lupus erythematosis.

The products can also be used for detection and diagnosis.
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Best Local Similarity
Matches 10; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the patient
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R92909
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                                                                                                                                                                                                                                                                                                                                                                                                                                 runpublic cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp: English.

Example: Page 20 AA; English.
                                                                                                                      HLA-B2702 84-75-84 palindrome.
HLA: p74: alphal-helix: human-leucocyte-associated antigen; inhibitor;
Tcell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx: cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Compsns. comprising lymphoid surface membrane proteins - which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunomodulating dimer péptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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(STRD ) UNIV, LELAND STANFORD JUNIOR.
(STRD ) UNIV, LELAND STANFORD JUNIOR.
(BELLOW R. Clayberger C, Krensky AM;
WPI: 98-086530/008.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W33778 standard; peptide; 20 AA.
                                                  R95428 standard; peptide; 20 AA.
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                                                                                              12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
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22-MAY-1997; U08689
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                                                                                                                                                                                                                                                           WÒ9513288-A1.
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WO9744351-Al.
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Best Local Si
Matches 113
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    RESULT
R95428
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R83061-R83085, R83090-R83096 and R92207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
CYtotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                    70.4%; Score 38; DB 1; Length 20; 55.0%; Pred. No. 0.16; 1; Indels ive 0; Mismatches 1; Indels
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(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R92909 standard; peptide; 20 AA.
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                                                                                                                                                 Query Match
Best Local Similarity 55.0
Matches 11; Conservative
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05-APR-1995; U04349.
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WPI; 95-358582/46.
liseason.
The products can a
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Gaps

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Homo sapiens.
WO9744351-A1.
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W33792
ID W3
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                  HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1, Page 19: 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                       Claybrays ( ) ...
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
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; Mismatches
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                                                                                                                                                                                                                        05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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22-MAY-1997. UO8689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                             R92908 standard; peptide; 20 AA.
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1 YRLAI ----- XRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                  Clayberger C,
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WO9744351-A1.
                                                                                                                                                                       Synthetic.
WO9526979-A1.
                                                                                                       16-MAY-1996
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the peptide-type compound comprises the formula; A-B, where A, B = (R a876-77), [a479-84] or A-B, where A, B = (R a876-77), [a479-84] or Or V; aa77 = (R a876-77), [a479-84] or Or V; aa77 = (R a876-77), [a479-84] or Or V; aa77 = (A a880 = 1 or N; aa81 = and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undestrably attacking cells in a host or Invitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, read for detection and diagnosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERION K, Lighberger C, Krensky AM;

WHI: 98-086530/08

New immunomodulating dimer peptide(s) - based on a Class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
reacting autoimmune diseases

Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
activity. A peptide-type compound or variant is claimed which has
activity. A peptide-type compound cor variant is claimed which has
certerminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula; A-B, where A, B = c

C -terminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula; A-B, where A, B = c

C small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino
acid sequence in the brackets may optionally be absent or truncated
at any peptide type bond within the brackets. The compounds comprise
amino acid sequences related to a Class I HLA-B alphal domain (positions)
39-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from
undesirably attacking cells in a host or in vitro. They can also be
used in combination with antigenic peptides or proteins of interest to
activate CTLs. They are also inhibit the proliferation of T cells in
cesponse to anti-CD3. The peptide can be used for preventing rejection
of transplants or for treating autoimmune diseases, e.g. diabetes,
considered to anti-CD3. The peptide can be used for preventing rejection
of transplants or for treating autoimmune diseases, e.g. diabetes,
considered to anti-CD3. The peptide can be used for preventing rejection
of transplants or for treating autoimmune diseases, e.g. diabetes,
considered to anti-CD3. The peptide can be used for preventing rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1998 (first entry)
Peptide B2702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.1%; Score 33; DB 1; Length 20; 50.0%; Pred. No. 1.6; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W33792 standard; peptide; 20 AA.
W33792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLAI-----XRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLATRINERRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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22-MAY-1997; U08689.
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Matches 10; Conserv
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DB 1; Length 20;

Score 33;

61.18;

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cytolysis; antigen presenting cell. Synthetic.
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| YRLAIRLNETRENLRIALR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAI-----XRIALR 11
                                                                                                                                                       Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc_difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sufficient to com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9744052-A1.
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Synthetic.
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W47261
AC W47261
DT 22-WAY DD 22-WAY DD 22-WAY Immunoof KW transpoor Synthem Store Synthem Syn
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HIA-B2702 84-757775-84T palindrome.
HIA-B2702 84-757775-84T palindrome.
HIA- p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for diagnosis and therapy of hepatitis GB virus
Example 5: Page 222: 661pp; English.
Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV infected tamarin plasma, using standard procedures, was used to prepare a lambda phage HGBV cDNA library. The cDNA clone T00049, which encodes the proteins R81447-50 and R82064/65 (the 6 possible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reading frames), was rescued from the lambda phage, searched against a sequence database and found to be an unique HGBV sequence. Reagents which comprise the HGBV DNA, or its protein prods. can be used for the diagnosis, therapy or in a vaccine t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Schlauder GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 111;
                                                                                                                                                                                                                                                02-JUL-1996 (first entry)
02-JUL-1996 (first entry)
Hepatitis GB virus (HGBV) clone 50 protein prod.
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A; non-B; non-C; non-D; non-E; clone 50; tamarin; infected plasma; lambda phage; cDNA library.
                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                note= "corresponding codon STOP codon"
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Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dawson GJ, Desai SM, Erker JC, L
3, Mushahwar IK, Pilot-Matias TJ,
  Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                               R81449 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R95430 standard; peptide; 20 AA.
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50.0%;
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                                                                                                      1 YRLAIRLNERRENLRTALRY 20
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                                                              1 YRLAI-----XRIALRY
                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1994; US-196030.
13-MAY-1994; US-242654.
29-UUL-1994; US-283314.
23-NOV-1994; US-344190.
23-NOV-1995; US-344185.
27-JAN-1995; US-344557.
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81 YLLRMSRVAIKY 92
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 95-293123/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T00049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9521922-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1995.
14-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buijk SL,
Muerhoff AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevent
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                                                                                                                                                                    RESULT 11
R81449
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While of the proteins of the proteins of the may multiply captured to the manufacture and differentiation of CTLS.

Frample: Page 12: 20pp: English.

R95413, and R95415-R9543 represent palindromes and fragments of the manufacture associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the LHA-B2702 84-757/75-84T palindrome. These sequences can be used to isolate the protein p74 from a T-cell activation in mammalian T-cells. The protein p74 from a T-cell activation in mammalian T-cells and is also immunologically cross reactive with the heat shock protein Escope particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an efficitly column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-48 (see R95416), induces calcium influx, and inhibits cytocoxic T lymphocyte (CTL) differentiation or cytolysis.

Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds can be employed binding between the candidate compound complexity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound composition containing T-cells and antigen presenting cells (APCS), by sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched
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1. .6
/note= "at least one of the amino acids is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 1; Length 20;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
10-NOV-1994; U12985.
10-NOV-1994; U2985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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23-ARR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDERGER C, KRENSKY AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplant rejection
Claim 10; Page 36; 41pp; English.
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Mew peptide(s) based on class I HLA antigen domains - used for modulating cytotox1 T-lymphocyte activity towards targets claim 11; Page 54; 61pp; English.

Claim 11; Page 54; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removating subsets of CTLs from T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
                                                       Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.
        15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
                                                                                                                                                            16-SEP-1993.
25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                           Clayberger CA, Krensky AM; WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a specifically claimed peptide which forms part (1 in sequence represents a specifically claimed peptide which forms part (2 it is sequence represents a specifically claimed invention. A peptide-type compound or variant is claimed which has immunomodulating activity.

Compound or variant is claimed which has immunomodulating activity.

Compound or variant is claimed which has immunomodulating activity.

Compound or variant acylated and/or C-terminal amidated or compounds to the compound or seterified forms of up to 60 amino acids, where the peptide-type compounds compounds compounds or N: aa79 - R or G; (aa84-79) (Laa77-76R); aa76 - E or V; aa77 - D, S or N; aa79 - R or G; ca80 - I or N; aa81 - a for N: aa18 - a for
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                  Gaps
donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.

Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.

Sequence 6 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1998 (first entry)

Peptide # I used in immunomdulating dimer peptide.

Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation: autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                          DB 1; Length 6;
1.5e+05;
hes 0; Indels
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                                                                                                                                                                                          Query Match 53.7%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 1.: Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NUV-1997;
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W33780 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                    7 RIALRY 12
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1 RIALRY 6
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WO9744351-A1.
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W33780
     866688
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Conservative

7 RIALRY 12

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RESULT 15 R41208 ID R4 AC R4

R41208 standard; peptide; 10 AA. R41208;

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                               Gaps
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          Length 10;
                               0; Indels
          Score 29; DB 1;
Pred. No. 4.8;
                              Mismatches
                                                                                                                  Search completed: February 8, 2000, 01:29:40 Job time: 1752 sec
53.7%; Scur
100.0%; Pre
                               Conservative
Query Match
Best Local Similarity
5, Conserve
                                                   7 RIALRY 12
                                                                       5 RIALRY 10
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

 ; Search time 117.7 Seconds (without alignments) 4.809 Million cell updates/sec February 7, 2000, 11:54:29 Run on:

US-08-653-294-19 54

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YRLAIXRIALRY 12 Title: Perfect score: Scoring table: Sequence:

142080 seqs, 47169319 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_62:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Result		* Query			SUMMAKIES	
- :	Score	Match	Length	BB :	DI	Description
	34		141	7	H71504	ribosomal protein
	34	63.0	309	7	G70882	probable oxidoredu
	33		142	7	C72053	L17 ribosomal prot
	32		253	7	E75055	Ω
	32		264	~	E71567	
	32		552	7	A64085	á.
	32		610	7	S77337	tran
	32	59.3	2242	~	A57541	
	31	57.4	190	~	F70410	hypothetical prote
	31	57.4	349	~	G70542	probable bioB prot
	31	57.4	356	~	S37356	spaS protein - Sal
	31	57.4	469	~	C69460	conserved hypothet
	31	57.4	578	~	B64012	hypothetical prote
	31	57.4	1166	7	A49201	adenylate cyclase
	31	57.4	18	~	A47202	adenylate cyclase
	31	57.4	1791	~	T02909	hypothetical prote
	30	55.6	88	~	C70200	ribosomal protein
	30	55.6	153	~	S08501	3-dehydroquinate d
	30	55.6	211	~	H64961	probable membrane
	30	55.6	283	~	JC6531	avermectin B 5-0-m
	30		286	П	B69290	rhamnosyl transfer
	30		313	7	JC5342	Na+/H+ antiporter
	30		331	7	S09800	hypothetical prote
	30		348	~	229990	유
	30	55.6	376	~	S75438	hypothetical prote
	30		377	~	A72350	ы
	30		394	7	S20905	hypothetical prote
	30		432	~	F70575	ble PurA
	30	55.6	497	~	D65189	٠ ي
	30		528	7	476	propionate catabol

6-1-0	ATMI protein precu	hypothetical prote	gene 30 protein -	pyruvate, phosphate	hypothetical prote	kinase-related pro	laminin alpha-1 ch	F11 protein - vacc	J5L protein - vacc	JSL protein - vari	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote
164134	554211	\$52564	WZBE30	F71652	G71329	TVHURS	S18253	QQVZEL	H42513	533096	A69219	H72464	T12893	E69149
c	۱ ۵	7	Н	~	~	П	~	٦	~	~	-	~	~	~
795	9069	754	770	880	1084	2347	3712	124	133	133	138	144	156	170
7. 7.	22.0	55.6	55.6	55.6	55.6	55.6	55.6	53.7	53.7	53.7	53.7	53.7	53.7	53.7
5	000	30	30	30	30	30	30	53	53	53	53	53	53	53
33	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1	
ribosomal protein L17 - Chlamydia trachomatis	
C;Species: Chlamydia trachomatis	
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999	9-1999
C; Accession: H71504; I40747	ı
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche	vind, L.; Mitche
Science 282, 754-759, 1998	
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t	ans: Chlamydia t
A; Reference number: A71570; MUID:99000809	•
A; Accession: H71504	
A; Molecule type: DNA	
A; Residues: 1-141 <arn></arn>	
A; Cross-references: GB: AE001323; GB: AE001273; NID: 93328931; PIDN: AAC68107.1; PID: 9332	8107.1; PID:9332
A; Experimental source: serotype D, strain UW-3/Cx	
R;Gu, L.; Wenman, W.M.; Remacha, M.; Meuser, R.; Coffin, J.; Kaul, R.	
J. Bacteriol. 177, 2594-2601, 1995	
A, Title: Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural	and structural
A; Reference number: I40743; MUID:95247702	
A; Accession: I40747	
A; Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molecule type: DNA	
A; Residues: 20-115, 'R', 117-141 <gul></gul>	
A; Cross-references: GB: L33834; NID: 9620026; PIDN: AAA74990.1; PID: 9620030	030
C;Genetics:	
A; Gene: r117	
C; Superfamily: Escherichia coli ribosomal protein L17	
C; Keywords: protein biosynthesis; ribosome	

ö Gaps ö 63.0%; Score 34; DB 2; Length 141; 54.5%; Pred. No. 3.7; 2; Indels :1ve 3; Mismatches 2; Indels Query Match 63.0 Best Local Similarity 54.5 Matches 6; Conservative

2 RLAIXRIALRY 12 ò

64 RLAVGRLMVRY 74 g

RESULT 2
g70882
probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
G;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 29-Sep-1999
C;Accession: G70882
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Naturors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua A;Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua A;Tieference number: A70500; MulD:98295987
A;Accession: G70882

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EFSULT 5
E71567
E7157
E7
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A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Titte: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nces: GB:U32749; GB:L42023; NID:g1573658; PIDN:AAC22321.1; PID:g1573663 unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable ATP-binding transport protein H10664 - Haemophilus influenzae (strain Rd KW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Sep-1999
C.Accession: A64085
      Gaps
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A;Experimental source: serotype D, strain UW-3/Cx
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F:355-549/Domain: ATP-binding cassette homology <ABC>
F:372-379/Region: nucleotide-binding motif A (P-loop)
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Pred. No. 38;
1; Mismatches
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Pred. No. 18;
1; Mismatches
         Mismatches
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C;Superfamily: hypothetical protein ybbP
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ilarity 70.0%;
Conservative
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70.0%;
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A; Residues: 1-552 <TIGR>
A; Cross-references: GB:U32749;
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Best Local Similarity
Matches 7; Conserv
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                                                                     1 YRLAIXRIALRY
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         Matches
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C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20.Aug-1999 #sequence_revision 20.Aug-1999 #text_change 20.Aug-1999
C;Accession: E75055
R;Annonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Beferinted to the EMBL Data Library, July 1999
A;Reference number: A75001
A;Accession: E75055
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-309 <CCD.>
A;Residues: 1-309 <CCD.>
A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129972
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2776C
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
F;9-211/Domain: cytochrome-b5 reductase homology <CBR>
F;240-297/Domain: ferredoxin [2Fe-25] homology <FER>
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A;Cross-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAD18764.1; PID:g437692
A;Cross-references: strain CWL029
C;Genetics:
A;Gene: rll7
C;Superfamily: Escherichia coli ribosomal protein Ll7
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A;Molecule type: DNA
A;Molecule type: 1-253 <KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50338.1; PID:e151623
A;Experimental source: strain Orsay
A;Genetics: AbB1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: C72053
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Superfamily: Escherichia coli ribosomal protein L17
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18;
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8;
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Pred. No.
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Pred. No.
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Pred. No.
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77.8%;
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66.78;
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54.5%;
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Best Local Similarity 77.5.
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Best Local Similarity
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Best Local Similarity
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65 YRIAIRRIA 73
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A; Status: prelimina:
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D.E.;

The Later

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Useful biob protein - Mycobacterium tuberculosis (strain H37RV)

C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Sacession: G70542
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davila, R.; Perkhill, M.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Mutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A, Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID: 98295987
A, Reference number: A70500; MUID: 98295987
A, Stetsus: preliminary: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Kesidues: 1-349 < COLD.
A; Cross-references: GB: 295586; GB: AL123456; NID: 93261785; PIDN: CAB09080.1; PID: e31716
A; Experimental source: strain H37RV
C; Superimental source: strain H37RV
C; Superfamily: biotin synthetase
                                 Cippenies Aquifex aeolicus
Cippenies Aquifex aeolicus
Cippenies Aquifex aeolicus
Cippenies 108-May-1998 #text_change 08-May-1998
Cipate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
Cipate: 08-May-1998 #sequence_revision 08-May-1998
Cipates 08-May-1998
Riberkert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A;Ittle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUD:9819666
A;Accession: F70410
A;Accession: 
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C; Species: Salmonella typhimurium
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Sep-1999
C; Accession: S37356
R; Groisman, E.A.; Ochman, H.
EMBO 7. 12, 3779-3787, 1993
A; Title: Cognate gene clusters govern invasion of host epithelial cells by Salmonella A; Reference number: S37304; MUID: 94008985
A; Accession: S37356
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Pred. No. 22;
3; Mismatches
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            aq_1277 - Aquifex aeolicus
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50.0%;
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54.5%;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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43 HNLAIQKVALR
                protein
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A. Status: 1-242 cHONA
A. Status: 1-2242 cHONA
A. Status: 1-2242 cHONA
A. Cross-references: GB.U18868; NID:9951095; PIDN:AAA74569.1; PID:9951096
C. Superfamily: rudimentary enzyme; aspartate/ornithine carbamoylransferase homology; Ba arbamoyl-phosphate synthase (ammonia) homology cRCPA
C. Statomain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology
F: 178 354/Domain: carbamoyl-phosphate. synthase (glutamine-hydrolyzing) large chain homology
F: 178 454/Domain: biotin carboxylase homology cBCl>
F: 939-1385/Domain: biotin carboxylase homology cBCl>
F: 1464-13808/Domain: Bacillus dipydrocrotase homology cBCD>
F: 1941-2239/Domain: aspartate/ornithine carbamoyltransferase homology cACT>
F: 252/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S74322; MUID:97061201
A; Reference number: S74322; MUID:97061201
A; Accession: S77337
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-610 < KRN>
A; Residues: 1-610 < KRN>
A; Rosidues: 1-610 < KRN>
C; Stoperferences: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17440.1; PID:d101817
A; NOTE: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfemily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C; Reywords: ATP; P-loop; transport protein
E; 380-574/Domain: ATP-binding cassette homology cassette homology
E; 337-404/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyrimidine synthesis multifunctional protein CAD - spiny dogfish
N;Contains: aspartate carbamoyltransferase (EC 2.1.3.2); carbamoyl-phosphate synthase (g
C;Species: Squalus acanthias (spiny dogfish)
C;Dete: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
C;Accession: A57541
R;Hong, J; Salo, W.L.; Anderson, P.M.
J; Biol. Chem. 270, 14130-14139, 1995
A;Tittle: Nucleotide sequence and tissue-specific expression of the multifunctional prote
A;Reference number: A57541; MUID:95294021
                                                                                                                                                                                                          R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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N:Alternate names: ABC transporter; protein sill/25
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Sep-1999
C;Accession: S77337
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Pred. No. 1.5e+02;
2; Mismatches 4; Indels
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Pred. No. 42;
1; Mismatches
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llarity 50.0%;
Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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2109 YLLTLYRVNLRY 2120
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508 RLAIARAAMR 517
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Best Local Similarity
Matches 6; Conserv
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RESULT F70410

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A; Accession: A425.

A; Residues: 7-1161 CPRE>
A; Experimental source: S49 lymphoma cells
A; Experimental source: S49 lymphoma cells
A; Note: sequence extracted from NCB1 backbone (NCBIN:119384, NCBIP:119386)
A; Note: sequence extracted from NCB1 backbone (NCBIN:119384, NCBIP:119386)
B; Note: Natl. Acad. Sci. U.S.A. 89, 6716-6720, 1992
A; Title: Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase from NCB-20
A; Reference number: A46187; MUID:92357702
A; Status: not compared with conceptual translation
A; Status: not compared with conceptual translation
A; Status: not compared with Signature (SC)
A; Accession: A46187
A; Status: not compared with conceptual translation
A; Status: not compared with conceptual translation
A; Status: not compared from NCB-20 cells
A; Cross-references: GB:M93422; NID:9191690; PIDN:AA37174.1; PID:9191691
A; Cross-reference extracted from NCB1 backbone (NCBIP:110233); the authors acknowledge C; Superfamily: human adenylate cyclase; quanylate cyclase; catalytic domain homology cGCC>
F; 925-1164/Domain: guanylate cyclase catalytic domain homology cGCC>
F; 925-1164/Domain: guanylate cyclase catalytic domain homology
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Advisor

Advisor

Advisor

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Advisor

C;Accession: Advisor

Advisor

R; Premont, R.T.; Chen, J.; Ma, H.W.; Ponnapalli, M.; Iyengar, R.

R; Premont, R.T.; Chen, J.; Ma, H.W.; Ponnapalli, M.; Iyengar, R.

A;Title: Two members of a widely expressed subfamily of hormone-stimulated adenylyl c

A;Reference number: Advisor; MUID:93028552

A;Reference number: Advisor

A;Residues: preliminary; not compared with conceptual translation

A;Residues: 1-1180 < PRE>

A;Repensence extracted from NCB1 backbone (NCBIP:115851)

A;Note: sequence extracted from NCB1 backbone (NCBIP:115851)

A;Title: Molecular diversity in the adenylylcyclase family. Evidence for eight forms
A;Accession: Ad5145

A;Accession: Ad5145
A;Accession: Preliminary
A;Accession: Ad5145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Lowered responsiveness of the catalyst of adenylyl cyclase to stimulation by A; Reference number: A49201; MUID:93076707
                                                                                                                                                                                                                                                                                                             adenylate cyclase (EC 4.6.1.1) type V, calcium-inhibitable - mouse
C;Species: Mus musculus (house mouse)
C;Decies: P-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A49201; A4618
R;Premont, R.T.; Jacobowitz, O.; Iyengar, R.
Endocrinology 131, 2774-2784, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 15-93,'K', 95-463,'V',465-551,'G',553-803,'I',805-1180 <KRU>
A;Cross-references: GB:L01115; NID:9202712; PIDN:AAA40676.1; PID:9202713
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Matches 5; Conserv
                                            1 YRLAIXRIAL 10
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886 AVGRVALKY 894
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R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, P. Felenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Weese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaect A; Reference number: A69250; MUID:98049343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: C69460
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-469 < KLE>
A; Cross-references: GB: AE000987; GB: AE000782; NID: 92689310; PIDN: AAB89565.1; PID: 9264887
C; Superfamily: hypothetical protein MJ0966
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C.Species: Haemophilus influenzae
C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997
C.Accession: B64012
C.Accession: B64012
R.Fileschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.D.; Scott, J. Shirley, R.; Liu, L.I.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A.Authors: Grehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.Aritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A.Accession: B64012
A; Molecule type: DNA
A; Residues: 1-356 <GRO>
A; Cross-references: EMBL:X73525; NID:9404286; PID:9404293
A; Cross-references: EMBL:X73525; NID:9404286; PID:9404293
B; Chote: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
C; Genetics:
A; Gene: space
C; Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology
C; Keywords: transmembrane protein
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A;Cross-references: GB:U32752; GB:L42023; NID:91573692; PID:91573700; TIGR:HI0698
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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2; Mismatches
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Best Local Similarity 60.04
المالية وفي Si Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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A; Residues: 1-578 <TIGR>
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C;Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology C;Reywords: phosphorus-oxygen lyase F;333-568/Domain: guanylate cyclase catalytic domain.,homology <GCC>F;939-1178/Domain: guanylate cyclase catalytic domain homology <GCC>
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ö Gaps Ouery Match 57.4%; Score 31; DB 2; Length 1180; Best Local Similarity 55.6%; Pred. No. 1.38+02; Matches 5; Conservative 3; Mismatches 1; Indels 0;

4 AIXRIALRY 12 |: |:|:| 900 AVGRVALKY 908

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Search completed: February 7, 2000, 11:54:30 Job time: 24340 sec

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us-08-653-294-19.rsp

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Programme Company

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Search time 63.71 Seconds (without alignments) 5.625 Million cell updates/sec 8, 2000, 00:59:57 February Run on:

US-08-653-294-19 54 Perfect score:

1 YRLAIXRIALRY 12 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 segs, 29864866 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description						ιΩ		ທ	haemo	homo	mus m	caen	Q01341 mus musculu								-				P09284 varicella-z	P08922 homo sapien		P07618 vaccinia vi	P21083 vaccinia vi		Q9zcv4 rickettsia		$\sim$	P78382 homo sapien
SUMMAKIES		A	RL17_CHLTR	- 1	Y664_HAEIN	PYR1_SQUAC	BIOB_MYCTU	SPAS_SALTY	YD45_SCHPO	PRPR_SALTY	YTFM_HAEIN	MNT_HUMAN	MNT_MOUSE	YPD2_CAEEL	CYA6_MOUSE	CYA6_RAT	LMA3_MOUSE	RS15_BORBU	3DHQ_EMENI	UL38_HCMVA	HLAF_MACMU	PURA_MYCTU	YIGC_ECOLI	PRPR_ECOLI	LDHD_HAEIN	ATM1_YEAST	PRTP_VZVD	KROS_HUMAN	LMA_DROME	VJ05_VACCV	VJ05_VACCC	VJ05_VARV	PTH_RICPR	NH10_YEAST	STRF_STRGR	CMST_HUMAN
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2; Indels

Score 34; DB 1; Length 122; Pred. No. 1.3; 3; Mismatches 7; Indels

Query Match 63.0%; Best Local Similarity 54.5%; Matches 6; Conservative 5

2 RLAIXRIALRY 12 |||: |: :|| 45 RLAVGRLMVRY 55

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HRMA. Pseudomonas syringae (pv. syringae). Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.

HRMA\_PSESY
1D HRMA\_PSESY STANDARD; PRT; 375 AA.
AC 008370;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DF HRMA PROTEIN.

SCORPETERS

P13750 pan troglod P30379 gorilla gor P30380 gorilla gor P30381 gorilla gor P10317 homo sapien P30487 homo sapien P30489 homo sapien P30490 homo sapien P30491 homo sapien P18465 homo sapien P18465 homo sapien		AA.	.e.) late)	Chlamydia.		R.U., COFFIN J.M., KAUL R.; the subunit: sequence and	OF RIBOSOMAL PROTEINS.	produced tics and ere are	. Usage by and for commerc http://www.isb-sib.ch/annour	.RC32;
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папапапапа				hlar	.; ;;	REMACHA RNA po	010	cop	int ise	, L17; 9 MW;
88888888888888888888888888888888888888		STANDARD;		trachomatis. Chlamydiales; C	A. SEROVAR L2	)2. W.M., REM nomatis RN	.s."; 2594-26 LONGS I	OT entry is copyright. It Swiss institute of Bioinfo Bloinformatics Institute. Profit institutions as lo	and this statement is not removed requires a license agreement (See in email to license@isb-sib.ch).	L33834; AAA74990.1; E: PSO1167; RIBOSOMAL_L PF01196; Ribosomal_L17; omal protein. ICE 122 AA; 13969 MW;
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00000000000000000000000000000000000000	•	JT 1 CHLTR RL17_CHLTR	10-FEB-1996 (Rel. 33, 01-FEB-1996 (Rel. 33, 15-DEC-1998 (Rel. 37, 50S RIBOSOMAL PROTEIN	Q. amydia teria;		MEDLINE; 95247702. GU L.J., WENMAN W.M., REMACHA M., MEU! "Chlamydia trachomatis RNA polymerase	structural analysis."; J. Bacteriol. 177:2594-2601(1995). -!- SIMILARITY: BELONGS TO THE L17P FAMILY	This SWISS-PROT entry between the Swiss Ins the European Bloinform use by non-profit i	ified ities send a	EMBL; L33834; AAA74990.1; PROSITE; PS01167; RIBOSOMAL_L17 PFAM; PF01196; Ribosomal_L17; 1 Ribosomal protein. SEQUENCE 122 AA; 13969 MW;
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091437;
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                                                                                                                              STRAIN-PSS61;
MEDLINE; 94100578.
HEUS., HUTCHESON S.W.;
Nucleotide sequence and properties of the hrmA locus associated with
"Nucleotide sequence and properties of the hrmA locus associated with
the Pseudomonas syringae pv. syringae 61 hrp gene cluster.";
Mol. Plant Microbe Interact. 6:553-564(1993).
-: FUNCTION: UNKNOWN. MAY SERVE A REGULATORY FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                    HUANG H.C., HUTCHESON S.W., COLLMER A.; "Characterization of the hrp cluster from Pseudomonas syringae pv. syringae 61 and TnphoA tagging of exported or membrane-spanning Hrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN H10664.
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58.3%; Pred. No. 7.3;
iive 1; Mismatches 4
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                                                                                         Mol. Plant Microbe Interact. 4:469-476(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence and tissue-specific expression of the multifunctional protein carbamoyi-phosphate synthetase-aspartate multifunctional protein carbamoyi-phosphate synthetase-aspartate transcarbamoyiase-dihydrocrotase (CAD) mRNA in Squalus acanthias."; J. Biol. Chem. 270:14130-14139(1995).
-:-FONCTION: THIS PROTEIN IS A "FUSION" PROTEIN ENCODING FOUR ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASE, CPSASE, ATCASE AND DHOASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CAD PROTEIN (INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE
SYNTHASE (EC 6.35.5); ASPRATATE CARBAMOYLTRANSFERASE (EC 2.1.3.2);
DIHYDROOROTASE (EC 3.5.2.3)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squaliformes; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- PATHWAY: FIRST TO THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
-:- SUBUNT: HOMOHEXAMER.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- TISSUE SPECIFICITY: PRESENT IN THE TESTIS BUT NOT IN THE LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: 2 ATP + GLUTAMINE + CO(2) + H(2)O = 2 ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTROLLED
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                                                                                                                                                                                                                                             PROSITE: PS00211; ABC_TRANSPORTER; FALSE_NEG.
PFAM; PF00005; ABC_tran; 1.
PFAM; PF00664; ABC_membrane; 1.
TRANSMEM 2.
TRANSMEM 2.
TRANSMEM 52 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: DHOASE ACTIVITY REQUIRES A ZINC ATOM.
ENZYME REGULATION: ALLOSTERICALLY REGULATED AND CONTROLL
PHOSPHORYLATION. PRPP IS AN ACTIVATOR WHILE UMP IS AN IN
OF THE CPEASE REACTION (BY SIMILARITY).
PATHWAY: FIRST TO THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORTHOPHOSPHATE + GLUTAWATE + CARBAMOYL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
C2D5CD9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                           42 PC 159 PC 159 PC 182 PC 223 PC 298 PC 61293 MV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=TESTIS, AND SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 70.v.
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METAL
SEQUENCE
                                                                                                                 SECUENCE
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SPAS_SALTY
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                  CPSASE (CARBAMOYL-PHOSPHATE SYNTHASE)
CPSASE A.
CPSASE B.
DHOASE (DIHYDROOROTASE)
MISCELLANEOUS: GATASE (GLUTAMINE AMIDOTRANSFERASE) AND CPSASE (CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE GLUTAMINE-DEPENDENT CPSASE (GD-CPSASE) (EC 6.3.5.5).
SIMILARITY: THE CESASE DOMAIN IS SIMILAR TO OTHER CPASES; THE DHOASE TO OTHER DHOASES.
                                                                                                                                                                                                                                                                     PFAM: PF001203; Creace, Lchain; 2.
PFAM: PF00744; Dihydrooratase; 1.
PFAM: PF00988; Cresse_sm_chain; 1.
Pyrimidine biosynthesis; Ligase; Transferase; Hydrolase; Zinc; Allosteric enzyme; Multifunctional enzyme; Phosphorylation.
DOMAIN 1 365
                                                                                                                                                                                                                                                                                                                                                                                                     ATCASE (ASPARTATE TRANSCARBAMYLASE).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
ZINC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                  SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-1 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
BIOD OR RV1589 OR MTCX336.15C
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C (POTENTIAL).
9F38F825 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB ;
Pred. No. 84;
2; Mismatches
                                                                                                                                                                                    PROSITE: PS00097; CARBAMOXITRANSFERASE; 1. PROSITE; PS00442; GATASE_IYPE_I; 1. PROSITE; PS00443; DIHYDROOROTASE_I; 1. PROSITE; PS00483; DIHYDROOROTASE_2; 1. PROSITE; PS00866; CPSASE_1; 2. PROSITE; PS00867; CPSASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                             LINKER.
                                                                                                                                                                                                                                                                                                                                           LINKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.3%;
50.0%;
                                                                                                                                                                    EMBL; U18868; AAA74569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
                                                                                                                                                                                                                                                      PFAM; PF00117; GATase; 1. PFAM; PF00185; OTCACE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLAIXRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=H37RV;
MEDLINE; 98295987.
                                                                                                                                                                                                                                                                                                                                                                                                                                    338
1478
1480
2242
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1797
1935
252
336
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006601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLE S.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
SEQUENCE
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
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DOMAIN
DOMAIN
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
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BIOB_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                       s:
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GROISMAN E.A., OCHMAN H.;
GROISMAN E.A., OCHMAN H.;

"COGNATE gene clusters govern invasion of host epithelial cells by salmonella typhimurium and shigella flexneri.";

EMBO J. 12:3779-3787(1993).

-I - FUNCTION: INVOLVED IN A SECRETORY PATHWAY RESPONSIBLE FOR THE SURREACE PRESENTATION OF DETERMINANTS NEEDED FOR THE ENTRY OF SALMONELLA SPECIES INTO MAMMALIAN CELLS.

-I - SUBCELLIGAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F.,
BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
BADYLES R., DEVLIN K., FELTWELL T., CENTLES S., HAMLIN N., HOLROYD ;
HORNESE Y., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L.,
OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
RUTTER S., SEBGERK K., SKELTON S., SQUARES S., SQARES R., SULSTON J
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=PASTEUR;
YU S., JACOBS W.R., JR.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: DETHIOBLOTIN + (S) = BIOTIN.
-!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
-!- PATHWAY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1; Length 349;
Pred. No. 19;
; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1ron-sulfur; Transferase.
1ron-sulfur; Transferase.
1son-Sulfur (POTENTIAL).
1son-Sulfur (POTENTIAL).
1ron-sulfur (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
SURFACE PRESENTATION OF ANTICENS PROTEIN SPAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31B0B9DA CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 AA; 37550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 295586; CAB09080.1; -. EMBL; AF041819; AAB96962.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%;
50.0%;
                                                                                                                                                                                                                                                                                                 Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotin biosynthesis;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAS_SALTY
P40702;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                              01-NOV-1997 (Rel. 35, Greated)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROPIONATE CATABOLISM OPERON REGULATORY PROTEIN.
                       STANDARD
                                                                                                                                                                            Salmonella typhimurium
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription
                                                                                                                                                                                                                           Salmonella.
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9
                       PRPR_SALTY
                                                                                                                                                                                                                                                                                            STRAIN-LT2
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SEQUENCE
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                                         P74839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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YTFM_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                       SOT THE TRANSPORT OF TH
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 50.5 KD PROTEIN C22H10.05C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
19;
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
26881BE1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 120 ATP (POTENTIAL).
456 AA; 50449 MW; 11934D38 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB Pred. No. 19; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                  EMBL, X73525; CAA51927.1; -.
PIR, S37356; S37356.
STYGENE; SG10471. SPAS.
PFAM; PF01312; Bac_export_2; 1.
Virulence: Transmembrane; Inner membrane.
TRANSMEM 29 49 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; ATP-binding. NP_BIND 113 120 ATP ()
                                                                                                                                                                                                                                                                                                                                                                                40093 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 269730; CAA93606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLAIXRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ||: | |:|
70 YSLAVFGIGLKY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 YKLSLSRLAL 214
                                                                                                                                                                                                                                                                                                                                                                              356 AA;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLAIXRIAL 10
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Q10299;
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TRANSMEM
TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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STRAINS—172;
MEDLINE: 97158691.
HORSWILL A.R., ESCALANTE-SEMERENA J.C.;
FORCH on the scampeling of scattering of the sigma-54 family of activators, and the encodes a member of the sigma-54 family of activators, and the prpROTE genes constitute an openon.";
J. Bacteriol. 179:928-940(1997).
INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF THE PROFIGNATION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF THE PROFIGNATION: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; DNA-binding; ATP-binding.
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY); 298D809F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STYGENE; SG7777; PRPR.
PROSITE; PS00675; SIGMA54_INTERACT_1; FALSE_NEG.
PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
PROSITE; PS00688; SIGMA54_INTERACT_4; 1.
PROSITE; PS00045; SIGMA54_INTERACT_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 1;
Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE ABEIN STANDARD; PRT; 578 AA. P44038; 01-NOY-1995 (Rel. 32, Created) 01-NOY-1995 (Rel. 32, Last sequence update) HYPOTHETICAL PROTEIN HI0698 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U51879; AAC44813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.08;
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Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 YRLSILRLTL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLAIXRIAL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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MEDLINE; 95350630
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RESULT

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FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERRACK T.R., HANNON M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ಥ
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MEDLINE: 97327566.
MEDLINE: 97327566.
MEDLINE: 97327566.
MEDLINE: DAILOND A., ALCALAY M., BORSANI G., TANIGAMI A.,
TONLORENZI R., LO NIGRO C., MESSALI S., ZOLLO M., LEDBETTER D.H.,
BRENT R., BALLABIO A., CARROZZO R.;
"Rox, a novel bilihizip protein expressed in quiescent cells that
"Rox, a novel bilihizip protein expressed in quiescent cells that
hetroclimerizes with Max, binds a non-canonical E box and acts as
transcriptional repressor.";
EMBO J. 16:2892-2906(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 49:275-282(1998).
-!- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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CAINARCA S., ENRICO F., STACK M., LEDBETTER D.H., LISCIA D.S.,
BALLABIO A., CARROZZO R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}."\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)
MNT OR ROX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN H10698.
8FCD6AF9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 1;
Pred. No. 32;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 AA.
                                                                                                                                                                                                                                                                                                                                                                Science 269.496-512(1995).
-!- SIMILARITY: STRONG, TO E.COLI YIFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65812 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32752; AAC22357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
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147 YKTAISRLAL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HI0698;
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                                                                                                                                                                                                                                                                        VENTER J.C.;
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Q99583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
5'-CACGTG-3' AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.
SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MERONI G., REYMOND A., ALCALAY M., BORSANI G., TANICAMI A.,
TONLORENZI R., IO NIGRO C., MESSALI S., 20LLO M., LEDBETTER D.H.,
BRENT R., BALLABIO A., CARROZZO R.;
BRENT R., BALLABIO A., CARROZZO R.;
heterodimerizes with Max, binds a non-canonical E box and acts as a
transcriptional repressor.";
EMBO J. 16:2892-2906(1997).
-!- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE 5'-CACGTG-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97152466.

HURLIN P.J., OUEVA C., EISENMAN R.N.;

"Mnt, a novel Max-interacting protein is coexpressed with Myc in proliferating cells and mediates repression at Myc binding sites."; Genes Dev. 11:44-58(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; Repressor; Nuclear protein; DNA-binding. 22 233 BASIC MOTIF (POTENTIAL). 34 270 HELIX-LOOP-HELIX MOTIF (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus muscilus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNT_MOUSE STANDARD; PRT; 591 AA.
008789; 997349;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).
MNT OR ROX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 1; Length 582;
Pred. No. 32;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUCINE-ZIPPER.
4ED96BBF CRC32;
                                                                                                                                                                                                                                                                                                                             JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                        EMBL; X96401; CAA65265.1; -.
EMBL; X13440; CAA73851.1; -.
EMBL; X13441; CAA73851.1; JOINED.
EMBL; X13442; CAA73851.1; JOINED.
EMBL; X13444; CAA73851.1; JOINED.
EMBL; X13444; CAA73851.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 II
62299 MW;
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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MEDLINE; 97327566.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription
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SEQUENCE
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PROSITE;
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MNT_MOUSE
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Hypothetical protein. SEQUENCE 833 AA; 9
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CYA6_MOUSE
ID CYA6_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                on regulation; Repressor; Nuclear protein; DNA-binding.
224 235 272 HELIX-LOOP-HELIX MOTIF (POTENTIAL).
236 272 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
273 301 LEUCINE-ZIPPER (POTENTIAL).
379 379 T -> P (IN REF. 2).
402 403 EE -> QQ (IN REF. 2).
414 414 G -> A (IN REF. 2).
431 431 V -> A (IN REF. 2).
455 465 A -> P (IN REF. 2).
555 555 G -> A (IN REF. 2).
558 558 G -> A (IN REF. 2).
551 AA; 63311 MW; 16BADBA6 CRC32;
         SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX. SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 93.8 KD PROTEIN COSDIL.2 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 WITH HIGHER AFFINITY, TO 5'-CACGCG-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                     EMBL; Y07609; CAA68878.1; -.
MGD; MGI:109150; MNT.
PROSITE; PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              833 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No.
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60.0%;
                                                                                                                                                                                       EMBL; U77356; AAB38687.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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-!- SIMILARITY: WEAK, TC
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                                                                                                                                                                                                                                         PFAM; PF00010; HLH; 1.
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260 LSVLRTALRY 269
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Best Local Similarity
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                                                                                                                                                                                                                                                      Transcription
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DOMAIN
CONFLICT
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YPD2_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOSHIMURA M., COOPER D.M.F.; "CLoning and expression of a Ca(2+)-inhibitable adenylyl cyclase from NCB-20 cells.";
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: MOST ABUNDANT IN HEART BUT WEAKLY DETECTABLE.
IN BRAIN, INTESTINE, LUG, AND SPLEEN.
-:- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-:- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
10-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENVLATE CYCLASE, TYPE VI (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(CA(2+)-INHIBITABLE ADENYLYL CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE, 93076707.

PREMOUT R.T., JACOBOWITZ O., IYENGAR R.;

"Lowered responsiveness of the catalyst of adenylyl cyclase to "Lowered responsiveness of the catalyst of adenylyl cyclase to stimulation by GS in heterologous desensitization: a role for adenosine 3',5'-monophosphate-dependent phosphorylation.";

Endocrinology 131:2774-2784(1992).

-i- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
-!- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR
CONCENTRATION RANGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; cAMP synthesis; Transmembrane; Glycoprotein; Duplication.
DOMAIN 1149 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                ö
                                                                                           Length 833;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 89:6716-6720(1992)
                                                                                           Score 31; DB 1;
Pred. No. 48;
508777F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1165 AA.
                                                                                                                                                            0; Mismatches
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PROSITE; PS00452; GUANYLATE_CYCLASES; 2.
PFAM; PF00211; guanylate_cyc; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
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93791 MW;
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EMBL; M96653; AAA37182.1; -.
PIR; A46187; A46187.
                                                                                               57.4%;
70.0%;
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Best Local Similarity
T; Conserve
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STRAIN-BALB/C; TISSUE-LUNG;
MEDLINE; 95394944.
MEDLINE; 95394946.
ABERDAM D., AGUZZI A., ORTONNE J.-P., MENEGUZZI G.;
"Cloning and complete primary structure of the mouse laminin alpha 3 chain. Distinct expression pattern of the laminin alpha 3A and alpha 3B chain isoforms.";
J. Biol. Chem. 270:21820-21826(1995).
                                                                                                                  EMBL; L01115; AAA40676.1; -.
EMBL; L01115; AA440678.1; ALT_INIT.
PIR; A45145; A45145.
HSSP: P19754; LAW.
HSSP: P19754; LAW.
PROSITE; P500452; GUANYLATE_CYCLASES; 2.
PRAM; PF00211; guanylate_CyC; 2.
Lyase, CAMP synthesis; Transmembrane; Glycoprotein; Duplication.
Lyase, CAMP synthesis; Transmembrane; Glycoprotein; Duplication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.4%; Score 31; DB 1; Length 1166;
55.6%; Pred. No. 69;
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ABERDAM D.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
K -> E (IN REF. 2).
K -> A (IN REF. 2).
G -> A (IN REF. 2).
I -> L (IN REF. 2).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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Best Local Similarity
Matches 5; Conserv
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886 AVGRVALKY 894
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LMA3_MOUSE
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-!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93028552.

PREMONT R.T., CHEN J., MA H.-W., PONNAPALLI M., IYENGAR R.;

Two members of a widely expressed subfamily of hormone-stimulated adenyly1 cyclases.";

Proc. Natl. Acad. Sci. U.S.A. 89:9809-9813(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADBWYLATE CYCLASE, TYPE VI (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
(CA(2+)-INHIBITABLE ADENYLYL CYCLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WATSON P.A.; "Molecular diversity in the adenylylcyclase family. Evidence for "Molecular diversity in the adenylylcyclase family. Evidence for eight forms of the enzyme and cloning of type VI."; J. Biol. Chem. 267:24858-24862(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL. CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
-!- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR CONCENTRATION RANGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 93077589.
KRUPINSKI J., LEHMAN T.C., FRANKENFIELD C.D., ZWAAGSTRA J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                              POTENTIAL.
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                          (POTENTIAL)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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69;
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Pred. No. 69;
3; Mismatches
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                                                          CYTOPLASMIC POTENTIAL.
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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"Developmental expression of nicein adhesion protein (laminin-5)

"Underelopmental expression of nicein adhesion protein (laminin-5)

"Underelopmental expression of nicein adhesion protein (laminin-5)

"Is ubunits suggests multiple morphogenic roles.";

cella Adhes. Commun. 2:165-129(1994)

"Is THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF

CELLS INTO TISSUES DURING EMBRYONIC DEPUEDMENT BY INTERACTING

WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

"IN THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION (I CELL ADHESION

"VA INTEGRIN ADPHA-3 PERTA-1 IN POCAL ADHESION AND INTEGRIN ALPHA-6/BETA-4 IN HEMIDESMOSOMES, (2) SIGNAL TRANSDUCTION VIA TYROSINE

PHOSPHORYLATION OF PP125-FAX AND P80, (3) DIFFERENTIATION OF

KERATINOCYTES (BY SIMILARITY).

"IN EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE

COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

THE ALPHA-3 CHAIN IS A SUBBNIT OF LAMININ-5 (EPILIGRIN/KALININ/

AND LAMININ-7 (KS-LAMININ).

"IN ELIN AND POSSIBLY ALSO A COMPONENT OF LAMININ-6 (K-LAMININ)

"IN THEIR N-TERRIATIVE PRODUCTS: THE TWO ISOFORMS A AND B, WHICH DIFFER

IN THEIR N-TERRIATAL ARE DERIVED BY ALTERNATIVE SPLICING OF THE

"IN THEIR N-TERRIANAL ARE DERIVED BY ALTERNATIVE SPLICING OF THE

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"IN THEIR N-TERRIANAL AND THE BASEMENT THE LARGER ISOFORM
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or send an email to license@isb-sib.ch).
                                                                                                     SEQUENCE OF 1052-1770 FROM N.A.
TISSUE-LUNG;
MEDILNE; 94363405.
ABERDAM D., AGUZZI A., BAUDOIN C., GALLIANO M.-F., ORTONNE J.-P.
MENEGUZZI G.;
                                              ABERDAM D., GALLIANO M.-F., MATTEI M.-G., PISANI-SPADAFORA A. ORTONNE J.-P., MENEGUZZI G.; "Assignment of mouse nicein genes to chromosomes 1 and 18."; Mamm. Genome 5:229-233(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:99909; LAMA3.
PROSITE; PSO0022; EGF_1; 4.
PROSITE; PSO1186; EGF_2; 1.
PROSITE; PSO1248; LAMININ_TYPE_EGF; 4.
PFAM; PF00052; laminin_B; 1.
PFAM; PF00053; laminin_EGF; 4.
PFAM; PF00054; laminin_G; 2.
[3]
SEQUENCE OF 1052-1770 FROM N.A.
TISSUE-LUNG;
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                                      MEDLINE; 94281750.
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MISSING (IN ISOFORM A).

MYDPRLERKHIRGHFTEORLIGEVGLEBASDTGSGPR
AHLVENGACPPDYTGDSC -> MLPAVRWSAWSTGKLWIFG
AALGOCLGYGSEOORVAFLORPSONHLOASYMELRPS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 X LAMININ EGF-LIKE REPEATS (DOMAIN III
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-11ke domain; Cell adhesion; Repeat; Signal; Alternative splicing.

NON_TER 1 1 1 1 28 POTENTIAL.

CHAIN 29 2569 LAMININ ALPHA-3 CHAIN.
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LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 6
LAMININ EGF-LIKE 7 (INCOMPLETE).
DOMAIN II AND I (HEPTAT REPEATS).
5 X LAMININ G-LIKE REPEATS (DOMAIN G).
LAMININ G-LIKE 1.
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CELL ATTACHENT SITE (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                 3.5 X LAMININ EGF-LIKE REPEATS.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4 (N-TERMINAL).
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INTERCHAIN (PROBABLE).
POTENTIAL.
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LAMININ ALPHA-3 CHAIN.
DOMAIN IV''.
DOMAIN III B.
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LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
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Gaps ; 0 Query Match

57.4%; Score 31; DB 1; Length 2569;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels

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SERAIN-ER-15;
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PAITAN Y., ORR E., RON E.Z., ROSENBERG E.;
"Genetic and functional analysis of genes required for the post-
modification of the polyketide antibiotic TA of Myxococcus xanthus.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132503: CAB46503.1;
SEQUENCE 325 AA; 35985 MW; 4CC64E85 CRC32;
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01-NOY-1996 (TrEMBLrel. 01, Created)
01-NAY-1999 (TrEMBLrel. 12, Last annotation update)
10-NOY-1999 (TrEMBLrel. 12, Last annotation update)
10-NOY-1999 (TrEMBLrel. 12, Last annotation update)
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Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q22063 caenorhabd1
Q8xeg1 gossyplum h
Q8xeg1 gossyplum h
Q8414 chlamydia t
Q84259 chlamydia p
Q84015 chlamydia p
Q84015 chlamydia t
C86606 streptomyce
P73400 synechocyst
O54741 mus musculu
O57313 aquifex aeo
Q88633 sphingomona
Q23555 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogyges oncorpyrchu
094545 schizosacch
P91495 caenorhabdi
06920 azotobacter
0923x8 pseudomonas
P76343 escherichia
                                                                               (without alignments)
3.980 Million cell updates/sec
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                                                                     ; Search time 209.03 Seconds
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
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sp_organelle:*
sp_phage:*
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sp_bacteria:*
sp_fungi:*
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seq length: 1000000
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DADLINE; 98295987.

MEDLINE; 98295987.

MEDLINE; 98295987.

GOLG S.T., BROSCH R., GAS S., BARRY III C. E., TEKAIA F., GONDON S.V., EIGLMEIER K., GAS S., BARRY III C. E., TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVILIN K., FREITWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNESY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., CLIVER S., SEEGER K., SKELTON S., SQUARES S., SOARES T., SULSTON J.E., TAYLOR K., WHITEHEAD S., BARRELL B.G.;

"Deciphering the blology of Mycobacterium tuberculosis from the complete genome sequence.";

"Ature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                           STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V., DAVIS R.W.;
Sequence of an Obligate Intracellular Pathogen of Humans: a trachomatis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL008967; CAA15591.1; -.
HSSP; P33164; 2PIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
HYPOTHETICAL 33.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2;
Pred. No. 19;
                                                                                                                                                                                                                                                                                  Score 34; DB 2;
Pred. No. 8.3;
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309 AA; 33517 MW; B152B590 CRC32;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                   63.0%;
54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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64 RLAVGRLMVRY 74
                               Science 0:0-0(1998)
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SEQUENCE 3(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=D/UW-3/CX;
STEAHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
DAVIS R.W.;
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                            WILD A.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases. EMBL; 281061; CAB02939.1; -. EMBL; 278413; CAB01697.1; -. EMBL; 281061; CAB01667.1; -. EMBL; 281061; CAB01667.1; JOINED. HSSP, P19491; 1GR2. PPFM; PF00060; 119_chan; 1. SEQUENCE 795 AA; 89703 MW; DD722166 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF085717; AAD25952.1; -.
SEQUENCE 1899 AA; 218627 WW; E695145F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE CALLOSE SYNTHASE CATALYTIC SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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                                                                                                                                                                                                                      Score 35; DB
Pred. No. 31;
3; Mismatches
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ilarity 63.6%; Pred. No. 7
Conservative 2; Mismatch
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
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50.0%;
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Best Local Similarity
Lac 6; Conserve
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Best Local Similarity
Matches 7; Conserv
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                               SEQUENCE FROM N.A.
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RESULT Q927S9

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SEQUENCE FROM N.A.
STRAIN=PCC6803;
MEDLIES; 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
KANEKO I., SATO S., KOTANI H., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI I., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINSHI H., HOPWOOD D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coellicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL, ALO31155; CAA20068.1;

SEQUENCE 310 AA; 33156 MW; 5AD2CED4 CRC32;
                                                                                                                                                                                                                                                                      Streptomyces coellcolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.3%; Score 32; DB 2; Length 310; 63.6%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
OLIVER K., HARRIS D.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ABC TRANSPORTER.
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Last annotation update)
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                              PRELIMINARY;
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249 RLAVFRWATRY 259
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83 RLALSRIRLR 92
                 2 RLAIXRIALR 11
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MEDLINE; 97000351
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STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                            KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L., GENMWOOD J., DAYLS R.W., STEPHENS R.S.;
"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
- SIMLARITY: BELONGS TO THE LITP FAMILY OF RIBOSOMAL PROTEINS.
EMBL; AEOOL647; AADL9676.11;
- PROSITE; PS01167; RIBOSOMAL_L17; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
Science 0:0-0(1998).
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EMBL; AE001276; AAC67602.1; -.
Hypothetical protein
SEQUENCE 264 AA; 29971 MW; COAD12DB CRC32;
                                                                                                                                                                                                                   RL17.
Chlamydia pneumoniae.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                              Last sequence update)
Last annotation update)
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01-NOV-1998 (TIEMBLrel. 08, Last sequence update)
01-NOV-1998 (TIEMBLrel. 08, Last annotation update)
HYPOTHETICAL 30.0 KD PROTEIN.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Pred. No. 14;
3; Mismatches
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Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AA; 16400 MW; 4839EC84 CRC32;
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                                                                                                                                            Created)
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Best Local Similarity 70.0%; Pr
Matches 7; Conservative 1;
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54.5%;
                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12, 50S RIBOSOMAL PROTEIN L17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                        PRELIMINARY;
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64 RIAIGRLMVRY 74
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein.
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65 YRIAIRRIA 73
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ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENSEN C.W., GARSTERLAND T., SAFFER J.D., FREDRICKSON J.K.;
"Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans strain F199.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFC)317; AAD03868.1;
Hypothetical protein; Jessmid 40CDF9F4 CRC32;
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01-JAN-1998 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE SERINE PROTEASE-LIKE PROTEIN.
DL4585C.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Virialplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                            DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAX M., HUBER FELDMAN R.A., SHORT J.M., OLLSON G.J., SWANSON R.V.; SHORT J.M., OLLSON G.J., SWANSON R.V.; SHORT J.A., OLLSON G.J., SWANSON R.V.; HUBER (JUL-1997), to the EMBL/GenBank/DDBJ databases. Hypothetical protein.

Hypothetical protein.

EFBGIENCE 190 AA: 22041 MW; EFBGIF50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pNL1.
Bacteria; Proteobacteria; alpha subdivision; Zymomonas group;
Sphingomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%; Score 31; DB 2; Length 243; 54.5%; Pred. No. 63; 1.1ve 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; Length 190;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel: 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 26.5 KD PROTEIN.
Sphingenonas aromaticivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.5.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.4
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                   Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| |::||
5 RLAQRRVTIRY 15
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43 HNLAIQKVALR 53
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085853
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023555
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                                                                                                                                                                                                                                                                                                                                                                Gaps
                                        Sequence, analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90906; BAA17440.1; -. HSSP; P13569; INBD.
PFAM; PF00064; ABC_membrane; 1.
SEQUENCE 610 AA; 67028 MW; 835D2045 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 97400527.
FERRIGNO O., VIROLLE T., GALLIANO M.F., CHAUVIN N., ORTONNE J.P.,
MENEGUZZI G., ABENDAM D.;
"Murine laminin alpha3A and alpha3B isoform chains are generated by
usage of two prompters and alternative splicing.";
J. Blol. Chem. 272:20502-20508(1997).
EMBL; Y08850. CAA70073.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 11; Length 42;
Pred. No. 10;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           Length 610;
                                                                                                                                                                                                                                                                                                                                                              2; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
LAMININ, ALPHA 3 (LAMININ 5 ALPHA3C CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 22.0 KD PROTEIN.
                                                                                                                                                                                                                                                                                                         Score 32; DB 2;
Pred. No. 1e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aquifex aeolicus.
Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AA; 4872 MW; 42FE6150 CRC32;
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                                                                                                                                                                                                                                                                                                           Query Match 59.3%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 RLAIARAAMR 517
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           2 RLAIXRIALR 11
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22 LSLFRIVLRY 31
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SEQUENCE
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054741
ID 054741
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Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                       MEDLINE; 99132290.
BRUNELLI J.P., THORGARD G.H.;
BRUNELLI J.P., THORGARD G.H.;
Sequence, expression and genetic mapping of a rainbow trout retinoblastoma cDNA.";
Gene 226:175-180(1999).
EMBL: AF102861; AAD13390.1; -.
                              Q9YGE5;
01-MAY-1999 (TFEMBLrel. 10, Created)
01-MAY-1999 (TFEMBLrel. 10, Last sequence update)
01-NOV-1999 (TFEMBLrel. 12, Last annotation update)
RETINOBLASTOMA 1.
                                                                                                                                                                                                                                                                                                                                       910 AA; 103531 MW;
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Best Local Similarity 50.0
Matches 6; Conservative
                PRELIMINARY;
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KETCHUM K.A., DODSON R.J., GWINN M., HICKEY EW., PETERSON J.D.,
RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., OUGACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENDEY K., ADAMS M.D., LOFFUS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W. D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
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                            SEQUENCE FROM N.A.
BEVAN M., STIEKENA W., MURPHY G., WAMBUTT R., POHL T., TERRYN N.,
KREIS M., KAVANGH T., ENTTAN K.D., RIEGER M., JAMES R.,
PUIGDOMENECH P., HATZOPOULOS P., OBERWAIER B., DUESTERHOFT A.,
JONES J., PALME K., ANSORGE W., DELSENY M., BANCROFT I., MEWES H.W.,
SULDMITTER C., CHALWATZIS N.;
SULDMITTER (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
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Pred. No. 1.3e+02;
1; Mismatches 4; Indels
                                                                                                                                                         SEQUENCE FROM N.A.
ED ARBIDOPSIS SEQUENCING PROJECT;
Submitted (2011.1999) to the EMBL/GenBank/DDBJ databases.
EMBL, 297342; CAB46052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 07, Last annotation update)
                                                                                                                                                                                                                                            9B2D1556 CRC32;
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SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE: 98049343.
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                                                                                                                                                                                                                                            407 AA; 46703 MW;
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469 AA; 53468 MW;
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368 YRLGNNRIALSF 379
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12 YRKGMKRIALVY 23
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Best Local Similarity
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01-JAN-1998 (
01-AUG-1998 (
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SEQUENCE 4
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Length 910; 4; Indels

Score 31; DB 13; Pred. No. 2.5e+02; 2; Mismatches 4;

57.4%;

CE74234B CRC32

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i AL121652 BAC sequence fro
i AC008810 Homo sapiens chr
i AL049831 Human chromosome
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LOCUS AC017966 8849 bp DNA HTG 09-DEC-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                        Three Drosophila melanogaster genes for transfer RNAs (Glu specific).
V00238 J01146
V00238.1 GI:8458
transfer RNA; transfer RNA-Glu.
                                                                                                                                                                                                                               fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Diptera; Brachycera; Muscomorpha; Ephydroidea;

Drosophilidae; Drosophila.

1 (bases 1 to 1050)

Hosbach, H.A., Silberklang, M. and McCarthy, B.J.

Evolution of a D. melanogaster glutamate tRNA gene cluster

Cell. 21 (1), 169-178 (1980)
 194430
214385
218956
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Gaps: 0
Percent Identity: 66.667
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464. :335
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262_.333
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2.3e+04
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/note="tRNA Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1050
 79.56
78.70
78.51
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Drosophila melanogaster
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AC017966.1 GI:6553224
HTG; HTGS_PHASE2.
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 36.00
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US-08-653-294-19 x DMRNA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_htg7:AC017966
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                                                                        seq_name: gb_in1:DMRNA3
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Ratio:
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 gb_pr2:CNS01DS2
gb_htg4:AC008810
gb_pr2:CNS00008
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AL035250 Human DNA sequence
AC009909 Drosophila melanoga
AC007807 Drosophila melanoga
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Homo sapiens chromo
Homo sapiens clone
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Homo sapiens clone
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Homo sapiens chromo
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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPCX=0.000 -GAPDP=4.500
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-OUTFWT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
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                                                                        About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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...2e+03
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                                                                                                                                                                                                                                                                                                                                                                                                      Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 11370.480000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block:
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                                    Date: Feb 8, 2000 4:43
                                                                                                                              Command line parameters:
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Query length: 12
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gb_ba1: WATO5666
gb_ba1: WATO5666
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57412
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61361
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 149304)

8 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Budota, B., Bouck, J., Brooks, A., Buhay, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
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Schen, R., Sandel, S., Sandel, S., Scherer, S., Shah, E.,
Schen, R., Sandel, S., Sandel, S., Scherer, S., Shah, E.,
Schen, M., Scherer, S., Sandel, S., Sand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster chromosome 3L/62Al clone RPC198-2701, ***
SEQUENCING IN PROGRESS ***, 89 unordered pleces.
AC010564 GI:5917942
HTG: HTGS_PHASE1.
                                                                                                                                    Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10212817 by the submitter. For more information on this record e-mail to fly@celera.com. * NoTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. 8849
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 8849) Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
| 1735 c 1884 g 2626 t
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Percent Identity: 66.667
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Direct Submission
Submitted (16-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
on Sep 22, 1999 this sequence version replaced gi:5916428.

* NOTE: This is a 'working draft' sequence. It currently
consists of 89 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                      831 bp in length
834 bp in length
835 bp in length
836 bp in length
848 bp in length
852 bp in length
853 bp in length
854 bp in length
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859 bp in length
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5469: C
6313: C
7273: C
8101: C
8941: C
11019: C
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Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K. R.H., Zhang, Park S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M. Sequencing of Drosophila chromosome JL, region 61F3-62A2 Unpublished (1997)

L. Unpublished (1997)

E. Chases I to 268369)

S. Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Baxter, E., Svirskas, R.R., Harris, N.L., Apdayani, A., Arcaina, T.T., Baxter, E., Slaragan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L., and Rubin, G.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Library locations: 11-34, 21-67, 44-36, 73-50, 92-76.
Location/Qualifiers
                                                                                                                                                                                                                                                                                            Submitted (22-007-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Pls 0283179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291 (D240)"
//note="These five Pls were completed as a project. The coordinateds are the pl ends for each Pl. DS03404 (D231)extends from bp 1 to bp 80,732. DS03179 (D226) extends from bp 32,734 to bp 117,954. DS06357 (D230) extends from bp 88,745 to bp 169,482. DS06562 (D232) extends from bp 197,117 to bp 209,427. DS07291 (D240) extends from bp 194,759 to bp 268,369."
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LOCUS MXA132503 4513 bp DNA BCT 01-JUL-1999
DEFINITION MYXCOCCUS Xanthus taB, taC, taD, taE and taF genes.
ACCESSION AJ132503.1 GI:5419951
KEYWORDS ACP synthase; acyl carier protein (ACP); membrane associated protein; taB gene; taC gene; taD gene; TaF gene.
SOURCE Myxcoccus xanthus.
ORGANISM Myxcoccus xanthus
Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="3L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="61F3-62A2
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US-08-653-294-19 x AC005847/rev
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Drosophila melanogaster (Subclones in tet from Pl clones DS03179
(D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291
(D240)) DNA.
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Drosophila melanogaster DNA sequence (Pls DS03179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291 (D240)),
AC005847 AC004331 AC004436 AC004488 AC004489
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 26836)
Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,
Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

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Percent Identity: 66.667
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/clone="RPC198-2701"
33523 c 32072 g 39042 t
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137892: contig of 5081
143914: contig of 6022
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LOCUS AC005847 2
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KEYWORDS
SOURCE
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Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
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Submitted (20-3NN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 25383)
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1 (bases 1 to 25383)
Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p DNA PRI 27-APR-199
clone U169D2 from Xp22.1-22.2, complete
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3 (bases 1 to 25383)
                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 12
Gaps: 0
Percent Identity: 58.333
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Genome Res. 8 (11), 1097-1108 (1998)
99063792
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                                                                          /note="TaF protein"
/codon_start=1
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Submitted (19-JAN-1999) D
University, 4444 Forest P
5 (bases 1 to 25383)
Waterston.R.
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4 (bases 1 to 25383)
Waterston, R.
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Homo sapiens cosmid cl
sequence.
U72788 U3:1575796
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/gene="taF"
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Waterston, R.
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/gene="taF"
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Direct Submission
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Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus. 1 (bases 1 to 4513)
Paitan,Y., Orr.E., Ron.E.Z. and Rosenberg,E. Genetic and functional analysis of genes required for the post-modification of the polyketide antibiotic TA of Myxococcus
                                                                                                                                                                    Direct Submission
Submitted (25-JAN-1999) Paitan Y., Molecular Microbiology and
Blotechnology, Tel Aviv University, G.S Wise Faculty of life
Siciences, Tel Aviv University, Ramat Aviv, 69978, ISRAEL
Location/Qualifiers
1. 4513
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Paitan, Y.
                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                      source
                                                                                                               JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                        TITLE
JOURNAL
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4.222
75.000
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US-08-653-294-19 x U72788
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
Direct Submission
Submitted (27-APR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Mashington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is from a chromosome X-specific cosmid library LLOXNCCO1 'U'. The source of the chromosomes was a human/hamster hybrid, GM07297-F, from Robert Nussbaum at the University of Pennsylvania School of Medicine. Please contact the Lawrence Livernore National Laboratory at http://www-bio.llnl.gov/genome to obtain the clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone was mapped by Grieff, M., Whyte, M. P., Thakker, R. V., and Mazzarella, R. Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX. Genomics 44:227-231 (1997).
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Location∕Qualifiers
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TITLE

COMMENT

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https://doce-representations.com/piessentity to Pasteurella
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B229_c3_246"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTISAVPGTIILAIETSCDETGVGIACLDDYGTVTLLADEVASS
VDEQARFGGVVPEIASRAHLEALGPTIRCALAAAGLTGSAKPDVVAATIGPGLAGALL
VGVAAAKAYSAAWGVPFYAVNHLGGHLAADVYEHGPLPECVALLVSGGHTHLLQVRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /traislation="Maeyslrsgavicervedtvalgsrlgeqlragdvvvlsgplga
GRTVLAKGIAVAMDVDGPVISPTYVLARVHLPRRLGTPAMIHVDVYRLLDHRDADLVG
ELDSLDLDTDLAEAVVVMEWGAGLAECLAARHLDIRLERVRYSDVRIATWQWVCSRDR
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                                  complement(3751. .4053)
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VARMMLTTETAVVDKPAKTEEHDHHGHAH"
complement(3751. .4053)
                                                                                                                                                        /product="chpa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA17310.1"
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                                                                                               /codon_start=1
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RUTUAGTDSERRADALIGIADALGYGRIAAARALTLRRVGASLAPAQLPAQYADRLAV
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RARVVAEAALAATGRLGLIPLRWALACLLIDIGSVTFSEPELSELP"
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REQRAKEMCRRCPVIEECRAHALDVGEPYGVWGGLSESERDLLLKGDLARSRSIPRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEGMNKVGTDGVVSVEESSTLDTELEFTEGVGFDKGFLSAYFVTDFDSQQAVLDDPLV 
LHOBKISSEDELLPMLEKVESGKPHLJVADBLDGBALATVVNSIKRTLKAYAVKS 
PFEGDRKRAFLEDLA IVTGGGVVNPETGLVLEEVGTDVLGSARRVVSKDDTITVDGG 
GSNDAVAKRVNQLRAEIEVSDSEWDREKLQERVAKLAGGVAVIKVGAVTETALKKRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MTSVSIVVEIGHTSAAEPMLAAAAFGNOPGRWPLPTATTPHQLW
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GPTITNDGVTVAREIDLEDPFENLGAQLVKSVATKTNDVAGDGTTTATVLAQALVKGG
LRMVAAGANPVALGAGISKAADAVSEALLAVATPVAGKDAITQVATVSSRDEQIGALV
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YWIATNAGLDGAVVVDKVSGLPAGHGLNASTLGYGDLVADGVVDPVKVTRSAVLNAAS
                                                                                         Mycobacterium.

1 (bases 1622 to 4514)

Rinke de Wit.T.F., Bekelie,S., Osland,A., Miko,T.L.,
Hermans,P.W.M., van Soolingen,D., Drijfhout,J.W., Schoeningh,R.,
Janson,A.A.M. and Thole,E.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-MAR-1994) Department of Genetics, Harvard Medical Submitted (10-MAR-1994) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
On Mar 31, 1994 this sequence version replaced gi:414226.
This sequence data was produced by the Genome Sequencing Center located at Collaborative Research Incorporated (1365 Main St., Maltham MA, 02159). 617-487-7979). Please contact Doug Smith (smith@cr.cric.com). The annotation should be considered preliminary and incomplete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-NOV-1993) Department of Genetics, Harvard Medical
School, 200 Longwood Avenue, Boston MA 02115
4 (Dases 1 to 36947)
                                                                                                                                                                                                                                           Mycobacteria contain two GroEl genes. The second Mycobacterium leprae GroEL gene is arranged in an operon with GroES Mol. Microbiol. 6, 1995-2007 (1992)
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Streptomyces coelicolor whiB); B229_F1_2"
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                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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1. .36947
Acoganisma-"Mycobacterium leprae"
Ab_xref-"taxon:1769"
Complement(1. .791)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
3 (bases 1 to 36947)
Robison, K.
                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 36947)
Smith, D.R.
      Mycobacterium leprae
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   ORGANISM
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complement(<1.
/gene="ansP"
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                                                                                                                                      Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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LADVQIAVSSVRQLDELLDAVRRTGRTATVTVKADTGLNRNGVVTDQYPAMLTALQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'translation="MSWPSLSATFTGELEPVAELCVALDKLAADNGLDIAVSVGAASG'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAETFDKTCLDKDEYPAAAPSNGAAYSMATGLYSRLGTQLRQPV
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MCDB533 40245 bp DNA BCT 27-AUG-1999
LOCUS
MCDB5330 40245 bp DNA B2533.

ACCESSION AL035310

VERSION AL035310 GI:4200258

KEYWORDS ansp: ATP-dependent RNA helicase; ATP-phosphoribosyl transferase;
ATPASAS; hisG 5-methyltetrahydrofolate-homocysteine methyl transferase; hisi: L-asraragine permease; meth; mttb;
                                                                                                                                                                                                                                                                                                                                                                                                      /note="Glutamate decarboxylase isozyme; B229_C2_202"
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Gaps: 0
Percent Identity: 72.727
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subunit proteasone beta subunit; protein translocation system; yecobacterium legrae.

Mycobacterium legrae.

Mycob
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AAFEGWNDASDAASGALEHLNAVWEADPIVEIDDEAYYDYQVNRPVIRQVDGVTRELV
WPAMRISYCRPPGSDRNVVLMHGVEPNMRWRTFCTELLIIADRLNVDTVVILGALLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYVSHPPNPKATVALLRRVEDVLDVEVPLADLPTQAEDWEGAITEIAAEDDELAEYVH
SLEGRGDAEVDVNDALGKIDGDALAAEFERYLRRRRPGFGR"
4004. .7555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:049797"
/translation="MPPHRAVTRHASSSALKPYADSVTLRDGGPDRGALPELHNTVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to M.tuberculosis Mpothetical protein 317 ad

Similar to M.tuberculosis Mpothetical protein R2125

(MTCY261.21) (EMBL:297559) (292 aa), fasta scores; opt:

1648 z-score: 2382.2 E(): 0, 84.1% identity in 290 aa

overlap. Also some similarity to M.leprae hypothetical

protein TR:Q49847 (29.7% identity in 279 aa overlap).

Annotated as ORF TR:Q49797, hypothetical protein in

M.leprae cosmid EMBL:U00017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MLCB2533.04, metH, probable
5-methyltetrahydrofolate-homocysteine methyltransferase,
/note="Pfam match to entry PF00324 aa_permeases, Amino
acid permease, score 501.80, E-value 5.1e-147"
1668. .2835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       len: 1183 aa; similar to many members of vitamin-B12 dependent methionine synthase family e.g. METH_ECOLI (EMBL:X16584) E.coli metH (1226 aa), fasta scores; opt: 1617 z.score: 1000.7 E(); 0, 31.6% identity in 1228 aa overlap. Equivalent to M.tuberculosis Rv2124c (MTCY261.20c, 88.7% identity in 1183 aa overlap). Annotated as METH_MYCLE, designated metH2 in M.leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                     complement(2903. .3856)
/gene="MLCB2533.03c"
/note="MLCB2533.03c, hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                /note="PS00218 Amino acid permeases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium leprae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"hypothetical protein MLCB2533.03c"
/protein_id="CAA22917.1"
                                                                                                                                                                                                                    /hote="conflict: C is CT in EMBL:ML017" complement(2500. .2592)
                                                                                           1668. .2835
/note="1168 bp perfect direct repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17534 TATCGATTGGCAAGTCGCAGAATATCTGCACGGTAT 17569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 40245
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                                                                                                                                                                                                                                                                                                                                             complement(2903. .3856)
/gene="MLCB2533.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"GI:4200261"
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Cosmid
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                                                                                                                                                                                       'qene-"ansP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4004. .7555
/gene="metH"
                                                                                                                                                                                                                                                                                     /gene="ansP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wycobacterium leprae U00017
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/gene-"metH
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US-08-653-294-19 x MLCB2533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.00
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Locus 000017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                     misc_feature
                                                                                           repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
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                                                                                                                                                                                                                                                                                                                                                    gene
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                      /note="MLCB2533.01c, ansP, probable L-asparagine permease, partial CDS, len: >366 as; highly similar to many amino-acid permease e.g. ANSP_SALTY (EMBL:U04851)
S.typhimurium AnsP, L-asparagine permease (L-asparagine transport protein) (497 as), fasts scores; opt: 1508 z-score: 1696.8 E(): 0, 61.2% identity in 366 as overlap. Equivalent to M:tuberculosis Rv2127, ansP (MTCY261.26, BS.7% identity in 356 as overlap). Also similar to M:tuberculosis permease Rv0346c, aroP2 (MTCY1810.06c, 75.1% identity in 345 as overlap). Probable integral membrane protein, contains PS00218 Amino acid permeases signature. Pfam match to entry PF00324 as_permeases acid permease. Annotated as ORF TR:049801, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          years auses 18.2 ansp2, probable L-asparagine permease, len: 505 as; highly similar to many amino-acid permeases e.g. ANSP_SALTY (EMBL:104881) S.typhimurium Ansp. L-asparagine permease (L-asparagine transport protein) (497 aa), fasta scores.opt: 1891 2-score: 2218.9 E(): 0, 58.9% identity in 477 aa overlap. Equivalent to M.tuberculosis Rv2127 (MTCV261.26, 83.7% identity in 485 aa overlap). Also similar to M.tuberculosis permease Rv0346c (MTCX13E10.06c, 69.8% identity in 473 aa overlap). Probable integral membrane protein, contains PS00218 Amino acid permeases signature. Pfam match to entry PF00324 aa_permeases, amino acid permeases. Annotated as ORF TR.049802, designated lysp in M.leprae cosmid EMBL:U00017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISVEWFGELEFWAALIKVCALMAFLVVGTIFLGGRYPVDGHNTGLSLWTSHGGLFPTG
VOLIVVSGOVHRYPANELEVGTAAGETVERKKIMPRAINSVIARIAFFYVGSVILLA
LLLPYSARRASESPRYFFSKVGFYGAGDLMVIVVLTAALSSLNAGLYATGRVMHSIA
INGSGPKFTARMSKNOPYGGILLAAVICLCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MATLAESPEPKSGASRAGVLGEEBGYHKGLKPRQLQMIGIGGAI
GTGLFLGAGGRLAKAGPGLFLVYAVCGVFVFLILRALGELVLHRPSSGSFVSYAREFF
GERAAYVVGWLYFLDWAMTAIVDTTAIATYLHRWTIFTALPQWTLALLALAAVVLVMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MatLaeSPEPKSGASRAGVLGEEAGYHKGLKPRQLQMIGIGGAI
GTGLFLGAGGRLAKAGPGLFLVYAVCGVFVFLILRALGELVLHRPSSGSFVSYAREFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAPLIVVSSGVMFAYAAVELVGTAAGETVEPKKIMPRAINSVIARIAIFYVGSVILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLPYSAFKASESPFVTFFSKVGFYGAGDLMNIVVLTAALSSLNAGLYATGRVMHSIA
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WGTIVLCQLRLHKMAKAGIMRRPRFFMPLAPYSGYLTLAFLFAVLVVMAFDKPIGTWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00324 aa_permeases, Amino acid permease, score 245.80, E-value 6e-70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="PS00218 Amino acid permeases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative L-asparagine permease"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative L-asparagine permease"
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/db_xref="GI:4200260"

    1168
/note="1168 bp perfect direct repeat"
complement(2. .991)
/gene="ansp"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ambiguous base T /G" complement(833. .925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1249. .2766)
/gene="ansP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1249. .2766)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ansP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"ansP2
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gene CDS

REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS JOURNAL AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

CDS

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QLWESQELITATQGALLKLRAAGVDIDPLDTPVVIASSSGVSSLRGSEDFLSILLSAI
GSRQANQFPYRPSRAEPTHRNVEPMGVITENSCWYLVGHDCDRNATRTFRLSRIGSE
VAPIGPAGAVTVPDGVDLRRIVSDAVAEVSTGATARVWVVDGRATALRHAGRPAGVRR
LGGRDGGVIELDIGSIDRLARDIAGHGADAVVLEPDALRDDVLIRLRRHAGTGPS
complement (3443. .3841)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MVGWYPWAWLAHRDAQTTSTLKDVQRRIMGIETEFGVTCTFHGH
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PHADAEKYRRLHVYTGSNWCETTFMLKVGTRALEMEWNETGYPFROFSLDNFRAIF
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complement(3861. .4871)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSFPYFISPEQAMREQRELARKGIARGRSVVALAYAGGGULFVAE
NPSRSLQKISELYDRVGFAAAGKFNEFDNLRRGGIOFADTRGYAYDRRDVTGRQLANV
YAQTLGTIFFEDAKPFEVELCVAEVAHYGETKRPELKRITYGGSINDEPHFWYMGGTT
ESIANALKESYAENASLTADALGIAVAALRAGSADAAGSDOFTLGVASLEVAVLDANRP
RRAFRRIIGSGLEALLERKDSKGSKGAQNPKGARDSKNSKSYGESTD"
complement(8047. 8922)
/note="proteasome, beta subunit; B2126_C1_173"
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AGYDIHAPDPQSAGRIVSFDAAGGWNIEEEGYQSVGSGSIFAKSSIKKLYSQVSDADS
SRMFERDKNELRDLGIPLEVGKVSALDPSEGYRINRDAYALPPVELTPDEAAAVAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mtrsfpDrlptnlafpGisvingssfvDllrrqapEllpvSLGG
GQSGGGQQLSHGTTIVVLKYPGGVVIAGDRRSTQGNMIAGRDVRKVYITDDYTATGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALRVAIEALYDAADDDSATGGPDLVRGIYPTAVTIGAEGAAEVTESRIAELAREIIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7253. .8050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(6569. .6862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6822. .7115)
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L Submitted (01-MAR-1994) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115

CON Mar 31, 1994 this sequence version replaced gi:414223.

This sequence data was produced by the Genome Sequencing Center located at Collaborative Research Incorporated (1365 Main St., Waltham MA, 02159). 617-487-7979). Please contact Doug Smith (smith@cr.cric.com). The annotation should be considered preliminary and incomplete.

Location/Qualifiers

1. 42157

/ Organism="Mycobacterium leprae"

/ Abxref="kaxon:1769"

/ Complement(133. .1086)

/ Complement(133. .1086)

/ Cocomplement(133. .1086)
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COMPLEMENT (1132. . 1398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MGSLSPWHWVVLVVVVVLLFGAKKLPDAARSLGKSMRIFKSELR
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VIDYYSASHDTLISRIVDPIRVLLVGDHSYLEAWSREAEGVRLFFFDRIVVARELDEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAPFDQFMLRIKVGMAAGIVLASPVWFYQLWAFITPGLYTKERRFTVAFVVPAAVLFA
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                                                                                                                                                                                                                                      Submitted (01-NOV-1993) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
3 (bases 1 to 42157)
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match to yigT E.coli; B2126_C1_182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQAPEALAYRVRNAAVAALESYQVTAQA"
complement(1701. .2444)
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                                                                                                                                             2 (bases 1 to 42157)
Robison, K.
                                                      (bases 1 to 42157)
                                                                                                                                                                                                                Direct Submission
                                   Mycobacterium.
                                                                                                                   Unpublished
                                                                                      Smith, D.R
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CDS

CDS

CDS

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Concess were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.orn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene.chcbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis BST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity to other proteins are named similarity to other proteins are named similarity to other proteins are named similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy, Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of genome washington.edu/RM/RepeatMasker.html). Regions of exons by GRAIL are anotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="WKQNIYAVDILLNQMRDRNIKLDSFVVSAIIETNCDRCRTEGAS
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                                                                 1 (bases I to 103125)
Rounsley,S.D., Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Mason,T.M.,
Shen,M., Ronning,C.M., Fraser,C.M., Somerville,C.R. and Venter,J.C.
Arabidopsis thaliana chromosome II BAC F219 genomic sequence
Unpublished
eudicotyledons; core
Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (23-007-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Oct 23, 1998 this sequence version replaced gi:3776582.
Address all correspondence to:
                                                                                                                                                                                                                                                                                                                    Submitted (29-AUG-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org 3 (bases 1 to 103125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC clone F219 is from Arabidopsis chromosome II and is near the molecular marker rga. The orientation of the sequence is from SP6 to T7 end of the BAC
     euphyllophytes; Spermatophyta; Magnoliophyta;
eudicots; Rosidae; eurosids II; Brassicales; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="predicted by genscan"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steve Rounsley
The Institute for Genomic Research
9712 Medical Center Dr,
Rockville, MD 20850,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e-mail: rounsley@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome-"II
                                                                                                                                                                                                                           2 (bases 1 to 103125)
Rounsley, S.D. and Lin, X.
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                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                          Rounsley, S.D.
                                                           Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
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REFERENCE
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                                                                                                                      AUTHORS
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                                                        APECTDPLDAVIWDKAGERVMEAAARHVASVPGAAKLQLYKNNVDGKGASYGAHENYL
MSRQTPFSAIIAGLTPFLVSRQVVTGSGRVGIGPAGDEPGFQLSQRSDYIEVEVGLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="NVIVKSERVADLLSSVLVVARNTDLGYORFGIRAGMGDAHDTVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS ATACO05560 103125 bp DNA PLN 23-OCT-1998
DEFINITION Arabidopsis thaliana chromosome II BAC F219 genomic sequence,
complete sequence.
ACCESSION AC005560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 12
Gaps: 0
Percent Identity: 66.667
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                                                                                                                                                                                                                                                                                         11019. .11611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:467024"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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US-08-653-294-19 x U00017/rev
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4.222
75.000
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Ratio:
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                                                                                                                                                                                                                                                                                               repeat_region
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complement(join(14358. .14616,15958. .16037,16158. .16307))
/gene="F219.5"
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RLHREVEELRAMKVGPTTVNSASSLTWGPRCERVTPAASPSRAVVPVPAKKTPPPQER
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LOCUS
LOCUS
CNS01DTM 191442 bp DNA
LOCUS
DEFINITION Homo saptens chromosome 14 clone R-80A15, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="POLY_A"
complement(13972. .14049)
/note="exon predicted by xgrail, quality marginal"
complement(join(<14358. .14616,15958. .16037,16158.
/gene="F219.5"
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Homo saplens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(16633. 16710)
/note="exon predicted by xgrail, quality excellent"
complement(16998. .17033)
                                                                                                                          quality excellent"
                                                                                                                                                                                                                                                                                                                                        quality excellent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality marginal"
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10803. .10939
/note="exon predicted by xgrail, quality
excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="exon predicted by xgrail, quality marginal_shadowexon" 13852. .13964
                                                                                                                                                                                                                                              quality
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                                                                             Length: 11
Gaps: 0
Percent Identity: 72.727
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/gene="F219.5"
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/rpt_family="AT_rich"
complement(16632. .16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: ATAC005560
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US-08-653-294-19 x ATAC005560/rev
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AL132800.1 GI:6272127
HTG; HTGS_PHASE2.
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Ratio: 3.455
Percent Similarity: 100.000
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VERSION
KEYWORDS
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ORGANISM
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/translation-3/053/14
/translation-3/053/14
/translation-3/053/14
/translation-3/053/14
/translation-3/053/14
/translation-3/053/14
/translation-3/053/14
/translation-3/052/14

                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="Aac67317.1"
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/Atranslation="MarscsiwTpvLislspvtgesprisrrvilatsigspoplle
Aktrenslation="MarscsiwTpvLislspvtgesprisrrvilatsigspoplle
Aktrepoklovldsbroysrrvilatslagelgginelngealearygrkenrkkalek
Lrakakessppnnksgnokiekelekeevfpllppplvveanllo"
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PVAIRVPLIASHFISTNDPYAMNERFYAADTLAGKINLALAWANILKNGSLEBWHI
FUFSLGSTLPWLIANGTPLIANGTYAGSLAW(VVVLQCIIWTLLELFERRGAKLI
IMBQFPETGASIVSFKVESDVVSLDGHDFLETDAEIGNDGKLHVYVRKSNASRRSLAM
PRPSMLTGAEIXSLSSTPRGSNFNHSDFYSYWEFPGRALSWFGPADLSVSSRFPT
PRPSMLTGAEIXSLSSTPRGSNFNHSDFYSYMFFPGRAFGRALSVGSRRFPT
PRPSMLTGAEIXSLSTPRGSNFNHSOFYSAMGSTPARGENGTAGATSVGSRRFPT
PRESNFEENNAVKYGFYNNTNSSVPAGGSTPRGGAGATSTFNKIPKENQQL
GEKDSRASHDARELHMYWSSSASPVSDVFGGGAGDNYATEQGEGGAGARIRMVSDQL
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LGMAMFSLGLFMALQPKIIACGNSVATFAMAVRFITGPAIMAVAGIAIGLHGDLLRIA
IVQAALPQGIVPFVFAKEYNVHPTILSTGVIFGMLIALPITLVYYILLGL"
SLGTYDVLLSGLEKTSDFQKEVALLRKEKKSLVASARFRENVHVEDKICDLLFATNLL
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7915. .8000,8140. .8407,8565. .9759))
/gene="F219.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1683. .1725)
/note="exon predicted by xgrail, quality marginal"
complement(<1769. .>2932)
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/protein_id="AAC67319.1"
/db_xref="G1:3785972"
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10586. 10649
/note="exon predicted by xgrail, quality
marginal_shadowexon"
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                                                                          /rpt_family="(IAAAA)"
join(<875. .994,1320. .>1640)
/gene="F219.2"
                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein"
                                                                                                                                                                                                                                       /note="predicted by genscan"
join(875. .994,1320. .1640)
/gene="F219.2"
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/rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6667. .>9759)
/gene="F219.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F2I9.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="F219.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F219.4"
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/gene="F219.2
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to reverse of: DVU57315 from: 1
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Percent Similarity: 100.000
                                                         to: CNS01DTM
   US-08-653-294-19 x CNS01DTM
                                                                                                                                                                                                                           seq_name: gb_inl:DVU57315
                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS DVU57315
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                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                          DEFINITION
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TITLE
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REFERENCE
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                                                                                                                                    Web : www.genoscope.cns.fr)
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                      Direct Submission
Submitted (04-NOV-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="AA194835"
/note="matching EMBL:AA194835; Identified using the e-PCR
software (G. Schuler)"
133712. 133887
                                                                                                                                                                                                                                                                                                            phage, etc.
Contig order: 13 10 12 11 14 15 9, 1000 N's separate segments
Contig 13: length 15976 bp
Contig 10: length 5980 bp
Contig 11: length 9512 bp
Contig 11: length 8124 bp
Contig 14: length 6723 bp
Contig 15: length 81177 bp
Contig 15: length 4117 bp
Contig 95: length 4117 bp
Contig 95: length 4117 bp
Contig 95: length 4117 bp
Contig 96: length 4117 bp
Contig 97: length 41
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/note="matching EMBL.R52665; Identified using the e-PCR
software (G. Schuler)"
154585. 154748
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/note="matching EMBL:M69137; Identified using the software (G. Schuler)"
132481. 132607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="matching EMBL:Z41390; Identified using the software (G. Schuler)" 133741. .133892
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Gaps: 0
Percent Identity: 50.000
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/note="matching EMBL:R39150;
software (G. Schuler)"
133768. _133909
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software (G. Schuler)"
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1. 191442
1. 191442
Acganism="Homo sapiens"
/db_xxef="taxon:9606"
/chromosome="14"
/clone_lib="RPCI-11"
/clone="R-80A15"
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41528 c 39774 g 50165
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   (bases 1 to 191442)
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ORIGIN
REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                     COMMENT
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Molecular and genetic analyses of lama, an evolutionarily conserved gene expressed in the precursors of the Drosophila first optic gangilon
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SLATHSYSLNFLPALSTISSSCDRDESSQKFCECVRNLLTRNYEQLKEQAAAMAEHDH
YWHQLHLILNQLEGMETGYIRGATRARSDLEEEIPLSDFLLMNAAADIQDLKIYYENY
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NFLLAGNSTWLANGVPYFDVILNASRISRDNYSEDQDLTPAEEAVPYNYSEDQDLTPA
EEAELINLEAVDKYLRNGGFRGDLLGDESIAYGNIDLKCYFSYNARLGMSDXHAFAGP
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QKRYKFHYHFSPDTRSNTVPGADITFTGYPGIIGSTDDFYVVKGRQVQSIVGGVCIKN
ENLALWEKVDVKNMYPLVARVMAANRIAQNRRTWARAMSRHPFTGAKQWISVDLNKLG
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                                                                                                                                                                                                                                                   21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila virilis
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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Perez,S.E. and Steller,H.
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USA
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Drosophila virilis LAWA (lama) gene, partial cds.
U57315.
U57315.1 GI:1314865
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Gaps: 0
Percent Identity: 72.727
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Submitted (30-APR-1996) Sharon E. Perez,
Massachusetts Ave., Cambridge, MA 02139,
Location/Qualifiers

    1911
    /organism="Drosophila virilis"
    /db_xref="taxon:7244"

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97047309
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ez, S.E. and Steller, H.
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US-08-653-294-19 x DVU57315/rev
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to: 1911

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repeat_region
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Submitted (04-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, Callo 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clone-request@sanger.ac.uk

On May 11, 1999 this sequence version replaced gi:4741514.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw:, SWISSPROT; Tr:, TREMBL

This sequence is the entire insert of clone 782123. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature the sequence elements (e.g. Alu). Where the feature is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<26. .108,605. .639,2393. .2486,4942. .5082,6225. .6286,6755. .6842,16087. .16197,16754. .16955,108085. .12525,21675. .24962,28335. .2835,19865. .18255,21673. .1865,33057. .33107,36418. .36490,
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                                                                                                                                                                                               HS782L23 123925 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 782L23 on chromosome 1p31.2-33
Contains start of HOOK1 gene, ESTs, STS and GSSs, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 123925)
Wallis, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="match: cDNAs: Em: AF044923; match: ESTs:
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/product="401782.23.1 (HOOK1)"
complement(26. .50318)
/gene="4J7822.23.1"
1. .123925
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPCI-4"
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                                                                                                                                                                                                                                                                                    sequence.
AL035416
AL035416.7 GI:4775629
HTG; CpG Island.
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                                                                                                               seq_name: gb_pr3:HS782L23
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                       seq_documentation_block:
LOCUS HS782L23 1
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/translation-"MEETOPPOPKLPLCDSIMIWLQTFNTASPCQDVKQLTSGVAMA
QVLHOIDAARTNESWLSRIKEDVGDWRIKASNVKYLOGINSYTHEFLGOOISEALI
PDLNOITECSOPVELGALLGCAINCEKKOEHIONIMITEESVOHVVWTAIQELM
SKEILGSPRNDAVGELEOOLKRALEELOEALAEKEEHRORCEELDWOYTTLQDEKNSL
VSENEMMURKLDQLDGSFDDPNTVVAKKYFHAOLQLEGOLGENFRLEAKDDYRPHCE
BLEKQLIEFORRNDEITSLAEETRALKDEIDVLRATSDKANKLESTYBIYROKLDDLN
DLRKQVKTLOETNMYMHYVSLEEELKRANAARTOLETYRROVQDLHVKLSSESKRA
DTLAFERKRLEEKHRALLKERRELIEORDTLKETNEELRCSOVQOHINOTDASATKS
YENLAAELMEYVEYREVEIRLIEORDTLKETNEELRCSOVQOHINOTDASATKS
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KOELIEDLQDPDINQN"
complement(<28 . . 638)
/gene" dJ782L23.1."
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7004="23 copies 2 mer aa 74% conserved"
2074. 2177
7004="2 copies 52 mer 86% conserved"
3183. 3362pies 52 mer 86% conserved"
3183. 3362pies 60 mer 96% conserved"
7004="3 copies 60 mer 96% conserved"
333. 3766
3346. 3966
7004="MIR repeat: matches 7. .237 of consensus"
7004="MIR repeat: matches 3. .139 of consensus"
7004="MIUD repeat: matches 1. .142 of consensus"
7004="AluJb repeat: matches 1. .308 of consensus"
7004="AluJb repeat: matches 142. .299 of consensus"
7004="AluJo repeat: matches 86. .262 of consensus"
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14324. .14604
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10921. .11230
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/note="L1M4 repeat: matches 14. .1352 of consensus"
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1231. .14323
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134. .253
/note="MIX repeat: matches 61. .188 of consensus"
complement(<601. .5013)
/gene="dJ782L23.1"
/note="match: ESTS H40247 T25043"
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/note="29 copies 2 mer aa 71% conserved"
                                                                                                                       /note="match: proteins: Tr:060561"
/codon_start=1
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                                                                                                                                                                                                                                                    /evidence=not_experimental
/product="da782123.1" (HOOK1)"
/protein_id="CAB52263.1"
/db_xxef="G1:5706448"
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.43412,50090.
                                                                  /gene="dJ782L23.1
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repeat_region
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14605. .15797

/note="LIMB7 repeat: matches 4281. .5403 of consensus"
/complement(15903. 16103)
/genne="dd7821231."
/note="match: STS: Em:AL009539"
/evidence=not_experimental
/evidence=not_experimental
/note="LIM4 repeat: matches 2693. .3042 of consensus"
/note="LIM4 repeat: matches 3035. .4224 of consensus"
/note="LIM4 repeat: matches 16. .362 of consensus"
/note="LIM4 repeat: matches 4276. .4883 of consensus"
/note="LIM4 repeat: matches 4276. .4883 of consensus"
/note="LIM4 repeat: matches 4276. .4883 of consensus"
/note="LIM4 repeat: matches 4883. .4897 of consensus"
/note="Match: GSS: Em:B761781"
/note="match: GSS: Em:B761781"
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24511. .24618
Anote-"MIR repeat: matches 119. .229 of consensus"
25107. .27565
Anote-"LIPA7 repeat: matches 3679. .6145 of consensus"
29303. .29618
Anote-"MERIB repeat: matches 2. .337 of consensus"
30133. .30371
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/evidence=not_experimental
join(30336 .30371,30559. .30682)
/gene="dJ782L23.1"
/note="match: GSS: Em:AQ263653"
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Percent Identity: 63.636
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30372. 30558_experimental
30702. 10558_experimental
30502. 105800.
31605. 12080
/gene="dJ782L23.1"
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/evidence=not_experimental
complement(3304).
/gene="dJY82L23.1"
/note="match: GSS: Em:AQ196444"
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evidence=not_experimental
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33388. .34107
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/gene="dJ782L23.1"
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Percent Similarity: 100.000
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US-08-653-294-19 x HS782L23
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Louis,
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3 (bases 1 to 187493)

S waterston, R.H.

Direct Submission

Louiversity School of Medicine, 4444 Forest Park Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louiv

MO 63108, USA

On Oct 29, 1999 this sequence version replaced gi:6007883.

SUBMITTED BY: WUGSC

Genome Sequencing Center
Department of Genetics

Washington University
St. Louis MO 63108, USA

Att.://genome.wustl.edu/gsc

mailto:sapiens@watson.wustl.edu
                                                                                                                                                                ACO1241 187493 bp DNA HTG 29-OCT-1999 HOMO Sapiens chromosome 2 clone NHO467P13 map unknown, WORKING DRAFT SEQUENCE, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                       Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhin!; Hominidae; Homo.
1 (bases 1 to 187493)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The attached annotation was produced using a purely automated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 187493)
Waterston,R.
The sequence of Homo sapiens unknown clone NHO467P13
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
                          /rpt_family-"L2"
3452. 3847
Tpt_family-"Retroviral"
3870. 3961
/rpt_family-"(TA)n"
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1. 187493
Arganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
ArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
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AC011241.2 GI:6139206
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323. .621
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                                                                                                 seq_name: gb_htg4:AC011241
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Locus Ac011241 1
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4939. 5132
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Align seg 1/1 to: AC011241 from: 1 to: 187493

1 TyrArgLeuAlaile\*\*\*ArgileAlaLeuArgTyr 12

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RATDLEQATGARIAFLIRFGTGVLPEPKTVLQAGDKVYIAAISGRAABAAAAAAAPPE
                                                                                               Chases 1 to 1692)
Chen, P. and Bishal, W.R.
Direct Submission
Submitted (23-SEP-1997) Molecular Microbiology and Immunology,
Johns Hopkins University, 615 N. Wolfe Street, Baltimore, MD 21205,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="Aac69359.1"
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                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynabacterinaea; Mycobacteriacae;
Mycobacterium; Mycobacterium tuberculosis complex.
I (bases 1 to 1692)
Chen, P. and Bishai, W. R.
Novel selection for isoniazid (INH) resistance genes supports a role for NAD+-binding proteins in mycobacterial INH resistance Infect. Immun. 66 (11), 5099-5106 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="TrkA homolog; complements the INH-sensitive phenotype of oxyR deletion mutant of E. coli" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mycobacterium tuberculosis"
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120136 TACTTATTTGCTATCACAAGAACAGCACTCAGATAT 120171
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1. .1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
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/transl_table=11
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                                                                                                                                                         (ceoC) gene, partial cds. AF026541
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Ratio:
Percent Similarity:
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                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AUTHORS
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MEDLINE
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JOURNAL
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DNA encoding a Bacillus thu
Human signal mediator prote
DNA encoding a Bacillus thu
Polynucleotide sequence fro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1998 (first entry)
Pig alpha 1-6 fucosyltransferase gene.
Alpha 1-6 fucosyltransferase; enzyme; pig; human; fucose transfer;
guanosine diphosphate; sugar chain synthesis; modification; antibody;
GlonAc; cancer diagnosis; ss.
Sus scrofa.
Location/Onalifica-
                                                                                                                                                                                           16-OCT-1996 (first entry)
Human gene signature HDMGSO8571.
Gene signature: messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
WO9514772.A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or recognising different cell types. 185 G; 102 T; sequence 382 Bp; 118 A; 72 C; 85 G; 102 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 12
Gaps: 0
Percent Identity: 58.333
   3453
3672
3867
4444
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1.7e+03
1.8e+03
2.1e+03
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                                                                                                                                                         BP
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ID T76573 standard; cDNA to mRNA; 1728
                                                                                                                                                         [2633] standard; cDNA to mRNA; 382
 91.84
91.31
90.87
89.67
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75.000
 31.00
31.00
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11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MAPES/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                   seq_name: N_Geneseq_36:T26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:T76573
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                                                                                                                                                                                                                                                                                                                                                                                                                           Okubo K;
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US-08-653-294-19 x T26331
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Ratio:
Percent Similarity:
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N_Geneseq_36:T61556
N_Geneseq_36:V38466
N_Geneseq_36:X20635
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                                                                                                                                                                             T26331;
                                                                                                                                                         HOKKEDAC
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32 : Human gene signature HUMGS08571
1728 : Pig alpha 1-6 fucosyltransfera
58 : D-A42d RNA sequence. L-nucleic a
1847 : Staphylococcus aureus contig s
1981 : Romaine lettuce violaxanthin d
9 1092 : Pseudomonas cepacia DSM 3401 1
6 1959 : Enterococcus faecalis genome c
2469 : Enterococcus faecalis genome c
8 3003 : Hereditary multiple exostose a
2 4114 : Enterococcus faecalis genome c
0 4114 : Enterococcus faecalis genome c
13110 : Enterococcus faecalis genome c
3 337 : Hepatitis GB virus (HGBV) clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 : Staphylococcus aureus contige 881 : Romaine lettuce violaxanthin 699 : Enterococcus faecalis genome 6410 : Enterococcus faecalis immusicalis immusicalis enterococcus faecalis immusicalis enterococcus faecalis faecalis
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Max-interacting protein coding
Encodes Babesia bovis 60kD imm
Babesia merozoite surface prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penicillium chrysogenum acetam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renal cancer associated gene.
Gene encoding enzyme with sta:
Mutant Aspergillus oryzae DEB
                                                                                                                             Command line parameters:
-MODEL-frame+p2n.model -DEV-xlp
-MODEL-frame+p2n.model -DEV-xlp
-O-cgn1_L/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-DB-N_Geneseq_36 -OFMT-fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GGAPOFT=6.500 -GGAPOXT=6.050 -CAPOP=10.000 -YGAPEXT=0.500
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-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-AALIGN=15 -MODE=LOOAL -OUTFMT=Pfs -NOCALGON=200 -THR SCORE-pct
-AALIGN=15 -MODE=LOOAL -OUTFMT=Pfs -NOCAME-ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                           About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110000
     out_format :
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1226
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12.50
66.13
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1.125.91
1.05.69
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36.38
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OM of: US-08-653-294-19 to: N_Geneseq_36:*
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Database sequences: 311585
Latabase length: 125096042
Search time (sec): 590.520000
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Query: US-08-653-294-19
                                       Date: Feb 8, 2000 1:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_36:V11310
N_Geneseq_36:V74678
N_Geneseq_36:V74678
N_Geneseq_36:T66241
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N_Geneseq_36:X13540
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N_Geneseq_36:X13127
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N_Geneseq_36:Q80775
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N_Geneseq_36:V16485
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N_Geneseq_36:Q24873
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N_Geneseq_36:V80372
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N_Geneseq_36:N60877
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N_Geneseq_36:Q33064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:T18995
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N_Geneseq_36:7
N_Geneseq_35:0
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Sequence
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misc_binding
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                                                                                   WO9808856-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Funds or page alpha 1-6 fucosyl:transferase and DNA encoding it - for synthesis and modification of sugar chains and used as an antigen

For production of diagnostic antibodies

Claim 5: Page 30-34; 61pp; Japanese

Claim 5: Page 30-34; 61pp; Japanese

Claim 5: Page 30-34; 61pp; Japanese

CT 76573 and T76574 represent the coding sequences for the pig and human

CC 176573 and T76574 represent the coding sequences for the pig and human

CC 176573 and T76574 represent the coding sequences for the pig and human

CC 176573 and T76574 represent the coding sequences for the pig and human

CC 176573 and T76574 represent the coding sequences for the pig and human

CC 176673 and T76574 represent the coding sequences for the followabeta

CC 176670 and 1-6 fucosyltransferases of the invention 1-6 followabeta

CC 1-3 Manbeta 1-4 followabeta 1-2 Manalpha 1-6) (GLONACbeta

CC 1-3 Manbeta 1-4 followabeta 1-2 Manalpha 1-6) (GLONACbeta

CC 1-3 Manbeta 1-4 followabeta 1-2 Manalpha 1-6) (GLONACbeta

CC 1-5 Manbeta 1-4 followabeta 1-2 Manalpha 1-6) (GLONACbeta

CC 1-5 Manbeta 1-4 followabeta 1-2 Manalpha 1-6) (GLONACbeta

CC 1-5 Manbeta 1-4 followabeta 1-2 Manalpha 1-6) (GLONACbeta

CC 1-5 Manbeta 1-4 followabeta 1-6 modern of the presence of 5 mW

CC 2 About 7.0 (pig) or 7.5 (human), and is stable over the pH range 4-10

CC 2 About 7.0 (pig) or 7.5 (human), and is stable over the pH range 4-10

CC 2 About 7.0 (pig) or 7.5 (human), and is stable over the presence of 5 mW

CC 2 About 7.0 (pig) or 7.5 (human), and is stable over the presence of 5 mW

CC 2 About 7.0 (pig) or 7.5 (human), and is stable over the presence of 5 mW

CC 2 About 7.0 (pig) or 7.5 (human), and inhibited in the presence of 5 mW

CC 2 About 7.0 (pig) or 7.5 (human), and modification of sugar

CC 3 About 7.0 (pig) or 7.5 (human), and modification of sugar

CC 4 About 7.0 (pig) or 7.5 (human), and modification of sugar

CC 4 About 7.0 (pig) or 7.5 (p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy;
perfume;
tumour;
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D-A42d RNA sequence.
L-nucleic acid; target; D-nucleic acid; optical antipode; diagnosis; biosensor; herbicide; food additive; analysis; flavouring; cosmetic; purification; dialysis; separation; viral infection; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9. .10
/*tag- b
/note= "Binds to nucleotides 46. .47"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 36.00 Length: 11
Ratio: 3.273 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 72.727
                                                 31-JUL-1997.
23-JAN-1997. J00171.
22-JUL-1996. JP-192260.
24-JAN-1996. JP-161648.
21-JUN-1996. JP-162813.
(TOYM ) TOYO BOSEKI KK.
Shiba T. Taniguchi N, Uozumi N, Yanagidani S;
P-PSDB; W22124.
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/note= "Binds to nucleotides 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      723 CGCCTTGGAATCTCACAATTGGCGCTACGCTAC 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: T76573 from: 1 to: 1728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID v11310 standard; RNA; 58 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .45
q=
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/*tag= c
29. .45
/*tag= d
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/*tag=
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US-08-653-294-19 x T76573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1728 BP;
                               WO9727303-A1.
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FIT MISC. Dinding (7.1829 - 8.100)

FIT MISC. Dinding (7.1829 - 10.100)

FIT MISC. Dinding (7.1829 - 10.100)

FIT MISC. Dinding (7.1820 - 10.100)

FIT MISC. Dinding (7.1820 - 10.100)

FIT MISC. Dinding (7.1820 - 10.100)

FIT MIND. DAMAGE (7.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820 - 10.1820
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D5-MAY-1997.

MOY-1995; UB-006315.

PROV-1995; UB-006315.

RO-AUG-1995; UB-006315.

RO-AUG-1995; UB-006315.

RO-AUG-1995; UB-006315.

RO-AUG-1995; UB-006315.

RO-AUG-1995; UB-006315.

RO-AUG-1996; UB-006315.

RO-AUG-1996; UB-006315.

RO-AUG-1996; UB-0063.

RO-AUG-1996; UB-00
  "bases 186-189 are illegible in Fig 1"
/note= "bases 186-189 are illegible in Fig

/*tag= f

/*tag= bases 226-227 are illegible in Fig

cds 235. 1656

/*tag= g
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Pseudomonas cepacia DSM 3401 lipD gene.
Lipase, LipD; Lipase modulator; limD; chaperone molecule; Lipolysis ergent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.00 Length: 10
3.889 Gaps: 0
90.000 Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID Q44280 standard; DNA; 1092 BP.
AC Q44280;
                                                                                                          /*tag= g
235. .609
/*tag= h
610. .1653
/*tag= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    712. .714
/*tag= d
734
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480
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481
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US-08-653-294-19 x T66241
                                                                                                                            transit_peptide 235
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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    Polynocleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S. aureus vaccines.

Claim 1: Page 1260-1261; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S. aureus. DNA sequences allows: putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can
                                                                                                                                                                                                                                                                                                                                                                                                                   be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1997 (first entry)
Romaine lettuce violaxanthin de-epoxidase cDNA.
Violaxanthin de-epoxidase; VDE; light; photosensitivity;
photoprotection; transgenic plant; zeaxanthin; antheraxanthin;
xanthophyll; lettuce; ss.
Lactuca sativa L. cv. romaine.
Key
Location/Qualifiers
misc_difference 26._29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference 147. .149
misc_difference 147. .149
misc_difference 186. .189
misc_difference 186. .189
/*tag= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "bases 26-29 are illegible in Fig 1"
misc_difference 66. .72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "bases 66-72 are illegible in Fig 1"
misc_difference 105. .110
           30-JUL_1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouality: 35.00 Length: 10
Ratio: 3.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: V74678 from: 1 to: 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GTTGCTATTTCTAAGATTGCATTGCGTTAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LeuAlaIle***ArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID T66241 standard; cDNA; 1981 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        627 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:T66241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block: |
US-08-653-294-19 x V74678
                                                                                                                                              WPI; 97-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sednence
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Claim 1; Page 413-414; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faccalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system commercial importance. The Enterococcus faccalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faccalis in samples. They can also be used for progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faccalis, or
                                                                                                                                                                                         Preph. of active lipase in high quantities - by subjecting to denaturation and restructuring in presence of chaperone molecule Example 10; page 43; 78pp; English.

Two genes were cloned and sequenced from Pseudomonas cepacia DSM 1401. The genes were designated lipp (044280) and limb (044281) and they code for a lipase and a lipase modulator protein, respectively. Due to the extreme GC content of the DNA, the sequence was difficult to determine (hence the "others" in the sequence). The limb start codon is positioned 3 bp downstream of the lipb stop codon. Lipp and climb were found to be homologous to Liph and LimA, respectively. In denaturation/renaturation experiments, LimA chaperone protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:41.
Enterococcus faecalis; contig; detection; Enterococcal infection;
                                                                                                                   Hobson A, Joergensen ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.00 Length: 10
4.250 Gaps: 0
80.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                   378 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: Q44280 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 353 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LeuAlaIle***ArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID x12978 standard; DNA; 1959 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             able to produce active LipD.
Sequence 1092 BP; 188 A;
                                                                                                                   Buckley CM, Diderichsen BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-653-294-19 x Q44280/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:X12978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                     08-JUL-1993.
18-DEC-1992; DK0391.
20-DEC-1991; WO-DK0402.
(NOVO) NOVO-NORDISK AS.
  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis. W09850555-A2.
                                                                                                                                     McConnell DJ;
WPI; 93-227318/28.
P-PSDB; R39396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                  WO9313200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
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claim 1, Page 1853-1855; 2084pp; English.

A computer readable medium has been developed which has recorded on it
A computer readable medium has been developed which has recorded on it
982 nucleotide sequences isolated from the Enterococcus faecalis genome.
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcal infection in an animal and monitoring
progression of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
  particular the
nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMA.) HUMAN GENOME SCI INC.

Barash SC. Dillon PJ. Kunsch CA:

WPI: 99-04517/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

New isolated Enterococcus for the detection of Enterococcus and for

used to develop products for the detection of Enterococcus and for

use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis genome contig SEQ ID NO:603.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide secan be used in vaccines to prevent or attenuate an Enterococcal
                                                                             749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738
                                                                                                                                                       Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 12
Gaps: 0
Percent Identity: 50.000
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                                                                             322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: X13540 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuAlalle***ArglleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                              1 TyrArgLeuAlaile***ArgileAlaLeuArgTyr
                                                                                                                                                                                                                                                                                           to: 1959
                                                                             341 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 C;
                                                                                                                                                                                                                                                                                             to: X12978 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      771 A;
                                                                               542 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-653-294-19 x X13540/rev
                                                                                                                                                       34.00
3.778
75.000
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:X13540
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3.091
91.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis.
WO9850555-A2.
                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-19 x X12978
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID X13540 standard; DNA;
                                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2469 BP;
                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                             1959
                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                       alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1998
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                                                            infection.
                                                                                                                                                                                                                                                                                             Align seg 1/1
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                                                                               Seguence
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Ratio:
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                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                       infection.
                         infection.
                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection.
                                                                                                                                                                                                                     Seguence
 claim 4; Pages 28:31; 31pp; English.

This cDNA encodes an isoform of the EXT2 gene associated with hereditary multiple exostoses and chondroarcoma. The polynucleotide is an isoform of the EXT2 gene described in Nature Genet., 14, 25, 1996. The polynucleotide can be used in the detection and treatment of EXT2-related diseases, and to identify compounds which activate or inhibit receptors for the encoded polypeptide. The polypeptide can be recombinantly the encoding nucleic acid.

730 C; 766 G; 756 T;
                                                                                         20-AUG-1998 (first entry)
Hereditary multiple exostose associated EXT2 gene isoform encoding cDNA.
Hereditary multiple exostose; EXT2; chondrosarcoma; human; isoform; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
Barash SC. Dillon PJ, Kunsch CA:
WPI: 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis genome contig SEQ ID NO:420.
Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                       P-PSDB; W44851.
Cloned human EXT2 gene - associated with hereditary multiple
exostoses or chondrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 13.00 Length: 11

Ratio: 3.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 54.545
1322 TICCAGCITCITCTAACGCGGGTTTCGCTTCGGTAT 1287
                                                                                                                                                                                          /product= "EXT2 gene isoform"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170 TACAAGCTGGCTGTGTCCCGGTTGTCATTGCAG 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: V19375 from: 1 to: 3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TyrArgLeuAlaIle***ArgIleAlaLeuArg 11
                                                                                                                                                       Location/Qualifiers
                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X13357 standard; DNA; 4114 BP. X13357;
                                                         seq_documentation_block:
ID V19375 standard; cDNA; 3003
                                                                                                                                                                                                                           26-AUG-1997; 306503.
21-OCT-1996; CN-121928.
(UYHU-) UNIV HUNAN MEDICAL.
                                                                                                                                                                 167. .2353
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1999 (first entry)
                                   seq_name: N_Geneseq_36:V19375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:X13357
                                                                                                                                                                                                                                                                 Deng HX, Fan CH, Xia J;
WPI; 98-219110/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-19 x V19375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis
WO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1998.
                                                                                                                                                                                                     EP-837127-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                   22-APR-1998
                                                                                V19375;
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Claim 1; Page 1639-1641; 2084pp; English.

A computer readable medium has been developed which has recorded on it

A computer readable medium has been developed which has recorded on it

R to mid to x13919 represent these nucleotide sequences which are primary

nucleotide sequences, also known as contigs. The computer based system

can identify fragments of the Enterococcus faecalis genome with

commercial importance. The products can be used to detect the presence

of Enterococcus faecalis in samples. They can also be used for

diagnosing Enterococcus infection in an animal and monitoring

progression of disease, and for identifying agents which can be used to

modulate the growth or pathogenicity of Enterococcus faecalis, or

another related organism, in vivo or in vitro. In particular the

polypeptides encoded by the Enterococcus faecalis nucleotide sequences

can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claim 1; Page 1021-1027; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences are also be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis.

12-NOV-1998.
12-NOV-1998;
14-NOV-1999;
16-MAY-1997;
15-MAY-1997;
15-MAY-1997;
16-MAY-1997;
16-MAY-1998;
16-MAY-1998;
16-MAY-1998;
16-MAY-1997;
16-MAY-1998;
16-MAY-1997;
16-MAY-1998;
16-MAY-
      and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faccalis genome contig SEQ ID NO:190.
Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.
to develop products for the detection of Enterococcus vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1226 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.00 Length: 11
3.667 Gaps: 0
81.818 Percent Identity: 54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 4114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1334 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X13127 standard; DNA; 11410 BP
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US-08-653-294-19 x X13357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4114 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
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us-08-653-294-19.rng

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seq_name: N_Geneseq_36:T41700
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NR WPI: 95-293123/38.

P-PSDB: R81447, R81448, R81449, R81450, R82064, R82065.

P-PSDB: R81447, R81448, R81449, R81450, R82064, R82065.

Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful
for diagnosis and therapy of hepatitis GB virus
Example 5: Page 193: 661pp; English.

Double stranded hepatitis GB virus
C prepare a lambda phage HGBV const library. The cDNA clone T00049,
which encodes the proteins R81447-50 and R82064/65 (the 6 possible reading frames), was rescued from the lambda phage, searched
c against a sequence database and found to be an unique HGBV
sequence. Reagents which comprise the HGBV DNA, or its protein
c prods. can be used for the diagnosis, therapy or in a vaccine to
  Ë
 4014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO) ABBOTT LAB.
Buijk SL, Dawson GJ, Desai SM, Erker JC, Leary TP;
Muerhoff AS, Mushahwar IK, Pilot-Matias TJ, Schlauder GG;
                                                                                                                                                                                                                                              02-070-1996 (first entry)
Hepatitis GB virus (HGBV) clone 50.
Hepatitis GB virus; HGBV, diagnosis; treatment; vaccine; reagents; non-A; non-B; non-C; non-D; non-E; clone 50; tamarin; infected plasma; lambda phage; CDNA library; ss.
  ö
                                                                                                                       Align seg 1/1 to reverse of: X13127 from: 1 to: 11410
1678
                                           Length: 11
Gaps: 0
Percent Identity: 63.636
                                                                                                                                            2328 C;
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/label= R81449
complement (1. .335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2. .336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3. .337)
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       /*tag= a
/label= R81447
2.336
/*tag= b
/label= R81448
  3374 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/label= R81450
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/label= R82065
                                                                                                                                                                                                                seq_documentation_block:
ID T00049 standard; DNA; 337 BP.
AC T00049;
                                                                                       alignment_block:
US-08-653-294-19 x X13127/rev
                                                        3.300
                                                                                                                                                                                          seq_name: N_Geneseq_36:T00049
                                                                                                                                                                                                                                                                                                                                                                                              .337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-1994; US-196030.
13-MAY-1994; US-242654.
29-JUL-1994; US-283314.
23-NOV-1994; US-344190.
23-NOV-1994; US-344185.
27-JAN-1995; US-3441857.
                                            33.00
  11410 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1995; U02118
                                                                                                                                                                                                                                                                                                       Hepatitis GB virus.
                                                                 Percent Similarity:
                                  alignment_scores:
Quality:
                                                         Ratio:
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WPI: 95-291133/38.

Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for diagnosis and therapy of hepatitis GB virus

Example 9; Page 286; 661pp; English.

Example stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV

Couble stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV

infected tamarin plasma, using standard procedures, was used to repare a lambda phage HGBV cDNA library. CDNA clones rescued from the lambda phage were searched against a sequence database and found to be unique HGBV sequences. Then a series of PCR experiments were performed to obtain additional HGBV sequences, i.e. T00156-28 Reagents which comprise the HGBV DNA, or its protein prods. can be used for the diagnosis, therapy or in a vaccine to prevent HGBV infection.

Sequence 337 BP; 99 A; 88 C; 79 G; 71 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leary TP;
, Schlauder GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-010-1996 (first entry)
Hepatitis GB virus (HGBV) clone.
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine; reagents; non-A; non-B; non-C; non-D; non-E; clone; tamarin; infected plasma; lambda phage; cDNA library; ss. Hepatitis GB virus.
                               71
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Gaps: 0
Percent Identity: 50.000
                                                                                                                                  32.00 Length: 12
3.200 Gaps: 0
83.333 . Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AGG-1995.

14-FEB-1995; U02118.

14-FEB-1994; US-19654.

13-FXZ-1994; US-242654.

29-JUL-1994; US-344190.

23-NOV-1994; US-344190.

23-NOV-1995; US-344190.

27-JAN-1995; US-344557.

(ABBO ) ABBOTT LAB.

Bujfk SL, Dawson GJ, Desai SM, Erker JC, Lear.

Muchoff AS, Mushahwar IK, Pilot-Matias TJ, Sci

Simons JN;
                            ΰ
                                                                                                                                                                                                                                                                                                                                                                                                            243 TATCTTCTGCGGATGTCACGAGTGGCAATAAAGTAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
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                               88
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ID T00127 standard; DNA; 337 BP.
prevent HGBV infection.
Sequence 337 BP; 99 A;
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83.333
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US-08-653-294-19 x T00049
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US-08-653-294-19 x T00127
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New vaccines for filarial parasite infection(s) - comprising C-terminal beta-tubulin amino acid sequence from a parasite Example 6, Page 51-53 67pp; English.

A CDNA clone (141700) codes for the beta-tubulin (R99425) of the filarial nematode Brugia pahangi. The C-terminal portion (see also R99420) of the beta-tubulin is useful in novel vaccines against filarial parasite infections.

Sequence 1347 BP; 381 A; 262 C; 337 G; 367 T;
                                    19-JAN-1997 (first entry)
Brugia pahangi beta-tubulin cDNA.
Filariasis; nematode; parasite; beta-tubulin; immunogen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viscolity (first entry)
Cotopus rhodopsin membrane protein.
Cotopus: rhodopsin; membrane; helix; OR; ss.
Location/Qualifiers
Location/Qualifiers
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/label= SphI
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Gaps: 0
Percent Identity: 70.000
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/note= "restriction enzyme site"
1371
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/label= NdeI
/hote= "restriction enzyme site"
1069. .1074
/*tag= d
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/label= MluI
/note= "restriction enzyme site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: T41700 from: 1 to: 1347
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                                                                                                                                                                           Bughio N, Faubert GM, Geary T, WPI; 96-476844/47.
P-PSDB; R99425.
seq_documentation_block:
ID T41700 standard; DNA; 1347 BP.
AC T41700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q12225 standard; DNA; 1371 BP.
AC Q12225;
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/label= BamHI
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                                                                                                             17-CCT-1996.
10-APR-1995; UG4838.
10-APR-1995; US-420982.
(UYMC-) UNIV MCGILL.
(UPJO ) UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:Q12225
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US-08-653-294-19 x T41700
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Quality:
Ratio:
Percent Similarity:
                                                                                         Brugia pahangi.
WO9632132-A1.
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AQ787789 HS_3072_A2_B11_T7C
AL080978 Arabidopsis thallan
AT000172 AT000172 Apple youn
                                                                                                                                                                                                                                                      Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 468)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry, R., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Other_GSSs: CIT-HSP-2343C10.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

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The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

The Institute for Genomic Research Genetics (info@resgen.com). BAC
end search page: Orgytdb/humgen/Dac_end_search/Dac_end_search.html.

    seq_documentation_block:
    476 bp
    mRNA
    EST
    09-DEC-1999

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    AV395907
    chlamydomonas reinhardtii c9 chlamydomonas reinhardtii cDNA clone CL51a05_r, mRNA sequence.
    ACCESSION
    AV395907

    VERSION
    AV395907.1
    GI:6550123

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Gaps: 0
Percent Identity: 66.667
   894
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262
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 280.01
112.23
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                                                                       seq_name: gb_gss8:AQ058120
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    Quality:
    Ratio:
    Percent Similarity:
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 gb_gss5:AQ787789
gb_gss1:CNS00MR8
gb_est21:AT000172
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AUTHORS
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AV395907 AV395907 Chlamydomonas
AA897834 NCP5EITP Perithecial N
B02005 CSRL-1470D11-u CSRL flow
H72837 ys06c01.s1 Soares fetal
AQ81552 EM-5348 AA_E006.SP6E RF
AQ851612 CPG1352B COGNAGADNAI
CAQ851612 CPG1352B COGNAGADNAI
AQ864396 nbeb0023D13f CUGI Rice
AA320981 EST23406 Adipose tissu
AL04008 Arabidopsis thaliana g
A1235399 EST231961 Normalized I
AQ210986 HS_2229_AZ_D06_MR CIT
AQ129594 HS_2254_AZ_B12_MR CIT
AI407553 EST235843 Normalized I
AN19172 MR4-SIQ069-080999-003-
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                                                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Search time (sec): 8553.360000
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Query: US-08-653-294-19
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9b_gss6:A0864396
9b_est12:AA320981
9b_est24:A1235399
9b_est24:A1235399
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9b_gss10.A0225567

9b_est14.AA43950

9b_est14.AA43950

9b_gss11.A0569045

9b_est40.AM442967

9b_est40.AM442967
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gb_est27.A1407553
gb_est44:AN170173
gb_est10:AA194167
gb_est35:A1826628
gb_est35:A184155
gb_est41:AN159605
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gb_estl:T04318
gb_est8:AA003505
gb_est4:R65508
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gb_est38:AL120179
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gb_est19:AA802027
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gb_gss6:AQ840156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_gss11:AQ327491
gb_gss4:AQ729455
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High quality sequence stop: 263
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Class: cosmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 214-648-1666
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3.800
83.333
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US-08-653-294-19 x AA897834
                                                                                                                    Seg primer: T7
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JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                             is Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A Large Scale Structural Analysis of CDNAs in a Unicellular Green Alga, Chlamydomonas rethnardtii. I. Generation of 3451 non-redundant Expressed Sequence Tags non-redundant Expressed Sequence Tags on Jun 5, 1998 this sequence version replaced gi:3189716. Contact: Yasukazu Nakamura The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.irce Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 575)
Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
Cushing,T., Errett,A., Flehatty,M., Gorman,M., Judson,R.,
Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S.,
Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S.
and Natvig,D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3055"
/db_xref="taxon:3055"
/clone="CL51a05_r"
/clone="Lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequences from conidial, mycelial, and sexual stages of
                                                           Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Jan 19, 1998 this sequence version replaced gi:2151810. Contact: Natvig.D.O./Nelson,M.A. Department of Biology University of New Mexico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Sordariales;
Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AA897834 575 bp mRNA EST
DEFINITION NCPSELT7 Perithecial Neurospora crassa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 80.000
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                Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C9"
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90.000
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US-08-653-294-19 x AV395907
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AA897834
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Ratio:
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/sex="Mating type a (fluiffy), fertilized"
/tissue_type="Perithecia" (fruiting bodies)"
/dev_stage="perithecia" (fruiting bodies)"
/note="mRNA isolated from 5 day old perithecia (fruiting bodies) of the fluify strain fl a (Mating type a), fertilized with conidia from 74-0R23-IV A (Mating type A).
cDNA directionally cloned into pBluescript SK(-) using the Dai-ZAP XN vector system (Stratagene, La Jolla, CA).

115 c 90 g 181 t
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1 (bases 1 to 263)

Evans, G.A., Burbee, D., Davies, C.; Hahner, L., Oliver, T., Gilbert, M., Jones, D., Mard, T., Gillilan, E., Schagemann, J., Probst, S., Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K., and Garner, H.R.
                                                                                             Email: ngp@blology.unm.edu
Deposited in GSDB at the National Center for Genome Resources with
accession GSDB:S:1146747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B02055 263 bp DNA GSS 13-JUL-1996 CSRL-147D11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-147D11, genomic survey sequence.
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Unpublished (1996)
Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
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PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 12
Gaps: 0
Percent Identity: 66.667
Castetter Hall, Albuquerque, NM 87131, 1
Tel: 505 277 3411
Fax: 505 277 0304
                                                                                                                                                                                                                                           102 TACAGACTGGATATATCTAAAGTCAAGTTAAGGTAT 137
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                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Perithecial"
                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:5141"
/clone="NP5E1"
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ĀQ815582
AQ815582.1 GI:5777975
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US-08-653-294-19 x H72837/rev
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                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                      /sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
/note="Vector: sCOs-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Oyary (CHO) monochromosomal
somatic cell hybrid, J1"
43 c 55 g 87 t 14 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H72837 504 bp mRNA EST 27-OCT-1995
ys06c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:213984 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 504)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Dubrquer,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Rucaba,T., Lacy,M., Le.M., Le.M., Le.M.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Trevaskis,E., Underwood,K., Wohldmann,P., Tan,F., Thlerry Meg,J.,
and Marra,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estewatson.wustl.edu
Insert Size: 528
High quality sequence stops: 380
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 528 Std Error: 0.00
Seq primer: Promega -21ml3
                                                                             /clone="cSRL-147D11"
/clone_lib="cSRL flow sorted Chromosome 11 specific
cosmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 8, 1995 this sequence version replaced gi:799648.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                            Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: B02055 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
1. .263
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LOCUS H72837
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ACTORNEL 1308 (ADD. ACCES-TORNEL 1308)

ALIGNMENT 120 (ADD. ACCES-TORNEL 1308)

ALIGNMENT 130 (ADD. ACCES-TORNEL 1308)

ACCESSION (ADD. ACCES-TORNEL 1308)

AC
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seq_documentation_block:
LOCUS AQ864396
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Ratio:
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                                                                                        264
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                   BASE COUNT
ORIGIN
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS
A0851612 724 bp DNA GSS 18-OCT-1999
DEFINITION CpG1352B CpIOWAgDNA1 Cryptosporidium parvum genomic similar to SKB1
homologue (negative regulator of mitosis) (regulator of Shk1, a
p21(Cd642/Rac)-activated kinase (PAK)), genomic survey sequence.
ACCESSION A0851612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/1d/CpTags/home.html
Seq primer: T3
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5807"
/db_xref="taxon:5807"
/clone_lib="CptOWAgDNA1"
/lab_host="E. coli XL2 Blue MRF'"
/note="Vector: pBlueScript II (SK-); Site_1: EcoRV; C.
parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a Light size distribution between 2-4 kb by Dr. Yoonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.stanford.edu/group/techdev/shear.htm). The randomly
sheared gDNA was chromatographed on Sephacryl S-400 to
remove any small Iragments and DNA eluting in the void
volume was subcloned into an EcoR V-digested, alkaline
phosphatase-treated pBlueScript II (SK-) vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryptosporidium parvum.
Cryptosporidium parvum.
Cryptosporidium parvum
Cryptosporidium parvum
Cryptosporidiudae; Alveolata; Aplicomplexa; Coccidia; Eimeriida;
Cryptosporidiudae; Cryptosporidium.

Strong, W.B. and Nelson, R.G.
Cryptosporidium parvum GSS Project
Unpublished (1997)
On Sep 10, 1998 this sequence version replaced g1:3553959.
Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
                                                                                                                                  /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
145 ç 123 g 144 t 20 others
1. .622
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=924 Col=12 Row=I"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                    Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 TATAGAACGCCCATAGAATAAGTGGCTCTAAGATAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 724
/organism="Cryptosporidium
/strain="IOWA"
                                                                                                                                                                                                                                                                                                                                                                                                                              to: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ851612.1 GI:6063307
                                                                                                                                                                                                                                                                                           4.111
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US-08-653-294-19 x AQ815582
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ORGANISM
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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/strain="Japonica"
/cultivar="Nipponbare"
/cultivar="Nipponbare"
/cultivar="Nipponbare"
/clone="nbeb0023013f"
/clone=lib="CUGI Rice BAC Library (ECORI)"
/tlssue_type="Leaf"
/lab_nost="E. Coli DH10B"
/note="Vector: pBACIndigo; Site_1: ECORI; Site_2: ECORI;
Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
Oryza sativa
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On fice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa,
transformed into E. coli strain XL2 Blue MRF'. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 brimers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oryza sativa genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae; Oryza.
1 (bases 1 to 794)
Ming.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ864396 794 bp DNA GSS nbeb0023D13f CUGI Rice BAC Library (ECORI) Or clone nbeb0023D13f, genomic survey sequence. AQ864396 1 GI:6214957
                                                                                                                                                                                                                                                                 4.111 Length: 11 Gaps: 0 81.818 Percent Identity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tal: 864 656 7288
Fax: 864 656 4293
Email: rwingelemson.edu
Seq primer: TAATACGACTATAGGG
Class: BAC ends
High quality sequence start: 84
High quality sequence stop: 408.
Location/Qualifiers
ce
1. 794
/organism="Oryaz aativa"
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                                                                                                                                244
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US-08-653-294-19 x AQ851612/rev
                                                                                                                                υ
                                                                                                         primers.
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seq_name: gb_gss1:CNS00WT6
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                                  FEATURES
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Butheria; Frimates: Catarini; Hominidae; Homo.

Stadms,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldher,R.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm.C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Moreno-Palanques,R.F., McDonald,L.A., Mquyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Ll.Y., Dimke,D.D., Foriggs,T.A., Utterback,T.R., Weidman,J.F., Ll.Y., Dimke,D.D., Koak,D.D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Rozak,D.L., Kunsch,C., Hungun,J., Li.H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu.C., Yu,G.L., Ruben,S.M., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nuclectides of CDNA sequence
No Sep 12, 1996 this sequence version replaced gi:1397790.

Contact: Kerlavage, AR
Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley! 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Sor clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AA320981 275 bp mRNA EST 19-APR-1997
DEFINITION EST23406 Adipose tissue, white II Homo sapiens cDNA 5' end, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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9712 Medical Center Drive, Rockville, MD 20850
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                 Length: 11
Gaps: 0
Percent Identity: 81.818
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AA320981
AA320981.1 GI:1973309
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3.700
90.909
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1 (bases 1 to 494)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Sanson, D., Saurin, W., Weissenbach, J. and Quetier, F.
Uppublished
2 (bases 1 to 494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thale cress. Arabidopsis thaliana Eukarbodopsis thaliana Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (25-UON-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EWRX cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                   4 others
                                                 /organism="Homo sapiens"
/db_xref="ATCC (inhost):121563"
/db_xref="taxon:9606"
/clone_lib="Adipose tissue, white II"
//tissue_type="adipose tissue, white"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 275
                                                                                                                                                                                                                                                                                                                Length: 12
Gaps: 0
Percent Identity: 50.000
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Gaps: 0
Percent Identity: 45,455
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/strain-"Columbia"
/db_xref="taxon:3702"
/clone_lib-"TAMU"
                                                                                                                                                                                                                   82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AA320981 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                  Location/Qualifiers
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177 c 114 g
                                                                                                                                                                                                                   61
Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĀL094008
AL094008.1 GI:5295162
                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-19 x AA320981/rev
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                                                                                                                                                                                                                                                                                                                                    3.273
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3.600
90.909
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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL COMMENT

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthbria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 502)
Manairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 508)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:

LOCUS AQ129594 508 bp DNA GSS 23-SEP-1998

LOCUS AQ129594 AZ_B1Z_MR CIT Approved Human Genomic Sperm Library D Homo

DEFINITION HS_2254_AZ_B1Z_MR CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=2254 Col=24 Row=C, genomic survey
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Location/Qualifiers
1. .502

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/ db_xref="taxon:9606"
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                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 row: G column: 12
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 others
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Gaps: 0
Percent Identity: 58.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AQ210986
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AQ129594.1 GI:3506760
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US-08-653-294-19 x AQ210986/rev
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                                                   Homo sapiens
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Ratio:
Percent Similarity:
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS A123539 502 bp mRNA EST 31-JAN-1999
DEFINITION EST231961 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVCR36 3' end, mRNA sequence.
ACCESSION A1235399 GI:3828905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ210986 18-SEP-1998 HS_3229_AZ_D06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=12 Row=G, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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/clone="lb="Normalized rat ovary, Bento Soares"

/note="Organ: ovary; Vector: pT/T3Pac; Site_1: EcoR1;

Site_2: Not1"

site_2: Not1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 502)
Lee.N.H.; Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
On Jan 19, 1998 this sequence version replaced gi:2151609.
Other_ESTS: TC5429
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 502
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Gaps: 0
Percent Identity: 75.000
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| CGAATGGCAGTAGTCAAGGTAGCCATGAGGTAC 448
                                                                                               2 ArgLeuAlaIle***ArgIleAlaLeuArgTyr 12
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AQ210986.1 GI:3619955
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US-08-653-294-19 x AI235399/rev
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4.000
75.000
                                                   to: CNS00WT6
    US-08-653-294-19 x CNS00WT6
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LOCUS AQ210986
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Ratio:
Percent Similarity:
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                                                   Align seg 1/1
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BASE COUNT ORIGIN

FEATURES

DEFINITION

ACCESSION VERSION

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alignment_block:
                     BASE COUNT
ORIGIN
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TITLE
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VERSION
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DEFINITION EST235843 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVELT 3' end, mRNA sequence.
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Lee.N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus sp."
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/note="Organ: ovary; Vector: p17T3Pac; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
On Feb 17, 1998 this sequence version replaced gi:2889619.
Contact: Lee, NH
ATCC
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 516-3818
Fax: (206) 516-3818
Fax: (206) 516-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2254 row: C column: 24
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                           2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 12
Gaps: 0
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                                                                                                                                                                                     High quality sequence stop: 508.
Location/Qualifiers
1. 508
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A1407553.1 GI:4251057
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Site_2: Smal; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
| 4 a | 113 c | 118 g | 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tal: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: satimpson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=MR4&t2=MR4-ST0069-080999-003-CO2&t23=1999-09-088t4=1)
Seq primer: puc lB forward
High quality sequence stop: 519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW179<u>1</u>72 520 bp mRNA EST 16-NOV-1999
MR4-ST0069-08099-003-C02 ST0069 Homo sapiens CDNA, mRNA sequence.
AW179172
AW179172.1 GI:6445209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saplens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 520)
HCGP http://www.ludwig.org.br/ORESTES.
The FARESP/LICR Human Cancer Genome Project
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5406194.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                     to: 511
                                                                                                                                               Length: 12
Gaps: 0
Percent Identity: 75.000
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Gaps: 0
Percent Identity: 50.000
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                         108
Site_2: NotI"
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US-08-653-294-19 x AI407553/rev
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                      151 a
                                                                                                                                                                      Ratio:
Percent Similarity:
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US-08-653-294-19 x AW179172

Align seg 1/1 to: AW179172 from: 1 to: 520

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GenCore version 4.5
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OM protein - protein search, using sw model

; Search time 122.56 Seconds
(without alignments)
2.706 Million cell updates/sec February 8, 2000, 01:29:40 Run on:

US-08-653-294-20 63 1 YRLAIRIXRILLRY 14 Title: Perfect score:

Sequence:

188963 segs, 23686106 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query	_			
Scor	a !	Length	8	ID	Description
4	. 99		н	542	-B2702 84-7
4	.99	1	Н	379	tide B2702.84
4	2 66.7		Н	W33799	겉
	65.	7	٦	290	ប
4	65.	7	٦	542	4
4	1 65.	2	٦	377	ati
3	7 58.	46	7	619	1 00
3	6 57.	7	٦	290	HLA-B2702 CTL modu
m	6 57.	7	Н	290	H
m	6 57.	7	Н	379	20
٣	6 57.	7	Н	379	02.8
٣	4 54.	2	Н	543	HLA-B2702 84-75T/7
3	4 54.	33	Н	594	Canine Y5 receptor
m	4 54.	33	-	6	Canis domesticus Y
m	4 54.	44	Н	523	euro
Ŕ	4 54.	44	Н	523	Ë
Ϋ́	4 54.	<b>4</b> 4	7	2097	Rat neuropeptide Y
c	4 54.	44	٦	260	ţ
m	4 54.	44	Н	290	Rat neuropeptide Y
m	4 54.	45	-	293	Human Y5 receptor.
m	4 54.	45	٦	944	Human hippocampal
m	4 54.	45	~	941	Human hippocampal
m	4 54.	45	-	709	Homo sapiens hippo
m	4 54.	45	٦	594	Rat Y5 receptor. M
m	4 54.	45	Н	44	Rat hypothalamic n
٣	4 54.	45	Н	941	Rat hypothalamic n
m	4 54.	45	Н	709	Canis domesticus Y
e	4 54.	45	Н	709	Rattus norvegicus
m	4 54.	46	Н	23	Mouse neuropeptide
٣	4 54.	8	Н	389	Thermotoga neapoli
m	4 54.	88	Н	390	
e	4 54.	88	Н	390	
m	4 54.	8	~	0	nea
ń	4 54.	8	П	391	Wild type Ine poly

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Gaps 5;

66.7%; Score 42; DB 1; Length 12; 78.6%; Pred. No. 0.045; tive 0; Mismatches 1; Indels

Query Match 66.7 Best Local Similarity 78.6 Matches 11; Conservative

1 YRLAIRIXRILLRY 14 ||||||| || ||| | YRLAIR--RIALRY 12

ò සු W33798 standard; peptide; 12 AA. W33798;

7

RESULT W33798 ID W3 AC W3

Mutant The polymerase The DNA polymerase	ALIGNMENTS	2-NoV-1996 (first entry) 2-NoV-1996 (first entry) LA-B2702 84-79-84 palindrome. Cell; aphal-Nellx; human-language shock protein; Hsc70; APC; cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; ynthetic. O9513288-A1. O9513288-A1. O-NOV-1994; UL2985. O-NOV-1993; US-150493.	(STRD ) UNIV LELAND STANFORD JUNIOR.  Glaybeager C, Krensky AM;  WPI: 95-194037/25.  Compsns. comprising lymphoid surface membrane proteins - which may inhibit yet/olytic activity and differentiation of CTLs.  Example: Page 12: 29pp; English and inferentiation of CTLs.  Example: Page 12: 29pp; English . This sequence represents the HAN-B2702 84-79-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the hear shock protein HSC70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable expressed on B and T cells. p74 can be isolated by lysis of a suitable coll with a mamphoteric detergent, and then passed through an affinity column containing a covalently bound HA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HA-B2702 60-84 (see R99416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of determining the amount of binding between the candidate composition of CTL activity can be inhibited in a cellular composition mix the extracellular portion of p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
W53919 W83978 W83974 W83980 W83981 W83981 W83988 W83988 W83988	ALIG AA.	drome. human-leucc human-leucc protein; ma cytotoxic inting ceil.	STANFORD JUNIOR.  Iyamphoid surface litivity and diffe pp; English.  colated antigens.  alindrome. Thes  alindrome. Thes  alindrome. Thes  in a T-cell lysate  inth T-cell activ  cross reactive  mited number of  cells. p74 can  mited number of  cells. p74 can  mited number of  covalently bound  into the extracel  te (CTL) differe  eened for their  g them with the  mit of binding be  tivity can be in  mid antigen prese  trivity can be in  nd antigen prese  reportion of p74  ding of the p74
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<i>-</i>	Ü	ry) pugg	ANFOR ANFOR ANFOR ANFOR VILY VILY ANTOR INCLUDE ANTOR
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	peptide;	1942.996 (first entry) A-B2702 84-79-84 palindrome. A: P74: alphal-helix; human-cell isate; membrane proteincell calcium influx; cytototofolysis; antigen presenting mithetic.	berger C, Krensky AM; berger C, Krensky AM; berger C, Krensky AM; 95-194027/25. sns. comprising lymphoid surfa blit cytolytic activity and di ple; Page 12; 29pp; English. 13, and R95415-R95431 represent n-leucocyte-associated antiger B2702 84-79-84 palindrome. Tr protein P4 from a T-cell lyst ein associated with T-cell act is found in a limited number of ssed on B and T cells. p74 with an amphoteric detergent, mn containing a covalently bou ositions comprising the extrac B2702.60-84 (see R95416), indi ctoxic T lymphocyte (CTL) diffect counds can be screened for their lation of CTL activity can be alming T-cells and antigen pre the extracellular portion of pri
00000000000	ີ່ຕ	(first 79-84 79-84 hal-he hal-he memb in find inf tigen Um 2985 US-150	ELA Kristi 11:255 11:255 11:25 1
	standard;	96 ( 84-7 alph alph sate; alciu alciu ant; Al. 94; U	o ) UNIV LELAN Nerger C, Kre 95-194027/Kre 116. 794027/Kre 116. 79404027/Kre 116. 7940415 116. 79415 116. 79415 117.00 124 127.02 8415 127.02 8415 127.02 8415 127.02 8415 127.02 80 B and With an ampho With an ampho
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 R95429 ID R95429	H H H K O O O H H H H H	PA (STRD) UNIV WINDS 95-1940 PI COMPSES. COMP PT COMPSES. COMP PT Inhibit cyto PT Example; and CC Human leucoc CC He Protein asso CC The Protein asso CC Protein asso CC Protein asso CC COMPOSITIONS CC CONTAINING T CC CONTAINING T

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New immunomodulating dimer peptide(s) - based on a Class I HLA-B PT New immunomodulating dimer peptide(s) - based on transplants or treating autoimmune diseases

Fracting autoimmune diseases

CC Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity, heptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or compensed forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = CC (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC or Small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid; account of the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions or undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CDS. The peptide can be used for preventing rejection of transplants or for treating autcommune diseases, e.g. dlabetes, consense for detection and diagnosis. The products can also be sensed for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 42; DB 1; Length 12; 78.6%; Pred. No. 0.045;
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                                                                                                                                                                                                        24-MAY-1996; US-653294.
(STR) JUNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
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24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w33799 standard; peptide; 12 AA.
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Best Local Similarity 78.6
Matches 11; Conservative
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| YRLAIR--RIALRY 12
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22-MAY-1997; U08689
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WO9744351-A1.
                                                                                                                              Homo sapiens
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19-JUN-1998
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claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proteins of interest to activate CTLS. They can also inhibit the close of the proteins of interest to activate CTLS. They can also inhibit autoimmune diseases, e.g. daabetes, rheumatoid arthritis and lupus erythematosis.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.
These sequences can be used to extend the period of acceptance by a reclipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R92907 standard; peptide; 20 AA.
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Matches 11; Conserv
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WO9526979-Al.
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PRI 195-194027/25.

Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example: Page 12: 29pp; English.

Example: Page 12: 29pp; English.

R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the LHA-B2702 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell activation in mammalian T-cells, and is protein associated with T-cell activation in mammalian T-cells, and is protein associated with T-cell activation in mammalian T-cells, and is protein massociated number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcum influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of etermining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition mix the extracellular portion of p74 and and mix the extracellular portion of p74, in an amount sufficient to compete containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing the binding of the p74 ligand.
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                                                                     HIA-B2702 84-75-84 palindrome.

HIAA-B274: alphal-helix: human-leucocyte-associated antigen; inhibitor;

T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;

cytolysis; antigen presenting cell.
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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22-MAY-1997; U08689.

24-MAY-1996; US-653294.

(STRD) UNIV LELAND STANFORD JUNIOR.

Beulow R, Clayberger C, Krensky AM:

WPI: 98-086530/08.

New immunomodulating dimer peptide(s) - based on a Class I HLA-B

alpha-1 domain, used for preventing rejection of transplants or
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                                                                                                                                                                           18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; U5-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C. Krensky AM;
             R95428 standard; peptide; 20 AA.
R95428;
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Best Local Similarity 55.0%;
Matches 11; Conservative 1
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                                                       12-NOV-1996 (first entry)
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                                                                                                                                                            WO9513288-A1.
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WO9744351-A1.
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RESULT
R95428
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(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                     of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W33791;
19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime modulate (or limited) period of the cyptotoxic I lymphocytes (CTLs) of the patient.
formation of biomass or a desired product, e.g. the product may be lactic acid which results in the acidification of dairy products. The method is more efficient than currently used methods of biomass production. Sequence 469 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                HIA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
Yototoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claybory C. Krensky Aw, runner Clayborger C, Krensky Aw, runner Clayborger C, WPI; 95-358582/46.

Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                              Score 37; DB 1; Length 469;
Pred. No. 13;
4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%; Score 36; DB 1
50.0%; Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1995.
05-APR-1995, U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                 R92909 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R92908 standard; peptide; 20 AA.
                                                                                                                                 58.7%;
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                                                                                                                                                                              Conservative
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05-APR-1995; U04349.
05-APR-1994; US-222851.
                                                                                                                                                                                                                        1 YRLAIRIXRILLRY 14
                                                                                                                                                                                                                                               | :|: |:| ||
362 YEVAMEVQRVLQRY
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Best Local Similarity
                                                                                                                                                    Local Similarity
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Synthetic.
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Matches
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Wet; servenosuouves.

Pur menunomodulating dimer peptide(s) - based on a class I HIA-B
alpha-1 domain, used for preventing rejection of transplants or
alpha-1 domain, used for preventing rejection of transplants or
by treating autofimmune diseases.

Example 1; Page 19; 41pp; English.

Example 1; Page 19; 41pp; English.

Peptides W3384-98 and W33778-9 were assayed for their immunomodulating activity, including the N-terminal acylated and/or
criminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B =
CC (R a376-771) (a379-44) or (a384-79) (Laa77-76R); aa76 = E or V; aa77 =
CD, S or N; aa79 = R or G; aa80 = I or N; aa81 = a hydrophobic or
Small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino
acid. The sequence in the brackets may optionally be absent or truncated
at any peptide type bond within the brackets. The compounds comprise
at any peptide type bond within the brackets. The compounds comprise
canino acid sequences related to a Class I HIA-B alphal domain (positions)
79-84). They can be used to inhibit cyctoxic I-lymphocytes (CIL) from
undesirably attacking cells in a host or in vitro. They can also be
used in combination with antigenic peptides or proteins of Interest to
activate CILs. They can also inhibit the proliferation of T cells in
response to anti-CD3. The peptide can be used for preventing rejection
cof transplants or for treating autoimmune diseases, e.g. diabetes,
cused for detection and diagnosis. The products can also be
considered.

Example 10 or 10
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                                                                                                                                                                                                                           Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.
These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to.a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Peptide B2702.84-75r/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Pred. No. 0.95;
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Parham P;
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22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
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          Clayberger C, Krensky AM,
WPI; 95-358582/46.
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Best Local Similarity 50.0 Matches 10; Conservative
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N-PSDB; T30435
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ID R
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The immunomodulating dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1: Page 19: Alpp: English.

Example 1: Page 10: Alph 10
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12-NOV-1996 (first entry)
HLA-B2702 84-757/75-84T palindrome.
HLA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                     Gaps
                                                                                                                                                                                                                                                19-JUN-1998 (first entry)
Peptide B2702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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             Length 20;
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               Score 36; DB 1;
Pred. No. 0.95;
                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1997: U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM:
WPI: 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytolysis; antigen presenting cell.
                                                                                                                                                                                                                  W33792 standard; peptide; 20 AA
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           57.1%;
50.0%;
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                                                                                                                         1 YRLATRINERRENLRIALRY 20
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                                                                                       1 YRLAIRI-----XRILLRY
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                                                     10; Conservative
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             Query Match
Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                               Synthetic
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While Strangerising lymphoid surface membrane proteins - which may thinbit cytolytic activity and differentiation of CTLs.

Example 12. 29pp. English.

Example 12. 29pp. English.

R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the card range of the Partol 84-77-84 palindrome. These sequences can be used too isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cells, and is also immunologically cross reactive with the heat shock protein Rsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphorteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Claims 58; F14 15; 235pp; English.
Claims F8; F14 15; 235pp; English.
Canine Y5 receptor (R95940), isolated as an 'atypical Y1
receptor. The receptor belongs to the G protein-coupled receptor
superfamily. It is encoded by a cDNA clone (see also T30435) that
was isolated by PCR amplification using primers (T30436-37) based
on human and rat cDNA clones (T30433-34). Recombinant canine Y5
receptor can be produced in prokaryotic or eukaryotic (e.g. COS,
293 or Sf9 insect) host cells. It is used to identify Y5 ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine IS receptor.

YS receptor; atypical neuropeptide Yl receptor; feeding behavior;
YS protein coupled receptor; agonist; antagonist; obesity;
bulinnia: anoraxia.

Canis familianis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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increases or decreases food consumption, for treatment of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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WPI; 96-277371/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1;
Pred. No. 2.2;
1; Mismatches
18-MAY-1995.
10-NOV-1994.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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06-JUN-1996.
01-DEC-1995, U15646.
02-DEC-1994; US-349025.
(SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIRINETRENLRIALR 19
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                                                                                                                                                     Clayberger C, Krensky AM;
WPI; 95-194027/25.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding canine hypothalamic atypical neuro:peptide Y/peptide YY receptor, Y5 - useful for identification of compounds which are apable of modifying feeding behaviour capable of modifying feeding behaviour capable of modifying feeding behaviour.

PS Claim 5; Fig 15; 273pp; English.

Claim 5; Fig 15; 273pp; English.

The sequence is that of a Y5 receptor (Y5-R).

The sequence is that of a Y5 receptor (Y5-R).

The sequence or reduce the activity of a Y5-R. In particular, inhibitors can be used to reat obesity and activity of a Y5-R. In particular, inhibitors can be used to treat obesity and activators can be used to treat anorexia. Antagonists capable of alleviating (by decreasing the activity of Y5-R) an abnormality can be identified by administering whether the substance alleviates the physical and behavioural abnormalities displayed by the transgenic mammal as a result of overactivity of a Y5-R. Agonists can be identified in a similar manner, but where the abnormality is alleviated by increasing the activity of but where the abnormality is alleviated by increasing the activity of the content of
                                                                                                                                                              ö
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W15232;
1-JUL-1997 (first entry)
Rat neuropeptide Y-Y5 receptor.
Neuropeptide Y-Y5; appetite; obesity; G-protein coupled receptor;
antiobesity; hypotensive; neuronal growth factor;
cardiovascular drug; anti-psychotic; neuroleptic; antidiabetic;
agonist; antagonist.
                                                                                                                                                              ö
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(agonists and antagonists) that can be used to treat obesity, bulinia or anorexia. Sequence 334 AA;
                                                                                         DB 1; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.0%; Score 34; DB 1; Length 334; 42.9%; Pred. No. 34; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y5 receptor; treatment; anorexia; bulimia; obesity;
feeding behavlour; modification; atypical neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1997.
04-JUN-1997; U09504.
21-FEB-1997; US-803600.
04-JUN-1996; US-668650.
(SYNA-) SYNAPTIC PHARM CORP.
Branchek T, Gerald CP, Walker MW, Weinshank RL;
WPI: 98-051901/05.
                                                                                                                  Score 34; DB ]
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W15232 standard; Protein; 445 AA.
                                                                                                                                                                                                                                                                                                                                                              W37094 standard; Protein; 334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1998 (first entry)
Canis domesticus Y5 receptor.
                                                                                                                    54.0%;
42.9%;
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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95 YRIAFTISLLLVQY 108
                                                                                                                                                                                                           1 YRLAIRIXRILLRY 14
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95 YRIAFTISLLLVQY
                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domesticus
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W15232
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PF 08-NOV-1996; AU0706.

PR (GARV-) GARVAN INST MEDICAL RES.

PI Herzog H;

BR WPI: 97-281029/25.

DR N-PSDB; 7-681029/25.

CC Anover rat hupothar and agonists, useful as anti-obseity agents, which is involved in appetite/obesity requiation. Its amino CC acid sequence was deduced from a CDNA CONE (F06911) isolated from CC acid sequence was deduced from a CDNA CONE (F06911) isolated from CC acid sequence was deduced from a CDNA CONE (F05911) isolated from CC acid sequence was deduced from a CDNA CONE (F05911) isolated from CC acid sequence for (ant)agonists of host (F06911) isolated from CC expressed on the cells uniface of host (F06911) isolated from CC expressed on the cells uniface of host (P06911) isolated from CC expressed on the cells uniface of host (F06911) isolated from CC expressed on the cells uniface of host (P06911) isolated from CC expressed on the cells uniface of host (B06911) isolated from CC expressed on the cells uniface of host (B06911) isolated from CC expressed on the cells can cC expressed on the cells uniface of the form of the form of the cells of the form of the for
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Search completed: February 8, 2000, 01:29:41 Job time: 1753 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model OM protein ; Search time 117.7 Seconds
(without alignments)
5.611 Million cell updates/sec February 7, 2000, 11:54:30 Run on:

1 YRLAIRIXRILLRY 14 US-08-653-294-20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

pir1:\* pir2:\* pir3:\* PIR\_62:\* 1: pir1: 2: pir2: 3: pir3: 4: pir4: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	H+-transporting	ď	hypothetical prote	УIС	ase	acyl-CoA oxidase (	conserved hypothet	COAC	COA	COA	ıtin	acyl-CoA oxidase (	acyl-CoA oxidase (	hypothetical prote	probable citrate 1	acetyl-CoA carboxy	acyl-CoA oxidase (	SEC7 protein - yea	ribosomal protein	AhyR protein - Aer	iron (iii) abc tra	H+-transporting AT	H+-transporting AT	probable phoR prot	probable coA ligas	otein	probable membrane	긎	5	hypothetical prote	
SUMMARIES	OI.	T09974	B70775	D72110	F64075	H70474	OXCKPM	B69327	OXCKAX	OXCKX4	OXCKX	S39842	OXCKP2	JC4563	F72612	F72721	A70404	OXCKX5	S49764	G72250	857939	G75035	S30597	S37547	A70706	G70986	A49282	S48405	T08868	T10296	D72509	
	88												П																			
	Query Match Length		486	133	194	478	709	96	502	709	709	3131	724	724	157	276	323	662	2009	149	260	331	470	478	485	532	1729	2376	2630	202	339	
de	Query	•	61.9	ď	ö	ċ	ö	ζ.	ζ.	Ľ.	7	ζ.	55.6	'n.	٠.	4	₹.	54.0	4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	ď.	50.8		
	Score	n	39	38	38	38	38	36	36	36	36	36	35	35	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	32	32	
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5489 1113 1113 1195 1220 224 224	334 343 351
$\begin{array}{c} 0.00444444444\\ 0.0000000000000\\ 0.0000000000$	4 4 9 . 2 4 9 . 2
	3113
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## ALIGNMENTS

RESULT 1		
T09974		
H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Mycobacterium leprae	- Mycobacterium leprae	
C;Species: Mycobacterium leprae	•	
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999	ext_change 20-Sep-1999	
C; Accession: T09974	•	
R; Robison, K.		
submitted to the EMBL Data Library, September 1994		
A; Reference number: 216911		
A; Accession: T09974		
A;Status: translated from GB/EMBL/DDBJ		
A; Molecule type: DNA		
A; Residues: 1-485 <rob></rob>		
A;Cross-references: EMBL;U15186; NID;a699323; PID;a699347	9347	
C; Keywords: ATP blosynthesis; hydrolase; membrane-associated complex	ociated complex	
Query Match 61.9%; Score 39; DB 2; Length 485;	ength 485;	
Best Local Similarity 57.1%; Pred. No. 3.7;	•	
	Indels 0; Gaps 0;	
Oy 1 YRLAIRIXRILLRY 14		

||:| : ||| || 376 YRVAQEVIRILQRY 389 g

probable atpD protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Accession: B70775
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Daviso, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hanlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Atuthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID: 98295987
A;Accession: B70775
A;Acce

Score 39; DB 2; Length 486; Pred. No. 3.7; 61.9%; 57.1%; Query Match Best Local Similarity

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Conserved hypothetical protein AF0618 - Archaeoglobus fulgidus
conserved hypothetical protein AF0618 - Archaeoglobus fulgidus
c) Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Accession: B69327
B; Accession: B69327
B;
                                                                                                                                                                                                                                              A; Residues: 1-478 <AQF>
A; Residues: 1-478 <AQF>
A; Cross-references: GB:AE000769; NID:g2984262; PIDN:AAC07790.1; PID:g2984264; GB:AE00
A; Experimental source: strain VF5
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase
R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
C;Species: Candida maltosa
C;Dacte: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 17-Feb-1995
C;Accession: A29441
R;Hill, D.E.; Boulay, R.; Rogers, D.
Nucleic Acids Res. 16, 365-366, 1988
A;Fitle: Complete nucleotide sequence of the peroxisomal acyl CoA oxidase from the A;Reference number: A29441; MUID:88124223
                                                                                           A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-709 <HIL>
A; Residues: 1-709 <HIL>
C; Genetics: A; CC 20184
C; Genetics: A; Gene: POX4
C; Superfamily: acyl-CoA oxidase
C; Superfamily: acyl-coA oxidase
C; Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
                                                                                                                                                      A;Accession: H70474
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <ATP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;163-170/Region: nucleotide-binding motif A (P-loop)
F;189-358/Domain: H+-transporting ATP synthase alpha chain homology
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Pred. No. 5.7;
3; Mismatches
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Pred. No. 8.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.3%;
50.0%;
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50.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
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308 YRMLARVSTIALRY 321
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                           C; Accession: F64075
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Googne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630
A; Accession: F64075
A; Status: nucleic acid sequence not shown; translation not shown.
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A;Start codon: GTG
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP synthase F1 beta subunit - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: H70474
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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   Indels
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   4
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Pred. No. 2.4;
6; Mismatches
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Pred. No. 1.7;
2; Mismatches
Mismatches
5
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61.5%;
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   Conservative
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377 YRVAQEVIRILQRY 390
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FKLGVRLLKIFIRY
                                                              1 YRLAIRIXRILLRY
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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C; Species: Candida tropicalis
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 30-Sep-1993
C; Accession: A29047
R; Murray, W.W.; Rachubinski, R.A.
Gene 51, 119-128, 1987
A; Title: The parimary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast A; Reference number: A29047; MUID:87248070
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-709 <MUR>
A; Residues: 1-709 <MUR>
A; Residues: 1-709 <MUR>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enniatin synthetase - fungus (Fusarium scirpi)
c;Species: Rusarium scirpi
c;Species: Rusarium scirpi
c;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: S39842; S35906; S65363
R;Haese, A.
Submitted to the EMBL Data Library, November 1992
A;Reference number: S39842
A;Accession: S39842
A;Molecule type: DNA
A;Residues: 1-3131 <AABE>
A;Residues: 1-3131 <AABE>
A;Cross_references: EMBL:218755; NID: 92729; PID: 92730
A;Cross_references: EMBL:218755; NID: 32729; PID: 92730
A;Cross_references: EMBL:218155; NID: 32729; PID: 92730
A;Cross_references: EMBL:218156; Nid: Zocher, R.
Mol. Microbiol. 7, 905-914, 1993
A;Title: Molecular characterization of the enniatin synthetase gene encoding a multif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental Source: strain ETH 1536/J5
R; Pieper, R.; Haese, A.; Schroeder, W.; Zocher, R.
Eur. J. Biochem. 230, 119-126, 1995
A; Title: Arrangement of catalytic sites in the multifunctional enzyme enniatin synthe A; Reference number: S65363; MOID: 95324513
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C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
                                                                                                                                                                                                                                               acyl-CoA oxidase (EC 1.3.3.6) AOx, peroxisomal - yeast (Candida tropicalis)
     Gaps
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A;Residues: 2029-2048;430-437;1011-1020;1021-1034;1677-1695;2294-2299
A;Experimental source: strain ETH 1536/J5
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C:Superfamily: gramicidin S synthetase I repeat homology;
C:Reywords: multifunctional enzyme; phosphopantetheine; ph
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Pred. No. 21;
2; Mismatches
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A;Molecule type: DNA
A;Residuae type: DNA
A;Residus: 499-1074;1572-1988;2423-2566 <HA2>
A;Cross-references: EMBL:218755
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50.0%;
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308 YRMLARMSTIALRY 321
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                                                        1 YRLAIRIXRILLRY 14
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Best Local Similarity
Matches 7; Conserv
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     Matches
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Proc. Natl. Acad. Sci. U.S.A. 83, 1232-1236, 1986
A;Title: Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis: pr A;Reference number: A94084; MUID:86149279
A;Accession: A25123
                                                                                                                                                                                                                                                                                                                                                                                                                                acyl-CoA oxidase (EC 1.3.3.6) POX4-2, peroxisomal - yeast (Candida tropicalis) (fragment NaMeste names: acyl-CoA oxidase II-2
C;Species: Candida tropicalis
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change II-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A28584; MUID:87280361
A;Accession: A28584; MUID:87280361
A;Accession: A28584; MUID:87280361
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A; Residues: 1-709 < OKA>
A; Cross-references: GB:M12160; NID:g170911; PIDN:AAA34362.1; PID:g170912
A; Experimental source: strain pK233, ATCC 20336
C; Comment: This enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation
; this reaction is the initial step of the peroxisomal beta-oxidation system. In C. trop
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ic reactions as well as the enzymes involved are usually different from the mitochondria
A;Molecule type: DNA
A;Residues: 1-96 <KLE>
A;Cross-references: GB:AE001062; GB:AE000782; NID:g2689385; PID:g2650002; TIGR:AF0618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: POX4-2
C;Superfamily: acyl-CoA oxidase
C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
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C;Superfamily: acyl-CoA oxidase
C;Reywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
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A.Residues: 1-502 <SMA>
A.Cross-references: GB:Y00623; NID:92672; PIDN:CAA68660.1;
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Pred. No.
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Pred. No.
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Pred. No.
                                                                                                                                       57.1%;
61.5%;
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50.0%;
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Matches 8; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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Gaps

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Indels

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Pred. No. 34;

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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Cacession: F72612
B;Kavarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-157 < KAM>
A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80356.1; PID:d1044142; PID:g
A;Experimental source: strain K1
C;Genetics:
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C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Dates 20-Salon: F72721
R; Kavarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Accession: F72721
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A;Experimental source: strain K1
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                                                                                                                                                                                                                                                                                                           hypothetical protein APE1362 - Aeropyrum pernix (strain K1)
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58.3%;
      50.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
      Best Local Similarity 50.(
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A; Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-276 <KAV
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A;Gene: APE1362
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C;Species: Candida maltosa
C;Species: Object: Candida maltosa
C;Accession: JC4563
R;Masuda, Y; Park, S.M.; Ohta, A.; Takagi, M.
Gene 167, 157-161, 1995
A;Title: Cloning and characterization of the Pox2 gene in Candida maltosa.
A;Reference number: JC4563; MUID:96144267
A;Reference number: JC4563; MUID:96144267
A;Residues: 1-724 cMAS>
A;Molecule type: DNA
A;Residues: 1-724 cMAS>
A;Cross-references: DDBJ:D21228; NID:9416286; PIDN:BAA04761.1; PID:d1005293; PID:9416287
A;Experimental source: P2DD
C;Comment: This protein is a member of the acyl-CoA oxidase family, and it is involved if C;Genetics:
C;Genetics:
A;Gene: pox2
C;Superfamily: acyl-CoA oxidase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-724 <0Khb.
A;Cross-references: GB:M18259; NID:g170909; PIDN:AAA34361.1; PID:g170910
C;Comment: This enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation
this reaction is the initial step of the peroxisomal beta-oxidation system. In C. trop
gene family.
C;Comment: The peroxisomes are eukaryote subcellular organelles that generate and degrad
ic reactions as well as the enzymes involved are usually different from the mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acyl-CaA oxidase (EC 1.3.3.6) PXP2, peroxisomal - yeast (Candida tropicalis)
C;Species: Candida tropicalis
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C;Accession: A: Tan, H:; Fukui, S.; Kubota, I.; Kamiryo, T.
Gene 58, 37-44, 1987
A;Title: Peroxisomal acyl-coenzyme A oxidase multigene family of the yeast Candida tropi
A;Reference number: A27331; MUID:88084444
F;1543-2574/Domain: gramicidin S synthetase I repeat homology #status atypical <GRS2> F;1603-2044/Domain: acetate--CoA ligase homology <ACL2> F;2507-2574/Domain: acyl carrier protein homology <ACP1> F;2601-2667/Domain: acyl carrier protein homology <ACP2> F;001-2667/Domain: acyl carrier protein homology <ACP2> F;1047,2538,2632/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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Keywords: FAD: fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
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                                                                                                                                                                                                                Score 36; DB 2; Length 3131; Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 724;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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2637 KLAVRIGRRLIRH 2649
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Best Local Similarity
Matches 7; Conserv
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Length 157;

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Score 34; DB 2 Pred. No. 12; 2; Mismatches

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Score 34; DB
Pred. No. 21;
2; Mismatches
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 54.0%;
50.0%;
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turkey ente escherichia caenorhabdi

P20530 P28544 O59300 P22654 P10525 P26626 P26626 P26133 P26133 P52133 P72980 P72980

YVAU\_VACCC RS8\_CHLTR RL13\_PXRHO YIOR\_CVBF YIOR\_CVBK YFIOR\_CVTKE YFJR\_ECOLI

bovine coro bovine coro

chlamydia

escherichia synechocyst pseudomonas

YAFY\_ECOLI LIP1\_SYNY3 HOLB\_PSEAE

227 AA

PRT;

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOSSE J.T., MACINNES J.I.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY FACILITATING NICKEL INCORPORATION.
-!- SIMILARITY: BELONGS TO THE UREF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AA; 25397 MW; 310CB946 CRC32;
                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
UREASE ACCESSORY PROTEIN UREF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPB_MYCLE STANDARD; PRT; 485 AA. P45823; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) ATP SYNTHASE BETA CHAIN (EC 3.6.1.34).
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Best Local Similarity 42.5
Best Local Similarity
6. Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
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97 YKLGVRLLKIFIRY 110
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SMITH D.R., ROBISON K.;
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Mycobacterium leprae.
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SEQUENCE
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UREF_ACTPL
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ATPB_MYCLE
TD PATPB_LYIN
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caenorhabdí
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6.563 Million cell updates/sec
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                                                                                                                              8, 2000, 00:59:58; Search time 63.71 Seconds
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                82229 seqs, 29864866 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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NYSR_CARRA
NYSR_ETG
NYSR_HUMAN
NYSR_RAT
NYSR_RAT
NYSR_RAT
NYSR_RAT
ANAWAR
SEC7_YEAST
ATPB_LACCA
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ATPB_LACCA
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CAO4_CANMA
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LMA3_MOUSE
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ATPB_ENTHR
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PACA_CLAMA
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Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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                                                                                                                                                                                                                                       1 YRLAIRIXRILLRY 14
                                                                                                                                                                                                  US-08-653-294-20
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Match Length DB
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Maximum DB seq length: 1000000
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Gaps

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Length 227; Indels

Score 42; DB 1; Pred. No. 0.16; 5; Mismatches

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Nickel.
SEQUENCE
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UREF_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                            SUBUNIT: F-TYPE ALPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BEATA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
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COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., COLE S.T., BROSCH R., PAS S., BARRY C.E. III, TERRIA F., GRADON S.V., EIGLMEIDER K., GAS S., BARRY C.E. III, TERRIA F., DAVIES R., DEVLIN K., FELWELL T., CENTIGE S., HAMILN N., HOLROYD S., HORNER T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MIRPLY I., HORNSHY T., JAGELS K., SEEGER K., SEEGER K., SEEGER K., SEEGER K., SELTON S., SQUARES S., SQUARES R., SULSTON J.E., TAYLOR K., WHITEHRAD S., BARRELL B.G.; SOURES S., SQUARES R., SCHEN T., MOULE S., SOURES S., SQUARES R., SALSTON J.E., MILTEHRAD S., BARRELL B.G.; MYCODACTETIUM TUDETCUIOSIS from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                       -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
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                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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07216783 CRC32;
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PFAM; PF00306; ATP-synt_ab_C; 1.
Hydrolase; ATP synthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ATPD SYNTHASE BETA CHAIN (EC 3.6.1.34).
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PS00152; ATPASE_ALPHA_BETA; 1.
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376 YRVAQEVIRILQRY 389
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Best Local Similarity
Lass 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                          SUBUNIT.
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Q10593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPB_MYCTU
SO DE PRESENTATION DE PRESENTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLEYAGES A.R., BULT C.J., TOMB J.F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIREY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNAM M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., GINE L.D., FRIYCHMAN J.L., FUHEMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIENCE 269-496-512(1995).
-!- FUNCTION: PROBABLY FACILITATING NICKEL INCORPORATION.
-!- SIMILARITY: BELONGS TO THE UREF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AA; 21960 MW; 44EB0D8E CRC32;
                                                                                                                                                                                                                                                                     EMBL; Z73419; CAA97743.1; -.
HSSP; P07677; 1SKY.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
PFAM; PF00006; ATP-Synt_ab; 1.
PFAM; PF00306; ATP-Synt_ab_C; 1.
Hydrolase; ATP Synthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A8001B2F CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 AA; 53094 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.9%;
57.1%;
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01-NOV-1995 (Rel. 32, Las
UREASE ACCESSORY PROTEIN
UREF OR H10537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrogen ion transport.
NP_BIND 171 178
SEQUENCE 486 AA; 5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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377 YRVAQEVIRILQRY 390
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P44395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBDUIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAWAA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                              STRAIN=VF5;
MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G., WARREN F.V., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDWAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATURE 392:353-358(1998).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98248216.
LUDWIG W., STRINK O., KLUGBAUER S., KLUGBAUER N., WEIZENEGGER M.,
PUEMAIER J., BACHLEITNER M., SCHLEIFER K.H.;
"Bacterial phylogeny based on comparative sequence analysis.";
Electrophoresis 19:554-568(1998).
                             15-DEC-1999 (Rel. 37, Last sequence update)
ATP SYNTHASE BETA CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0152, ATPASE_ALPHA_BETA; 1.
PFAM; PF00006; ATP-SYNt_ab.
T.
PFAM; PF00306; ATP-SYNt_ab_C; 1.
Hydrolase; ATP SYNthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ATP SYNTHASE BETA CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                    Bacteria; Aquificales; Aquificaceae; Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Aquificales; Aquificaceae; Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478 AA; 53321 MW;
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Best Local Similarity 50.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 YEVAMEVKRILORY 382
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                   Aquifex aeolicus
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                          15-DEC-1998
15-DEC-1998
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050292;
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SEQUENCE
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SOT WEEK WAS A PROCESS OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT:
-:- THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNIT:- ALPHA(3), BTA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
-:- SIMILARITY:- BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUDWIG W., NEUMATER J., KLUGBAUER N., BROCKMANN E., ROLLER C., KLUGBAUER S., REFIZ K., SCHACHTNER I., LUDVIGSEN A., BACHLEITNER M., FISCHEFR U., SCHLEIFER K.H.; "Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.";
Antonie Van Leeuwenhoek 64:285-305(1993).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpetosiphon aurantiacus (Herpetosiphon giganteus).
Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 471;
Pred. No. 2.3;
3; Mismatches 4; Indels
                       Length 194;
                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TP (BY SIMILARITY).
AAE39561 CRC32;
                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NOV-1995 (Rel. 32, Created)
NOV-1995 (Rel. 32, Last sequence update)
NOV-1995 (Rel. 32, Last annotation update)
SYNTHASE BETA CHAIN (EC 3.6.1.34).
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HSSP; P07677, 1SKY.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
PFAM; PF00006; ATP-Synt_ab, 1.
PFAM; PF00306; ATP-Synt_ab_C; 1.
Hydrolase; ATP synthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                             471 AA.
                                                        .9
                                                                                            Mismatches
                       Score 38;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                             PRT;
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50.0%;
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Matches 7; Conservative
                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 YRVATEVORMLORY 377
                                                                                                                                                                                         64 FKLGVRLLKIFIRY 77
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                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HPGA1;
MEDLINE; 94368062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Greer
Herpetosiphon.
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                         ATPB_HERAU
P42466;
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SEQUENCE
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ATPB_HERAU
                                                                                         Matches
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Gaps

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Score 38; DB 1; Length 478; Pred. No. 2.4; 3; Mismatches 4; Indels

478 AA.

STANDARD;

ATPB\_AQUAE ID ATPB\_AQUAE

P (POTENTIAL). 0E23DB68 CRC32;

ATP

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55528 MW;
                                                                                                                                                                                                                                                   60.3%;
50.0%;
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50.0%;
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Best Local Similarity 50.0.
                                                                                                                                                                                                                                                   Query Match 60.3
Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                      Multigene family.
INIT_MET 0
SEQUENCE 708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - COFACTOR: FAD
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P11355;
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P06598;
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CAO3_CANTR
ID CAO3_CANTR
DO CAO3_CANTR
OT 01-JUI
DT 01-JU
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AN WAR OS
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                                                  SUBUNIT:
-:- SUBUNIT:
-:- SUBUNIT:
-:- SUBUNIT:
-:- SUBUNIT:
-:- SUBUNIT: F.TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MIN SUBUNITS: A, B AND C.
-:- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ATCC 20184;
MEDLINE: 8812423.
HILL D.E., BOULAY R., ROGERS D.;
Complete nuclectide sequence of the peroxisomal acyl CoA oxidase from the alkane-utilizing yeast Candida maltosa.";
Nucleic Acids Res. 16:365-366(1988).
-:- CATALYIC ACTIVITY: ACYL-COA + O(2) = TRANS-2,3-DEHYDROACYL-COA + H(2)O(2) (ACYS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FROM R TO 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: FAD.
-!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
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01-MXY-1992 (Rel. 22, Last sequence update)
01-MXY-1992 (Rel. 22, Last annotation update)
ACYL-COENZYME A OXIDASE POX4 (EC 1.3.3.6) (ACYL-COA OXIDASE) (AOX).
FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida maltosa (Yeast).
Eukaryota; Fung1: Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.3%; Score 38; DB 1; Length 478; 50.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y15786; CAA75780.1; -.
PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
PFAM: PF000005; ATP-SYNt_ab; 1.
PFAM: PF00306; ATP-SYNt_ab C; 1.
Hydrolase; ATP synthesis; CF(1); ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
8F8ADBE9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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SEQUENCE 478 AA; 53393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SUBUNIT: HOMOOCTAMER.
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369 YEVAMEVKRILQRY 382
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Matches 7; Conserv
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P05335;
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MEDLINE; 87280361.
SMALL G.M., LAZAROW P.B.;
SMALL G.M., LAZAROW P.B.;
Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of Candida tropicalis.";
J. Cell Biol. 105:247-250(1987).
-!- CATALTIC ACTIVITY: ACYL-COA + O(2) = TRANS-2,3-DEHYDROACYL-COA + H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FROM 8 TO 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
EMBL; X06721; CAA29901.1; -.
PIR; A29441; OXCKPM.
Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A28584; OXCKAX.
Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE II (EC 1.3.3.6) (ACYL-COA OXIDASE) (PXP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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Eukaryota: Fungi: Ascomycota: Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 135, Last sequence update)
ACYL-COENZYME A OXIDASE POX4-2 (EC 1.3.3.6) (ACYL-COA OXIDASE)
                                                                                                                                                                                                                            Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; 'DB 1; Length 502;
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                            Score 38; DB 1;
Pred. No. 3.6;
2; Mismatches
                                                                                                              0 0 BY SIMILARITY.
708 AA; 78242 MW; D5E344D2 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708 AA.
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-1- SUBCELLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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A. M.

STRAIN=RR1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- CATALYTIC ACTIVITY: ACYL-COA + O(2) - TRANS-2,3-DEHYDROACYL-COA + H(2)O(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FROM 8 TO 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
Multigene family.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE POX2 (EC 1.3.3.5) (ACYL-COA OXIDASE) (AOX).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88084444.

WARAZAKI K., TAN H., FUKUI S., KUBOTA I., KAMIRYO T.;

"Percoxisomal acyl-coenzyme A oxidase multigene family of the yeast Candida tropicalis; nucleotide sequence of a third gene and its
                                                                                                                                                                                                                 Candida tropicalis (Yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
                                                                               01-JUL-1989 (Rel. 11, Created)
01-MXY-1992 (Rel. 22, Last sequence update)
01-NOV-1997 (Rel. 35, Last nonotation update)
ACYL-COENZYME A OXIDASE PXP-2 (EC 1.3.3.6) (ACYL-COA OXIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 723;
15;
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                             723 AA.
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Pred. No.
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                                PRT;
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50.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Gene 58:37-44(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=IAM 12247;
MEDLINE; 96144267.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMALL G.M., LAZAROW P.B.;
"Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of Candida tropicalis.";
J. Cell Biol. 105:247-250(1987).
-:- CATALYTIC ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY: ACTIVITY SON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH
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                                                                                                                                                                                                                                                                                                                                 "Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis: primary structures deduced from genomic DNA sequence."; Proc. Natl. Acad. Sci. U.S.A. 83:1232-1236(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 87248070. MEDLINE; 87248070. MURAX W.W., RACHUBINSKI R.A.; MURAX W.W., RACHUBINSKI R.A.; The primary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast candida tropicalis pK233.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN REF. 2 AND 3).
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G -> A (IN REF. 2).
E -> S (IN REF. 2).
ELA -> DLV (IN REF. 2).
Q -> E (IN REF. 2 AND 3).
W; D97A4EC8 CRC32;
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Pred. No. 9.2;
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P -> A (IN F
N -> K (IN F
FRAMESHIFT
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EMBL; M12160; AAA34362.1; --
EMBL; Y00623; CAA68660.1; --
EMBL; Y00623; CAA68661.1; ALT_INIT.
EMBL; Y00623; CAA68662.1; ALT_INIT.
PIR; A25123; OXCKX4
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ММ
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50.0%;
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STRAIN-ATCC 20336 / PK233;
MEDLINE; 86149279.
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Best Local Similarity
Matches 7; Conserv
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Gaps

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Indels

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B 16/:15/-161(1995).
CATALYTIC ACTIVITY: ACYL-COA + O(2) = TRANS-2,3-DEHYDROACYL-COA +
                                                                                                                                                                                                                                                            MASUDA Y., PARK S.M., OHTA A., TAKAGI M.; "Cloning and characterization of the POX2 gene in Candida maltosa."; Gene 167:157-161(1995).
Eukaryota; Fungl; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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CONFLICT CONFLICT SEQUENCE

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Local Similarity
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062729;
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DOMAIN
TRANSMEM
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CARBOHYD
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INCLUE 392.358(1998).

INCLUE 393.353-358(1998).

(2)Q(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FROM 8 TO 18). COFACTOR: FAD.
                                                               PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHMAD DE., OVERBEEK R., SHEDDAN R.A., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT ALPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 724;
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                  Multigene family. –
SEQUENCE 724 AA; 82273 MW; 1AE92F21 CRC32;
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                                                                                                          SIMILARITY).
                                                                                                        SUBUNIT: HOMOOCTAMER (BY SIMILARIT SUBCELLULAR LOCATION: PEROXISOMAL.
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Best Local Similarity
'-hac 7; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          species homologs.";
Regul. Pept. 75:45-53(1998).
-!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADBNYLATE
CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD
BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                       Gaps
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SEGULNE; 99017379.
BOROWSKY B., WALKER M.W., BARD J., WEINSHANK R.L., LAZ T.M.,
VAYSSE P., BRANCHEK T.A., GERALD C.;
"Molecular biology and pharmacology of multiple NPY Y5 receptor
"Molecular biology and pharmacology of multiple new Y5 receptor
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NEUROPEPTIDE I RECEPTOR ITPE 5 (NPY5-R) (NPY-Y5 RECEPTOR) (Y5
RECEPTOR) (NPY5).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                     Length 323;
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PFAM: PF00001; 7tm_1; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein
Phosphorylation; Lipoprotein; Palmitate.
DOMAIN 139 EXTRACELULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                  Score 34; DB 1;
Pred. No. 10;
4; Mismatches
                                                            4A96C81E CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                  446 AA
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CYTOPLASMIC (P
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EMBL; AE000728; AAC07216.1; --
Fatty acid biosynthesis; Ligase.
SEQUENCE 323 AA; 36198 MW: 4
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                                                                                                                                     54.0%;
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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POTENTIAL

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Search completed: February
Job time: 3787 sec
 TRANSMEM
DOMAIN
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DOMAIN
CARBOHYD
CARBOHYD
DISULFID
LIPID
SEQUENCE
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                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JION Y., MINEZAMA M.;

"Sus scrofa gene for neuropeptide Y receptor type 5, complete cds.";

"Sus scrofa gene for neuropeptide Y receptor type 5, complete cds.";

"Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE Y: THE ACTIVITY

OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE

CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD

BE INVOLVED IN FERDING DISORDERS (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANT PROTEIN.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        WRAITH A., TORNSTEN A., CHARDON P., HARBITZ I., CHOWDHARY B.P., ANDERSON L., LARHAMMAR D.;
"PORTIGE NBY receptors NPYIR, NPY2R and NPY5R: cloning, mapping and comparative analysis.",
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                    15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NEUROPEPTIDE Y RECEPTOR TYPE 5 (NPY5-R) (NPY-Y5 RECEPTOR) (Y5
                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                        Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                     Indels
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EMBL: AB019185; BAA34055.1; -.
PROSITE: PSO0237; G_PROTEIN_RECEPTOR; FALSE_NEG.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
BY SIMILARITY.
PALMITATE (POTENTIAL).
7D2CD74A CRC32;
                                                                                        Score 34; DB 1;
Pred. No. 14;
                                                                                                                                                                                                                                                           446 AA
                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                           PRT;
                                             51012 MW;
                                                                                        54.0%;
42.9%;
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SEQUENCE FROM N.A.
STRAIN-LWD: TISSUE-KIDNEY;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                     11:1 | :|::|
207 YRIAFTISLLLVQY 220
                                                                                                                                                   1 YRLAIRIXRILLRY 14
                                             446 AA;
                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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NPYSR OR NPYRS.
CARBOHYD
DISULFID
LIPID
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097969;
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FT TRANSMEM 369 391 6 (POTENTIAL).
FT TRANSMEM 405 428 CYPOCENTIAL).
FT TRANSMEM 405 428 (POTENTIAL).
FT TRANSMEM 405 446 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 POTENTIAL.
FT CARBOHYD 17 17 POTENTIAL.
FT CARBOHYD 17 17 POTENTIAL.
FT LIPID 442 442 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (POTENTIAL).
SQ SEQUENCE 446 AA; 50474 MW; 79A4E2F3 CRC32;

QUERY MATCH 54.0%; Score 34; DB 1; Length 446;
Best Local Similarity 42.9%; Pred. No. 14;
Best Local Similarity 42.9%; Pred. No. 14;
MATCHES 6; CONSERVATIVE 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 YRIAFIELLINQY 220
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8, 2000, 00:59:58

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Wed Feb

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2000, 13:17:48; Search time 209.03 Seconds (without alignments)

4.644 Million cell updates/sec

Title: US-08-653-294-20
Perfect score: 63
Sequence: 1 YRLAIRIXRILLRY 14
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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225878

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

225878 seqs, 69334122 residues

Searched:

Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: SPTREMBL\_12:\*
1: Sp\_archea':\*
2: sp\_bacteria:\*
3: sp\_tungi:\*
4: sp\_lumman:\*
5: sp\_lumman:\*
6: sp\_lumman:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_organelle:\*
10: sp\_plant:\*
11: sp\_rodent:\*
12: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_vertebrate:\*

SUMMARIES

	Description	Q9z903 chlamydia p	Q20456 caenorhabdi	045019 caenorhabdi	029637 archaeoglob		070073 agrobacteri	Q00869 fusarium sc	Q44541 azotobacter	Q57090 corynebacte	Q9xil2 arabidopsis	050159 streptococc	O49025 gracilaria	Q9yc92 aeropyrum p	P94457 bacillus st.	Q9yfd0 aeropyrum p	093237 cyprinus ca	Q9zj01 streptococc	O15451 homo sapien	O15450 homo sapien	Q9x1g5 thermotoga
	Ð	Q9Z903	020456	045019	029637	074720	070073	698000	044541	057090	Q9XIL2	050159	049025	Q9YC92	P94457	Q9YFD0	093237	092701	015451	015450	Q9X1G5
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фP	Query	60.3	60.3	58.7	57.1	57.1	57.1	57.1	55.6	55.6	55.6	55.6	54.0	54.0	54.0	54.0	54.0	54.0	54.0	54.0	52.4
	Score	38	38	37	36	36	36	36	35	35	35	35	34	34	34	34	34	34	34	34	33
	Result No.	П	7	m	4	Ŋ	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20

P71815 mycobacteri 004376 arabidopsis P72007 mycobacteri 0977b1 pichia past 055319 acyrthosiph 008534 sugar bet 054741 mus musculu 094889 aeropyrum p 02882 chiamydia p 023072 arabidopsis 09326 caenorhabdi 089906 beet yellow 066739 saccharomyc 070180 ratus norv 056739 saccharomyc 06739 caenorhabdi 069408 aeropyrum p 094081 aeropyrum p 094081 aeropyrum p 08412 treponema p 093780 caenorhabdi 062070 pseudomonas 062676 podospora a	•
P71815 004376 0977807 097781 055319 064833 088630 092863 0933072 0933072 093306 005139 007180 007180 007180 007180 007180 007180 007180 007180 007180 007180	
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44444444444444444444444444444444444444	

## ALIGNMENTS

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Gaps
                                                                                                                                                                                                         KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L., GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;
"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AE001604; AAD18334.1;
Hypothetical protein.
SEQUENCE 133 AA, 16132 MW; 8DA54C6A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                     Query Match 60.3%; Score 38; DB 2; Length 133; Best Local Similarity 61.5%; Pred. No. 4.3; Matches 8; Conservative 2; Mismatches 3; Indels
                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL 16.1 KD PROTEIN.
CPN0181.
CRAIN DRUMONIAE.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                  133 AA
                  PRT;
                PRELIMINARY;
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88 RIPWRLKRILLRY 100
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             Q92903
Q92903;
Q9Z903
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Best Local Similarity 61.5%; Pred: No. 4.3;
Matches 8; Conservative 2; Mismatches 3; Indels 0; G

QY 2 RIARIXRILLRY 14

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Db 88 RIPWRLRILLRY 100

RESULT 2
020456
ID 020456
ID 020456
DT 01-NOV-1996 (TEMBLE-1 01, Created)
DT 01-NOV-1999 (TEMBLE-1 10, Last sequence update)
DT 01-MAY-1999 (TEMBLE-1 10, Last annotation update)
DF HUM-4 PROTEIN.
GN HUM-4.
CS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

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Archaeoglobus.
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SEQUENCE 96
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01-JAN-1998
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                                                                                                                      MEDLINE: 94150718.
MEDLINE: 94150718.
MISCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MISCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER I., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN N., LAIRRILLE P.,
LIGHTWING J., LLOYD C., MCHURRAY A., MORTHMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULZON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.).
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 2810;
86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                              COTINGE A.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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"The sequence of C. elegans cosmid ZC123.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AF043706; AAB97603.2; -.
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Last sequence update)
Last annotation update)
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Pred. No. 8
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PROSITE; PS00028; ZINC_FINGER_C2H2; 6.
PFAM; PF00096; Zf-C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).

EMBL; 266563; CAA91469.1; -.

PFAM; PF00613; IQ; 2.

PFAM; PF00063; myosin_head; 4.

PFAM; PF0784; MYTH; 2.

SEQUENCE 2810 AA; 323526 MW;
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Science 282:2012-2018(1998).
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Best Local Similarity
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                                          SEQUENCE FROM N.A.
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Gaps
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KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUGH J., LEE N.H., SUTTON G.G., GILL S.,
KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A.,
OVERBERK R., GOCANTE J.D., WEIDMAN J.F., MCNONALD L., UTTERBACK T.,
GOTTON M.D., SPRIGGS T., ARTIACH P., KINIE B.P., SYKES S.M.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
Homeobox; DNA-binding; Nuclear protein; Zinc-finger; Metal-binding.
SEQUENCE 1592 AA; 178053 MW; BAFDE8CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390.364-370(1997).
EMBL: AE001062: AAB90622.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                  Length 1592,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TIEMBLIEL. 08, Created)
01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-NOV-1998 (TIEMBLIEL. 08, Last annotation update)
LINBAR PLASMID PDHIJ, ORFI AND ORFZ, PARTIAL (FRAGMENT).
Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l protein.
96 AA; 10892 MW; 76C3565A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                         96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 AA.
                                                                                                  Score 37; DB 5
Pred. No. 77;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB Pred. No. 7.6; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONSERVED HYPOTHETICAL PROTEIN
                                                                                                  58.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 05, C (TrEMBLrel. 05, I (TrEMBLrel. 07, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%;
61.5%;
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STRAIN-ATCC90624, CBS7848;
                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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51 YRLAIKISTELLK 63
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                                                                                                                                                                                                                                                        477 RVAIRLMRILL 487
                                                                                                                                                                                                        2 RLAIRIXRILL 12
                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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Bacteria; Proteobacteria; gamma subdivision; Azotobacteraceae;
  Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes; Hypocreales; Hypocreaceae; anamorphic Hypocreaceae; Fusarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 89123097.

MEDLINE: 89123097.

JACOBSON M.R., BRIGLE R.E., BENNETT L.T., SETTERQUIST R.A., WILSON M.S., CASH V.L., BEYNON J., NEWTON W.E., DEAN D.R.;

"Physical and genetic map of the major nif gene cluster from Azotobacter vinelandill.",

J. Bacteriol. 171:1017-1027(1989).

EMBL; M20568; AAA64728.1;

PROSITE; PROSITE; PROBLEMAREPETRANSFERASES; 1.
                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 3; Length 3131;
Pred. No. 2.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium xerosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
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Last sequence update)
Last annotation update)
                                                          SEQUENCE FROM N.A.
STRAIN=LAMBOTTE ET FAUTREY;
HARSEA A., SCHUBERT M., HERRMANN M., ZOCHER R.;
MO1. MICTODIO1. 010-0(1922).
EMBL, Z18755; CAA79245.1; -.
EMBL, Z18755; CAA79245.1; -.
EMBL, Z0784; FUSSE7; 3105, 20784.
PROSITE; PS00455; AMP_BINDING; 2.
PRAM; PF00560; AMP-Dinding; 2.
PFAM; PF00568; DUF4; 2.
PFAM; PF005154; AMP-Dinding; 3.
PRINTS; PROMISE; PP-Dinding; 3.
PRINTS; PROMISE; PAMPBINDING.
SEQUENCE 3131 AA; 346891 MW; 00949DB9 CRC32;
                                                                                                                                                                                                                                                                                                      3131 AA; 346891 MW; 00949DB9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00132; hexapep; 3.
SEQUENCE 265 AA; 28346 MW; OCE25212 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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044541;
01-100-1996 (TrEMBLEEL. 01, C.
01-100-1996 (TrEMBLEEL. 01, L.
01-100-1999 (TrEMBLEEL. 01, L.
ORF 7.
                                                                                                                                                                                                                                                                                                                                                                       53.8%;
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Best Local Similarity 57.1%;
Matches 8; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.1
Best Local Similarity 53.8
Matches 7; Conservative
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2637 KLAVRIGRRLIRH 2649
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40 YRLANRIWRAAWRY 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLAIRIXRILLRY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Azotobacter.
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Q57090;
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  SOR REPORTED OCC
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                                                                     STRAIN-ATCCO0624, CBS7848;
MEDLINE; 97344364.
FUKUDA K., MAEBUCHI M., TAKATA H., GUNGE N.;
FUKUDA K., MAEBUCHI M., TAKATA H., GUNGE N.;
The linear plasmid pDHL1 from Debaryomyces hansenii encodes a protein highly homologous to the pGKL1-plasmid DNA polymerase.";
Feast 13:613-620(1997).
EMBL; AJ011124; CAA09498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piasmid pTiChry5.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                              Length 248;
                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
GUNGE N.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CHRYS;
OGER P.M., VAUDEQUIN V., DESSAUX Y.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ANT4;
OGER P.M., VAUDEQUIN-DRANSART V., DESSAUX Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065242; AAC17432.1;
EMBL; U67851: AAC12800.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
PUTATIVE PERIPLASMIC PROTEIN CHTH.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens, and Agrobacterium sp.
                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 3;
Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                           248 27239 MW; 54CD45A4 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                 Query Match 57.1%;
Best Local Similarity 75.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, ENNIATIN SYTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobiaceae; Agrobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Matches 6; Conserv
                                                              SEQUENCE FROM N.A.
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Fusarium scirpi.
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SEQUENCE
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SEQUENCE
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Q00869;
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070073
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Q00869
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.6%;
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Best Local Similarity 35.7
Matches 5; Conservative
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Plasmid Gch7220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gracilaria.
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SEQUENCE
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049025
AC 049025
AC 049025
DT 01-JUN
DT 01-JUN
DT 01-JUN
DC 01-JUN
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                                                                                                               TAUCH A., KASSING F., KALINOWSKI J., PUHLER A.;
"The Corynebacterium xerosis composite transposon Tn5432 consists of
two identical insertion sequences, designated IS1249, flanking the
erythromycin resistance gene ermCx.";
Plasmid 34:119-131(1995)
EMBL: U21300; AAC95477.1;
EMBL: U21300; AAC95477.1;
EMBL: U21300; AAC95444.1;
EEMBL: U21800; AAC95444.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Watyryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; euphyllophytes: Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots: Rosidae: eurosids II: Brassicales: Brassicaeea.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
pUTATIVE CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC
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Pred. No. 49;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.6%; Score 35; DB 2; Length 402; 60.0%; Pred. No. 49;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 12, Last annotation update)
PROTON-TRANSLOCATING ATPASE, BETA SUBUNIT (EC 3.6.1.34).
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Streptococcus bovis.
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Best Local Similarity
Matches 6; Conserv
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    FROM N.A.
                                                                          MEDLINE; 96117603
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SEQUENCE FR
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09XIL2
10 09XIL2
10 01-NOV.
DT 01-NOV.
DT 01-NOV.
DE 5.21.8
DE 5.21.8
DE 7.21.8
DE 7.2
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050159
AC 050159,
DT 01-JUN-
DT 01-JUN-
DE PROTON-
GN ATPD.
CS Streptc.
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Eukaryota; Rhodophyta; Florideophyceae; Gracilariales; Gracilariaceae;
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UMEMORI J., MIWA T., NAGAMINE T., OGATA K., TAKENAKA A., HINO T.;
Submitted (NOV.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB009314; BAA2375E.JI.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
PFAM; PF00006; ATP-SYNt_ab; 1.
PFAM; PF00306; ATP-SYNt_ab._C; 1.
Hydrolase; Hydrogen no transport.
SEQUENCE 469 AA; 51219 WW; A4170D3F CRC32;
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BEDINE: 99310339.

KAWARBARASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,

JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,

HOSOYAMA A., FUKUI S., NAGAI Y., NISHJJIMA K., NAKAZAWA H.,

TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
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Pred. No. 8.6;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                Length 469;
                                                                                                                                                                                                                                                                                                                                                          Indels
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SEQUENCE FROM N.A.
GOFF L.J., MOON D.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034719; AAC04733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
PLASMID GCH7220, COMPLETE SEQUENCE.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
157AA LONG HYPOTHETICAL PROTEIN
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                                                                                                                                                                                                                                                                                             Score 35; DB 2
Pred. No. 57;
3; Mismatches
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                                                                                                                                                             Gaps
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EMBL: Y08751; CAA699998.1;
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
NOMURA N., SAKO Y., KIKUCHI H.;
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KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,
TAKAMIYA M., MASUDA S., FUNHARASHI T., TAMAKA T., KUDOH Y.,
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
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STRAIN-NOIB 8224:
MEDLINE: 94113715.
SAKANYAN V. DESMARRE I., LEGRAIN C., CHARLIER D., METT T.,
KOCHIKYAN A., SAVCHENKO A., BOYEN A., FIRARD A.,
                       "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP0000061; BAA80356.1; -
SEQUENCE 157 AA: 17942 MW; CIF4AB62 CRC32;
                                                                                                                              Score 34; DB 1; Length 157;
Pred. No. 30;
2; Mismatches 3; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
276AA LONG HYPOTHETICAL CITRATE LYASE BETA CHAIN.
APE0311.
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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Archaea; Crenarchaeota; Aeropyrum.
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01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                             Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                               PRELIMINARY;
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32 YRLEMKTTEKLLRY 45
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SEQUENCE
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P94457;
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P94457
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Q9YFD0
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NOMURA N., SAKO Y., KIKUCHI H.;
"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP000059; BAA79266.1; -.
                                                                                                                                                                                   Score 34; DB 1; Length 276;
Pred. No. 53;
2; Mismatches 5; Indels
                                                                                                                         276 AA; 30725 MW; 4B749B21 CRC32;
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Best Local Similarity 50.0%;
Matches 7; Conservative
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259 YRLALNLLRRASRY
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54 i ALO49835 Human chromosome
80 i 299113 Bacillus subtills
! AB017564 Arabidopsis thallan
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1 (bases 1 to 84056)

Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W., Fasman,K.H. and Lander,E.S.
Genomic sequence from Mouse 11
Unpublished

2 (bases 1 to 84056)

Es (bases 1 to 84056)

Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J., Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J., Marquis,N., McDermott,J., Moloney,N., Mororow,J., Nachman,A., Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J., Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-Mar-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases I to 84056)

Hawkins,T.L., Rever,W.P., Christoffersen,A., Birren,B.W., Fasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barna,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J., Gage,D., Geralgery,K., Hagos,B., Jacotot,L., Lane,M., MacKenzie,J., Marquis,N., McDermort,J., Moloney,N., Morrow,J., Nachman,A., Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J., Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and
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Research, 320 Charles Street, Cambridge, MA 02141, USA
(Dases 1 to 84056)
Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B. M.,
Fasman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P.,
Barna, N., Chang, A., Cooke, P., Daly, M.J., Forrest, C., Fripp, W.J.,
Gage, D., Geralgery, K., Hagos, B., Jacotot, L., Lane, M., MacKenzie, J.,
Marquis, N., McDermott, J., Moloney, N., Morthan, A.,
Naglor, J., O'Connor, T., Peterson, K., Rollins, G., Spencer, J.,
Stilwell, J., Stone, C., Strickland, C., Sydney, K., Wilmer, F. and
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                                                                                                                                                                                                            10-JUL-1997
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
Location/Qualifiers
                                                                                                                                                                                                   AC002121 84056 bp DNA ROD
Genomic sequence from Mouse 11, complete sequence.
AC002121
AC002121.1 GI:2133880
   187564
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    /organism="Mus musculus"

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      gb_pr2:CNS0000E
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M16893 Methanococcus vannielii

AF064589 Homo saplens melanoma

X07793 Methanococcus voltae mc

235133 B.subtilis 168 pks gene

AC012410 Drosophila melanogast

AC012410 Drosophila melanogast

AC01541 Drosophila melanogast

AC01544 Drosophila melanogast

INT186 Mycobacterium tubercul

U15186 Mycobacterium leprae c

AC00547 Drosophila melanogast

AC00547 Drosophila melanogast

AC00548 Arabidopsis thallana

AL01355 Arabidopsis thallana

AL013555 Arabidopsis thallana

AL013559 Drosophila melanoga
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                                                                                                                                                                                                                                 Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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9b_p11:YSCREV3

9b_p11:YSCREV3

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gb_pl2:ATAC007187
gb_pl2:ATF4110
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gb_htg2:AC008259
gb_pr3:HS326L12
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gb_pr4:AC007262
gb_htg5:AC011614
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gb_ba1:MVOMCR
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gb_bal:MVMCR1
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gb_bal:MLU15186
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complement(11657. .11708)
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complement(11768. .11934)
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// Tpt_family="BIDIO"
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to reverse of: AC002121 from: 1 to: 84056

Align seg 1/1

1 TyrArgLeuAlaIleArgIle\*\*\*ArgIleLeuLeuArgTyr 14

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1408 C 162 g 1693 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 6715)
Bosse,J.T. and MacInnes,J.I.
Direct Submission
Submitted (18-FEB-1997) Pathobiology, University of Guelph, Guelph, Ont NIG 2W1, Canada
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                                                                                                         seq_documentation_block:
LOCUS APU89957 6715 bp DNA BCT 03-FEB-1998
DEFINITION Actinobacillus pleuropneumoniae urease operon (ureABCXEFGD) genes,
                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Actinobacillus pleuropneumoniae"
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Bosse, J.T. and MacInnes, J.I.
Urease genes of Actinobacillus pleuropneumoniae
Unpublished
44056 TATAGATCAGCAGTGACAATTGCCAGGGTCCTGCTCAGGCAC 44015
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U89957
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ORGANISM
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TITLE
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Mammalia;

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Street, Waltham, MA 02453, USA
Street, Waltham, MA 02453, USA
On Dec 8, 1999 this sequence version replaced gi:6456128.

**NOTE: This is a "vorking draft, sequence. It currently
** consists of 28 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
                                                                                               Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 172450)
Smith, Da
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contig of 4701 bp in length
gap of unknown length
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contig of 1267 bp in length
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of 2488 bp in length
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of 2337 bp in length
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of 4247 bp in length
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of 5247 bp in length
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of 5904 bp in length
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contig of 8155 bp in length
gap of unknown length
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Direct Submission
                    Homo sapiens
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Euthoria: Primates: Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 5066)

E 1 (bases 1 to 5060)

E 2 (bases 1 to 5060)

E 2 (bases 1 to 5060)

E 3 (bases 1 to 5060)

E 4 (bases 1 to 5060)

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E 8 (bases 1 to 5060)

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E 9 (bases 1 to 5060)

E 1 (bases 1 to 5060)

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Homo sapiens genomic DNA, chromosome 21q21.1-q21.2, clone:B662K22,
LL56-APP region, complete sequence.
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Gaps: 0
Percent Identity: 66.667
Percent Identity: 42.857
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/db_xref="taxon:9606"
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HTG; HTGS_PHASE1.
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AP000657.1 GI:6252989
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Percent Similarity: 100.000
                                                                                           Align seg 1/1 to: APU89957
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US-08-653-294-20 x APU89957
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LOCUS AP000657
Percent Similarity:
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QVHKTLEVKIRASFKRKKDDKHDLAGDKLGNLNFVADVSVVKGIPFYGYHVGWNLFYK
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NREKLQHRDIHHDFLEKLGDISDIPVKPYVSSARDMINELTMQREELSLKEYKEPPET
KRHVSGHQWQSSGEFEAFYKKAQHKTSTFDGQIPNFENFIDKNQKFSAINTPYEALPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae
Bukaryota; Fungil, Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae: Saccharomyces.
1 (bases 1 to 4828)
Burnelle, B., Coster, F. and Goffeau, A.
Unpublished
2 (bases 1 to 4828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (28-MAY-1996) Data collected by MIPS on behalf of the Submitted (28-MAY-1996) Data collected by MIPS on behalf of the European yeast chromosome XVI sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Maxinsried, FRG; E-mail: Mewes@mips.embnet.org
Location/Qualifiers
1. 4828
//organism="Saccharomyces cerevisiae"
//db_xref="taxon:4932"
//chromosome="XVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS SCYPL167C 4828 bp DNA PLN 11-AUG-1997
LOCUS SCYPL267C ACCUSTANTION S.GETEVISIAE CHROMOSOME XVI reading frame ORF YPL167C.
ACCUSSION 273523 UG0094
VERSION 273523.1 GI:1370352
others
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Percent Identity: 50.000
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/protein_id="CAA97873.1"
/db_xref="GI:1370353"
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/db_xref="SGD:S0006088"
complement(84. .4598)
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/note="ORF YPL167c"
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                                                                                             FEATURES
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VMAGGLRYCKRAFYYGEPPFGYODILNKLEDEGFPKIDYKDPFFSINPVOLENKPYAYA

GRRPEISSTHYSTRIPVORGGETVSYYNRPFEDMESSMKYALKPPTOAVOKKYNKYP

SMGNKRTESOISMHTPHSKPLYKRASDVSGKORKKSSVHBSLHTLILEIHANTRSDK

IDPPAIDEYSMIJWCLEBEPFPLOLDIAYECIMÍVHKASEDSGTFPTKOHÇINEIPWK

OFRTKLESOISMHTPHSKPLYKRASDVSGKORKKSSVHBSLTHTLILEIHANTRSDK

OFRTKLESOISMHTPHSKPLYRASDVSGKORKKSSVHBSLTHTLILEIHANTRSDK

OFRTKLESOISMHTRUEPREFPLOLDIAYECIMÍVHKASEDSGTFPTKOHÇINEIPKK

OFRTKLESOTWARTSOFFETHILDPOLLSGFETHNFSWGYIIERCOYLARNIPGARLICIDFHS

VLDPGSTYNGASFLIRICKSESFILLSFGKKOYRGKALECVPLVMEPESAFTKSPLI

VLDPGSLYNGWARTSOYRSTLSKMLTDILDVRVNIKTWHRIGDDUTTLKRCDNYTLKKIDYNIA

PNGVYPARTSOYRSTLSKMLTDILDVRVNIKTWHRIGDDUTTLKRCDNYTLKKIDYNIA

ANTTIGTTSARSTSCRAPCSOLLADSIVOTGRETLEKFEKAIDIIEKKÉFTMNNKOLALKLL

ANTTIGTTSARSTSCRAPCSOLLADSIVOTGRETLEKFEKAIDIIEKKÉFTWNNKOVYGOTDSL

FVYLPGKTTSASFSCRAPCSOLLADSIVOTGRETLEKFEKAIDIIEKKÉFTWNNKOVYGOTDSL

FVYLPGKTTSASFSCRAPCSOLLADSIVOTGRETLEKFEKVYHPSILIEKKFYVGFSYESF
                                                                                                                                                                                                                                                                                                                                                                                            SQTLPIFDAKGIETVRRDGIPAQOKIIEKCIRLLFQTKDLSKIKKYĞONEFFKIQIGK
SAQDPCFAKEKKLGAYKSEKTAPAGAVVKRRINEDHRABDQYKERIPLUVGKQG
QLLRERCVSPEEFLEGENLELDSEYINKILIPPLDKLFNLGINVGWAQEYKKSKA
ASTTITKVENIIRVGTSATCCNCGEELIKICSLQLCDDCLEKRSTTLSFLIKKLKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYQTLKTVCRTCSYRYTSDAGIENDHIASKCNSYDCPVFYSRVKAERYLRDNQSVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M84605.1 GI:189391
Opioid receptor.
Homo sapiens female placenta cDNA to mRNA.
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria: Primates; Catarrhin; Hominidae; Homo.
1 (Dases 1 to 4839)
Goldstein,A., Xie,G.-X. and Miyajima,A.
Expression cloning of CDNA encodding a seven-helix receptor from human placenta with affinity for opioid ligands
Proc. Natl. Acad. Sci. U.S.A. 89, 4124-4128 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMOPIODRE 4839 bp mRNA PRI Human putative opioid receptor mRNA, complete cds. M84605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            helixes (numbers are AA residues):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: SCYPL167C from: 1 to: 4828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.00 Length: 14
3.727 Gaps: 0
78.571 Percent Identity: 57.143
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II 93. .114

IV 177. .156

V 221. .245

VI 275. .296

VI 310. .334

serine-rich cytoplasmic tail: 35

Possible glycosylation sites: 7,

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="placenta"
94. .1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 9
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US-08-653-294-20 x SCYPL167C/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pr1:HUMOPIODRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1381 a
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Quality:
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Percent Similarity:
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92237319
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Wed Feb

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seq_name: gb_pl1:SCLACHXVI
                                                                                                                                                                                                                                                                                                                    hromosome XVI.
                                                                                                                                                                                                                                                                                              1770 a
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
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                                                                                                                                  AFADAAMAALNALVNFIYALHGEWYFGANYCRFQNFFPITAVFASIYSWTAIAVDRYM
ALIDPLKREATARTVIGSTWILAFPCLLAFPGCIYSKIKWYNGERILCYQWPDGSRQ
HFTYHMIVIVLVYCFPLLMGITYTYGITLWGGELPGDTCDKYQDGLKAKRKYVKWM
IIVVYTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLASFWLAMSSTWNPIIYCCL
WRFPRAFERRAFRWCPFIHYSSYDELELKAFRLHPWRQSSLYTVTRWBSMSVVFDSND
GDSRRSSHQRRGTTRDVGSNVCSRNSKSTSTTASFVSSSHMSVEGS"
1099 C 965 9 1326 L
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SLLNBOCZERKISELIRDGKIFGKRFFETESHFFYLLQWADPNLFGOSGNINDDROFF
RSPVLNSILDIDKLTINDDLQLLLDRFCDFKONVLSREDFPRYGNGILEIDILDOFIN
NREKLOHRDIHHDFLEKLGDISDIPVKPYVSSARDMINELTMQREELSLKEYKEPPET
KRYSGHOWGSSGEFRAKTROHKTGFFDGOIPNFENFINDKNKFFSATNTPYBALPQ
LWPRLAPOIEINNNSWODKYKTGYFFDGOIPNFENFINGNKOFFSATNTPYBALPQ
STASFKDSTILLDHGYTKYNTINFSMOCAMTONMASKRKLRSSVSANKTSLSSSVSHE
SIASPKDSTILLDHGYTKYNTINFSMOCAMTONMASKRKLRSSVSANKTSLSKRKKK
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GKRFEISSTHVSTRIPVQFGGETVSVYNKPTFDMFSSWKYALKPPTYDAVQKWYNKVP
SWGNKKTESQISMHTPHSKFLYKFASDVSGKQKRKKSSVHDSLTHLTLEIHANTRSDK
                                                                                       /translation="MASPAGNLSAWPGWGWPPPAALRNLTSSPAPTASPSPAPSWTPS
PRPGPAHPFLQPPWAVALWSLAYGAVVAVAVLGNLVVIWIVLAHKRMRTVTNSFLVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. cerevisiae DNA.
Saccharomyces cerevisiae
Eukaryota: Fungi: Ascomycota; Saccharomycetales;
Saccharomycetacee; Saccharomyces.

1 (bases 1 to 5056)
MONITION.A. Christensen,R.B., Alley,J., Beck,A.K., Bernstine,E.G.,
Lemontt,J.F. and Lawrence,C.W.
REV3, a Saccharomyces cerevisiae gene whose function is required
for induced mutagenesis, is predicted to encode a nonessential DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mSRESNDTIQSDTVRSSSKSDYFRIQLNNQDYYMSKPTFLDPSH
GESLPLNQFSQVPNIRVFGALPTGHQVLCHVHGILPYMFIKYDGQITDTSTLRHQRCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPDPAIDEVSMIIWCLEEETFPLDLDIAYEGIMIVHKASEDSTFPTKIQHCINEIPVM
FYESEFEMFEALTDLVLLLDPDILSGFEIHNFSWGYIIERCQKIHQFDIVRELARVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSCREV3 5056 bp DNA PLN 27-APR-1993
S.cerevisiae DNA polymerase (rev3) gene, complete cds.
M29683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 5056
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
305. 4819
/note="DNA polymerase (pot.); putative"
/codon_start=1
product="putative opioid receptor"
/protein_id="AAA36395.1"
/db_xref="GI:189392"
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 76.923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 4839
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90008808
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/db_xref="G1:172387"
                                                                                                                                                                                                                                                                       965 g
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US-08-653-294-20 x HUMOPIODRE
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3.417
92.308
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Ratio:
Percent Similarity:
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LOCUS
DEFINITION
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ORGANISM
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ORIGIN
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MEDLINE
FEATURES
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QIKTKLSDTWGYAHSSGIMITGRHMINIWRALRSDVNLTQYTIESAAFNILHKRLPHF
SFESLTHWWNAKKGTTELKTVLNYWLSRAQINIQLERQDYIARNIEGARLIGIDFHS
VYYRGSQFKVESFLIRICKSESFILLSPGKKDVRKOKALECVPLVWBPESAFYRSPLI
VLDGOSLYPSIMIGYNYCYSTMIGRYREINLTENNLGVSKFSLPRNILALLKNDYTIA
PUGDYYAKTSVRKSTLSKMLTDILDVRVMIKKTMNEIGDDNTTLKRLLNNKQLALKL
ANVTYGYTGARFSGRMPCSDLADSIVOTGRETLERA DIERCEPTWRKYVYGDTBSL
FYLDGKTALEFSGRMPCSDLADSIVOTGRETLERA DIERCEPTWRKYVYGDTBSL
FYLLDRYARGIETVRRGIPAQOKIIEKCIRLEFGYRULSKIRYLCORFFKIQIGK
SQLLDFIDAGIETVRRGIETVRAGESYINKILIPPLRAFQYRELSKERITYVKGKOG
QLLERCVSPEEFLEGENLELDSEYINKILIPPLRAFQYRENLIGINGKAGG
QLLERCVSPEEFLEGENLELDSEYINKILIPPLRAFQYRENLIGINVGNWAQEIVKSKR
ASTTTTKVBNITRVGTSATCORGEBELTKICSLQLCDDCLERRSTTLELELIKKLRO
KEYQTLKTVCRTGSYRYTSDAGIENDHIASKCNSYDCPVFYSRVKAERYLRDNOSVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BEM4 gene; CDC66 gene; KES1 gene; KIP2 gene; OVE3 gene; PAL1 gene; PRJ PEP4 gene; PXA1 gene; REV3 gene; ribosomal protein L37a; RPL37A gene; SNR17B gene; spk1 gene; SVS1 gene; u3 small nuclear rna. baker's yeast.

Saccharomyces cerevisiae

Eukaryota; Fung1; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

El (bases 1 to 55786)

S Purnelle, B., Coster, F. and Goffeau, A.

The sequence of 55 kb on the left arm of yeast chromosome XVI identifies a small nuclear RNA, a new putative protein kinase and two new putative regulators

L Yeast 12 (14); 1483-1492 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (22-MAR-1996) B. Purnelle, Unite de Blochimie
Submitted (22-MAR-1996) B. Purnelle, Unite de Blochimie
2/20, 1348 Louvain-la-Neuve, BELGIUM
Overlapping sequences: L29279, M29683, D50278, L27816, X62878,
Z11963, M3358, M55629, L34491, U17065, U03913, X57969, X054988.
Location/Qualifiers
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    .55786
    /organism="Saccharomyces cerevisiae"
/strain="AB972"

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Gaps: 0
Percent Identity: 57.143
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/chromosome="XVI"
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Purnelle, B.
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a 856 c
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3.727
78.571
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US-08-653-294-20 x YSCREV3
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CDS

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FYESEFEMFEALTDLVILLDPDILSGFEIHNFSWGYIIERCQKIHQFDIVRELARVKC
QIKTKLLSDTWGYAHSGIMITGRHMINIWRALDSDVULTQYTIESAARNILHKRLPHF
SFESLTNWWNKKSTTELKTVLNYWLSRAQINIQLLRKQDYIARNIEQARLIGIDFHS
VYYRGSQFKVESFLIRICKSESFILLSPGKKOVROKALECVPLVMBPESSAFYKSPLI
VLDFQSLYPSIMIGYNYCYSTMIGRVREINLTENNLGVSKFSLPRNILALLKNDVTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNGVVZAKTSVRKSTLSKMLTDILDVRYMIKKTMNEIGDDNTTLKRILINNKOLALKIL
ANVIGYTSASFSGRMPCSDLADSIVQTGRETLEKAIDIIEKDETWNAKVYGDTDSL
FVILOKATATEAFSIGHAMAERYTQNRPRIELEKEKYYPESTLISKRRYVGFSYSES
SQTIPTDAKGIETVRRDGIPAQQKIIEKOTRLIFOTKDLSKIKKYLONEFFKIQIGK
VSAQDPCFAKEVKLOAKSEKTAPAGAVVVKRRIUDHRAEPOYKBIPYLVKKKQ
QLLRERCVSPEFLEGENLELDSEYYINKILIPPLDRIFNLIGINVGNWAQEIVKSKR
ASTITTKVENITRVGTSATCCNCGEELTKICSLQLCDDCLEKRSTTLISFLIKKLKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGMSDLIHKYTPTLQNDNLLNVSASPLTTERQDSEEVETEVTNEALQHLOTSKILNIH
KYEDSERVRPDKLLKDGINKEMECGSSDDDLSSSLSVSKSALEEALMDRLQF"
COMplement(11127 . .12248)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSEHCRTSTLOIDNITELIECYEILLHHFPSMIKKTNYTSEQEEKLNSILISENVIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-'msqhirkidsdvseriksqactvslasavreivonsvdahatti
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Vedminidpvrrriikeeppprtentikadmioliumhemislanvoytprklrimfev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYQTLKTVCRTCSYRYTSDAGIENDHIASKCNSYDCPVFYSRVKAERYLRDNQSVQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLFKHYQSEFKKWGIGYET IEGTMETSLLEIKTLPEMLTSKYNGKDYLKMYLLQHAH
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LGGSSTDFATRLLMANDNREQLLNI'S SPOROFSSYNDSTIPBETVLDEDQTPARĞTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVPMNNSVIIASDLLTVRAYSTGAMKTASIAIAQPPQQQASVLPQVASMNPNITTPPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="REV3 (also called PSO1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1485. .1943
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CDS

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02-SEP-1999

14

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http://webace.sanger.ac.uk/cgi-
bin/display?db-wormace&class-Sequence &object=E02Al0
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current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone E02Al0. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C14Cl0 is at 23796 in this sequence. The true right end of clone F45D3 is at 107 in this sequence. The strue india of clone F45D3 is at 107 in this sequence. The start of this sequence (1. 108) overlaps with the end of close E78063.

The end of this sequence (23793. 23889) overlaps with the start of sequence E78063.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 23889)
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Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Bonfield, J., Cardner, J., Carder, S., Durbin, R., Favello, A.,
Johnston, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Lardell, P., Lighthing, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Staden, R., Sulston, J., Therry-Mag, J., Thomas, K., Vaudin, M.,
Waughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P., Weinstock, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Submitted (21-0CT-1996) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
fon Dec 12, 1996 this sequence version replaced gi:1627715.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                    Z81053.1 GI:1729531
HTG; Calmodulin-like protein; Mitochondrial ribosomal protein
Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                              seq_documentation_block:
LOCUS CEE02A10 23889 bp DNA INV 02-SEI
DEFINITION Caenorhabditis elegans cosmid E02A10, complete sequence
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complement(11007. .12594)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ture 368 (6466), 32-38 (1994)
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                                                                                                           seq_name: gb_in1:CEE02A10
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ORGANISM
                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                              DNA HTG 03-NOV-1999
.*** SEQUENCING IN PROGRESS ***, in ordered
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This sequence was identified as CDM:10214157 by the submitter.
For further information on this sequence you may e-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Inse
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 3727)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 55786
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 14
Gaps: 0
Percent Identity: 57.143
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Percent Identity: 57.143
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847 c 880 g
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                                                                                                                                                                                                                                                                                                                                /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster,
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HTG: HTGS_PHASE2.
fruit fly.
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US-08-653-294-20 x SCLACHXVI/rev
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3.727
78.571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AC013211
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complement(join(11007. .11504,11551. .11813,11984. .12016,

CDS

to: 3727

from: 1

to: AC013211

Align seg 1/1

02-SEP-1999

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CDS

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bin/displayabe-wormscesclass-sequence sobject-MOIFI
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note. Imporrant: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

It may be shorter because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases 1 to 36355)
I
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4240. .4330,4518. .4667,4911. .4990,5046. .5155,5277. .5533,
5651. .5706,5757. .5807,6111. .6251,6299. .6382))
/gene="MOIF1.1"
                                                                                                                                                                                       HTG; Glucose transport protein; L13P ribosomal protein; Lipoic acid synthase; Ysy6.
Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The end of this sequence (36252. .36355) overlaps with the start of sequence 277131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The true left end of clone MOIF1 is at 1 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For a graphical representation of this sequence and its analysis
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beta-1,2-N-acetylglucosaminyltransferase"
                                                                      Caenorhabditis elegans cosmid MO1F1, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-OCT-1994) Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="III"
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/gene="M01F1.1"
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94150718
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Sims, M.
                                          36355 bp
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Z46381.1 GI:561920
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       seq_documentation_block:
LOCUS CEM01F1
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7500 22537, 22577, 22896. .22982, 23039. .23136, 23285. .23644)
/gene="E02A10.3"
/note="predicted using Genefinder; Similarity to C.elegans
                                                                                                                 /codon_start=1
/protein_id="CAB02877.1"
/db_xref="G1:3875441"
/db_xref="sPTREMBL:093424"
/tb_xref="sPTREMBL:093424"
                                                                                                                                                                                                                                                                                                                                            /note-"predicted using Genefinder; Similarity to Yeast mitochondrial ribosomal protein S5 (SW:RT05_YEAST); cDNA EST EMBL:065461 comes from this gene; cDNA EST EMBL:068901 comes from this gene; cDNA EST yk43244.3 comes from this gene; cDNA EST yk43244.3 comes from this yk554d6.3 comes from this gene; cDNA EST yk554d6.3 comes from this gene.
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EADVDGNGVIDYDEFTYMVKNYMTDDDIV"
join(278063.1:36566. 36692,Z78063.1:36740. 36890,
Z78063.1:36943. 37434,109. 194,841. 947,998. 1132,
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mklefaglnapirmretenqnlmsiaeqtedeirdsmggtkkileerdtgkkkrnnek
LHPMERGFSGTQLVGQKLGAPPPLDGVNFDDFETYCLEVKRTSNMTNVFGRVHTMSAL
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YRPROARRAFORGLTCHPRLKICEAGINDIYKVBGSTKNTLALTHAFVTGLLNQE
THQQLAERKGLHVVBASPSRHFLPOIVASPISTELKTBETLERLDDRALALDDFYGEGRY
PLRKPKSLPFSNLEGHLDARWRKHPFRNQESTMIRLIADNWVPRWTRDARAAWADQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mtnSVFYSDPLLSQHLLEGYSEEELQEYRQVFNMFDADRSGAIA
IDELEAAIKNLGLEQTRDELDKIIDEVDQRGNHQIDFDEFCVVMRRLTMKKSNMNEVV
                                                                                                                                                                                                                                                                                                         (2064. .12174,12220. .12258,12324. .12443,12501. .12594))
//gene="E02alo.2"
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/gene="E02A10.1"
join(z78063.1:36566. .36692,z78063.1:36740. .36890,
z78063.1:36943. .37434,109. .194,841. .947,998. .1132,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEEEKKDEEPKKEEEKKEEEEKKEDEVEEKSEKVEEKELEPKKDEETKKN"
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Gaps: 0
Percent Identity: 61.538
                                                                                  'note="predicted using Genefinder"
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/protein_id="CAB02878.1"
/db_xref="G1:3875442"
/db_xref="SPTREMBL:P90802"
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/db_xref="GI:3875443"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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BASE COUNT ORIGIN

/protein\_id-"CAA86513.1"

gene

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alignment_block:
US-08-653-294-20 x CEM01F1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.636
84.615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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/ John Est Embl. 1.37 family ribosomal protein; CDNA EST EMBL: M19788 comes from this gene; CDNA EST EMBL: D71976
comes from this gene; CDNA EST EMBL: D71976
comes from this gene; CDNA EST EMBL: D73026
comes from this gene; CDNA EST EMBL: D70036
gene; CDNA EST EMBL: C08236 comes from this gene; CDNA EST EMBL: C09324
comes from this gene; CDNA EST EMBL: C00304
gene; CDNA EST EMBL: C08236 comes from this gene; CDNA EST EMBL: C09304
comes from this gene; CDNA EST EMBL: C00700
comes from this gene; CDNA EST Yk40664.3 comes from this gene; CDNA EST Yk40664.3 comes from this gene; CDNA EST Yk40664.3 comes from this gene; CDNA EST Yk40664.3 comes from this gene; CDNA EST Yk40664.3 comes from this gene; CDNA EST Yk406043.3 comes from this gene; CDNA EST Yk40603.3 comes from thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(16047. .16243,16291. .16443,16496. .16754))
/gene="MOIFI.2"
/db_xref="Sptrembl:021450"
/tanslation="mhissyrificity informerious additioned additione
                                                                                                                                                                                                                                                                                             DPSLWCYTAWNDNGKPENIDLKSNATLYRSDFFAGLGWAMTRKTWEELBIWPNGFWD
DWMREPVORKQRCIRPEISRTGMKYGKEGTSKGQFFSDHLEKIKVNDLPVDFSQIN
LDYLQKNEFESRLSLDIRNAVPUDIDLTYPDWKPDYEGMKAIIYYTGRTDFVAKADR
LSLMHDFRAGVPRTANGIVYCFYKGTRIFLVPDRSKVPGYDSSW"
complement(12635. .15694)
                                                                                                                                                                                                                                                       NLQKFKPYYY ISRHYKLALNHIFSNSNNYSSVIITEDDLDIAPDFFSYFSNTRYLLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAPPNPQVPSTSAWNIAPTPTPVTVQRPLRKPVTPQPVKSAFQAOKPPPIDGFDDFDS
SRCACARFRENTANTYRKNNPKCIFSQPCFEGALKIKYLNQIHEELTVKREGEVDV"
Complement (16047. .16754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(12635. 12768,13939. 14239,15031. 15225,
15281. 15487,15533. 15694))
/gene="MOIF1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/db_xref="SPTREMBL:Q21451"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQFNARKATTVDIEVGDKLSQMANYELAWVGTELKFIKQGRMLVAEGAVINIPDDKAQ
YMFVDWKYTKNPPTLAKVCGNIPGYTKPLTTNVFVTRATVRPDVEKLTEMFKFGQRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVAREQAPNERGVCWRAALATDEYHDIAIDVPNAHGRQTYRVIPKAGVCPPAPLQQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="cDNA EST yk415a9.3 comes from this gene; cDNA EST yk415a9.5 comes from this gene; cDNA EST yk463b4.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="M01F1.8"
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CDS

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from this gene; cDNA EST yk298a4.3 comes from this gene; cDNA EST yk298a4.5 comes from this gene; cDNA EST yk330b10.3 comes from this gene; cDNA EST yk330b10.5 comes from this gene; cDNA EST yk330b10.5 comes from this gene; cDNA EST yk330b10.5 comes from this gene; cDNA EST yk300b7.5 comes from this gene; cDNA EST yk300b7.5 comes from this gene; cDNA EST yk310a3.3 comes from this gene; cDNA EST yk313a3.5 comes from this gene; cDNA EST yk252e3.5 comes from this gene; cDNA EST yk235b1.3 comes from this gene; cDNA EST yk235b1.5 comes from this gene; cDNA EST yk235b1.5 comes from this gene; cDNA EST yk235b1.3 comes from this gene; cDNA EST yk235b1.3 comes from this gene; cDNA EST yk235b1.3 comes from this gene; cDNA EST yk2311a2.5 comes from this gene; cDNA EST yk2311a2.5 comes from this gene; cDNA EST yk231a2.3 comes from this gene; cDNA EST yk238e5.3 comes from this gene; cDNA EST yk238e5.3 comes from this gene; cDNA EST yk538e5.3 comes from this gene; cDNA EST yk539f3.3 comes from this gene; cDNA EST yk699c7.3 comes from this gene; cDNA EST yk609c1.3 comes from this gene; cDNA EST yk609c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MGLSNRAITIDGKNHLLGRLASIVAKKLLQGDKVVVLRAEBIVI
SANTBHRSKLKYMSFLRKRCNINPARGAFHYRAPGKIFWRTVRGMLPHKTNRGNBALKN
LRAYEGVPAKYQKTKSLHAPSASRFRLQPRRKFCVVGRLSHEVGWQFQDVVAKLBARR
KVRGAAXFRQKKKMNKLAVQAKKNAPKIAQYQKIIEALGYN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="Caa86516.1"
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GKLKLEKGDRRLRLPPWLKKEKILPSENENVSRLKKQLKHLKLATVCQEARCPNLGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(16937 .17265,17322 .17557,17602 .17903,
17948 .18045,18095 .18194))
/gene="MOIF1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to lipolc acid synthase; cDNA EST yk283b6.:
comes from this gene; cDNA EST yk283b6.5 comes from this
gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3 comes
from this gene; cDNA EST yk476e7.5 comes from this gene;
cDNA EST yk543al.3 comes from this gene; cDNA EST yk588ql1.3 comes from this gene; cDNA EST pk642d9.3 comes from this gene; cDNA EST pk65d9.3 comes
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Gaps: 0
Percent Identity: 69.231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA86515.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4482 TITGAGCIGAAAAITCGAAITCTGCGCGATITGTIACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuAlaileArgile***ArgileLeuLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: CEM01F1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="M01F1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
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join(15683. 15783,16328. 16412,16458. 16849,16892. 16923,
17029. 17093,17175. 17660,17707. 17846,17897. 18136.
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complement(join(12390. .12479,12525. .12655,12727. .12817))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSVGGSALSSNASATTLLSIEVRSEAFLRHVLPLIAEFGHQCAQQRISRLLIARAKNA
SVTEATTPTQLSECIKLVKEFQSKCDKEGWYSTQNQKVGGLGRSVNKLSMDYIEKFHA
ARKIRIGNMLDTELWKATDVSIVDQNIVDMAMETGQLRNTKRIDDGPIKKSFKRTESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTIDSTTSTSNQIQGVIVDEENYVVVGSSITMIQLLSDYCEAISEMPSFSQDWNSRVV
ELKTENSECCOLILGAGALQLYGGKTISVRNGIALKEYPLAGRSLELVCREIPNVH
DEMDRYLPENRKSLLEXFKQVESEXRDHVNETAARLISVIAHYTHOCLGMWDYKGVIP
SPEFQQICRHMLKFHNGLVGIMPROQIEALFRQVHENFKANLREHVTGMGITPHDPLK
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TRSTQNNTYDTPKSMSHSSKSKRIGHVAKMLIDREXTHLQEDRTOTPTASVSITPQVTPQ
TRSTQNNTYDTPKSMSHSSKSKRIGHVAKMLIDREXTHLQEDRTOTPTASVSTAPSTHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mSHTILLLQPTDNIESRSWSDYENTTECLEGICRVYEEYLKKKV
PAQNEITYDISHLFEFIDDLKDLSMLVLDNTTYTYVPHNKQYVKESIYKLMNNRLNNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"msglshagrqvariavrqasshshdshavwkeinrlgsbgrwdn
vnnmpkmflegeakqettaayrainkdpdffrqspygqylkivwrlallegiikagtv
vydfavpeeqrlkyryrnhghhghddahd"
                                                                                                                                                                                                                                                  /translation="MKSMDDRTVGLISASSSRASLKIQPEIGYPRICDYCQPIIELMT
ASEFARHIRQDHTTKEGGSFLCRYGEHGVCQKLPLEGVCDLDFEAHIRRCHTSSQPAG
                                                                                                                                                                                                                                                                                                                                            YSSPTSSLVASYTEDSEETASLRSIRLTSDRDTPTIEKKKFTLHSFTQNLSAVLADPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="cDNA EST EMBL:T01297 comes from this gene; cDNA EST
yk257f11.3 comes from this gene; cDNA EST yk257f11.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(10754. .10853,11143. .11271,11317. .11594,
11645. .11775,11821. .11928,12049. .12112))
            ESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similarity to drosophila hypothetical protein PIR accession number S50341; cDNA EST yk391d9.3 comes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similarity to the drosphila discs large protein repeats; cDNA EST EMBL:T01372 comes from this gene" /codon_start=1
    gene; cDNA EST EMBL:C10882 comes from this gene; cDNA EMBL:C12782 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDDVPRTPRKPLSLLDPRNNSWLTEALYVSIGLGALTISGYLAYRFIRGRR*
complement(12390. .12817)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13113. .14343
/gene="12109.5"
join(13113. .13183,13598. .13730,14152. .14343)
/gene="12109.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGYVTKDYMFYQQNVKNMESCRNLELESLNDIMFE"
complement(10754. .12112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /proteIn_id="CAA97332.1"
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/db_xref="SWISS-PROT:022640"
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/db_xref="G1:3880015"
/db_xref="SPTREMBL:Q22639"
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/db_xref="GI:3880017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="T21C9.1"
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/gene="T21C9.6"
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Caenorhabditis elegans.

Bukaryota; Metasoa; Nematoda; Secernentea; Rhabditla; Rhabditida;

Bukaryota; Metasoa; Nematoda; Secernentea; Rhabditla; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 37545)

Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,

Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,

Coulson,A., Craxton,M., Deors,S., Du,Z., Dutbin,R., Favello,A.,

Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,

Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,

Latraille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,

O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,

Staden,R., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,

Staden,R., Sulston,J., Thierry-Mieg,J., Thomas, K., Vaudin,M.,

Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,

Wilkinson 'Sproat,J. and Wohldman,P.,
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Current sequence finishing criteria for the C. elegans genome sequence finishing criteria for the C. elegans genome sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

In sequence It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone T2LC9. The true right end of clone F3ZC8 is at 17256 in this sequence. The start of this sequence (1. 105) overlaps with the end of sequence 772509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.2 Mp of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-MAY-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu coding sequences below are predicted from computer analysis, usin predictions from Genefinder (P. Green, U. Washington), and other available information.
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    CET21C9 37545 bp DNA INV 02-SEP-1999 Caenorihabditis elegans cosmid T21C9, complete sequence.
                                                                                                                                                                      Myosin heavy cl
dependent GABA
                                                                                                                                                                 HTG; Discs large; GTP cyclohydrolase I; KIPI; IB; pyruvate, water dikinase; Sodium/chlorine
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/db_xref="taxon:6239"
/chromosome="V"
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/gene="T21C9.2"
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Nature 368 (6466), 32-38 (1994)
94150718
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                                                                                                                               GI:1313944
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                                                                                273098
273098.1
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clone:MXN24.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
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Lin,X., Kaul,S., Shea,T.P., Fujli,C.Y., Shen,M., VanAken,S.E.,
Lan,X., Kaul,S., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.,
Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C.,
Fraser,C.M. and Venter,J.C.
Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-JUN-1999) to the DDBJ/EMBL/GenBank databases.
Yasikazu Nakamura, Kazusa DNA Research Institute, Laboratory of
Gene Structure 2; 1332-3, Yana, Kisarazu, Chiba 292, Japan
(E-mail:ynakamu@kazusa.or.jp, Tel:+81-438-52-3935,
     clone: MZN24,
                                                                                                                                           Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACO07070 86017 bp DNA PLN 06-APR-1999
Arabidopsis thallana chromosome II BAC T22F11 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                Structural Analysis of Arabidopsis thaliana Chromosome 3. II Unpublished (1999)
2 (bases 1 to 82348)
Nakamura,Y.
     Arabidopsis thallana genomic DNA, chromosome 3, Pl
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Gaps: 0
Percent Identity: 50.000
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/organism="Arabidopsis thaliana"
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13968 c 13880 g 27438 t
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/db_xref="taxon:3702"
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Location/Qualifiers
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/clone="MZN24"
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AC007070
AC007070.3 GI:4567237
                                                                                        AB028622.1 GI:5041975
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                               complete sequence.
AB028622
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71.429
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US-08-653-294-20 x AB028622
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                                                                                  /note="similar to pyruvate, water dikinase; cDNA EST
EMBL:D64535 comes from this gene; cDNA EST EMBL:D67561
comes from this gene; cDNA EST EMBL:D67645 comes from this
gene; cDNA EST PX4350e8.3 comes from this gene; cDNA EST
yk350e8.5 comes from this gene; cDNA EST yk397f12.3 comes
from this gene; cDNA EST yk397f12.5 comes from this gene;
cDNA EST yk295f7.3 comes from this gene; cDNA EST yk295f7.5 comes
from this gene; cDNA EST yk27f10.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VITKLEDSFPEYHATESEKMKSYVSFNIRACQDKMLTGGKGANLARLQAITDDFHUPP
GIVYTAARTKHYIANPNYLEBIKLLDINDKNARFYEDGKRTEGLLFSESEVSGELGK
EIVYTTAARSAKRHYIANPNYLEBIKLLDINDKNARFYEDGKRTEGLLFSESEVSGELGK
EIKEWLPRSTYRSANGEDGALGSAGQLESYLDVIEIDIVDKIKLCWGSNBRRE
VLNYRKNYGQOLNPSMAVVIQEMDRNGVAGVMFTANPVKLDRGEIVINALKGSGEQIV
SGCTTPPDEITYNRIHKTVYNINKVGROCCLDDVGIEKLTKVGRYETLRIRGKSGEQIV
SCGTTPDEITYNRIHKTVYNINKVGROCCLDVGIEKLTKVGRYLDRIFGY
RNOWYNIVQSRDITGLDKETQFEMCTEFYNSFILDKEILTNARVGEYLPVPVNAMEAH
NLTGMFDKVIASMTFQELNDVVPAHTSIGFSVAHRKIFFNLGEVVLRIMFLVEKDRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLIFLFLELSAPLCKFVLYPVIYAFLKWRHPVKKFTAPTAKIR
DIINPDKEEWELEHIKNEEILTISGSGEDNSFVYIQVITKNEIHFAHIRVFEKGILYS
GSYKAVFSDNRTISCGPLLIELRNPFRKWRINFRGYLNDAKGNSHFVILSGWWKCVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFHTYLSDANAISYRVNSVDEKKSVSHGVGFRSDHSARPIIIDNSHSLESDNMLPVQF
KYVSRGLLPLEMRKGRKLCHFTFIREDNKVVDVTALEVNSAIFTGVGFVVRVREAIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIVIAGETLENAEMFOQAAHOYGKVSPFFPLKRMFNMIKLIYFTSNSVKAKIVKIDEE
AKKLVPNDKMTIEIVFKKYDELEKLMCDASHCHTSLSMFSSFTYVLCGMLIRGSDNGP
LSNDNISDFANVFSNNSRGDVISADVPNSLKKLAKTIREESIDKEFCAAEDDEALKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLYEKGYLPDPNLWMHFSMDELKELNATRSAKLVSRAIRRKQISSKFEGLQFPLVSHG
YMNPIKIEIAETDANIGIILRGTTVCEGKVRARARVAKTLEEAKETKPGEILITKYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYVENMYTFANSFYTLRAPONTCNNCTFAFLFERNSSTEEDNFPLQVFFTIHYCMAFI
QYFMTFLSSLNRLTMYFFYDSYEKIMRPSLPFLIMIVIIFPMIMTWPIATNNAYFIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICWSPFFPIISGIVTEIGGLLSHGAVVAREYGLPSLIAVSNATYHFKTGDLVELDSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(21064. .21207,21256. .21444,21587. .21724,
21806. .22039,22442. .22585))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVSFVSFIIQLLALGDTLILRAAPSEGMSVGAQTAKALMPFVSDILTFNHPWTIMYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARFFYSNALLKSFNEIYNDKPTALIENLKTIEKYRKGNVLNQMGLRHRNPLDLETSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGKKSSDELRRFLELHGHRGPKELYLDATTWEEDTNLLVHTIKSMLACPETSGKTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDDI I DNLKCK PTG I RRRLLKY FIGQTHRGVS FRETAKNHLVSTTHSLRKACRMVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MLTPLFFLPAAYGVASSYLYTLIILMMIRRWNEYNTAFFKLFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTLGGFATKTVANSTEVLNSLVTFMIVFTLFTATANIVSIIRLTLLPTRISGAERNLF
18184. .18403,18484. .18801,18852. .19332,19645. .20053,
20104. .20239,20283. .20825)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 14
Gaps: 0
Percent Identity: 57.143
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                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"SPTREMBL:Q22649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 37545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"SPTREMBL:022642"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(21064. .22585)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(23002. .23649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA97334.1"
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LOCUS AB028622 82348 bp
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4.000
71.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-20 x CET21C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pl1:AB028622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio
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/foce="T22F11.3"
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5675 .5695,6086 .6478))
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KLQDFGYLGPERNEEGGIFNRRKLDVKKNTWTKRIYVLPFMWWNIVATTKLRIVGMIG
TSEIVLSPYDLSDPYYLFYYNLETNNVREVGIQGLGAFETSTVVHLFVDYEEDVKLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /pocedi_1d="Aad23653.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSDNIHCSFVCRWTQRPITÄTIANNCRCVRLIAKNFSDQÄLRSLIAGDYR<mark>TFWSLNOR</mark>
RWEDLLWYVAGFSRQRQANDGCLNSIITGDIFNSKGBESSPAAKFWDNVYYRLEKFKG
LVWYEAVADDVEKAVKAGFVAICDEKDNILHEIKESLRDIEISRRGVEIMALVYRGLS
ESFDLGMRNYVIYCDDWIYQSIIGRGKSKKKIDHLVEEVQGILEKMALIDALVYRKI
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PVCKKLRSGTEPTCLEYGCKFKLTLERCSKVLTIKLIEMWKOKNKEDSIPAAERIYCPY
PVCKMLMSKTELSSEADLSVYTCVKCCGLFCIDCKVPSHTDLSYDDYKKLHPDPLVD
DLKLKSLANDKMWCOVKCHHMIELSHGCNHMTCSYDAPRDDDDVYYKYPSPEQFFSE
ERNADGDDYIWDDYNNYGGLIGDKGGFDEGFFRDYYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
4680 ..4760
/rpt_family="(AAT_n)
complement(join(<4693 ..4846,4930 ..5142,5399 ..5666,
5675 ..5699,6086 ..>6478))
/gene="T22Fil.3"
complement(<4693 ..>6478)
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6849. .6914
/rpt_family="AT_rich"
complement(foin(<7046. .7232,7601. .8334,8950. .9450,
9922. .>10140))
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/note="predicted by genscan"
complement(join(7046. 7232,7601. 8334,8950. 9450,
                                                                                                                                                                                                                                                                                                                                                                                                               /anticodon (pos: 2966, 2968, aa: Ala)
complement(2929, 3001)
/gene="T22F11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hypothetical protein"
/codon_start=1
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/gene="T22F11.4"
/note="hypothetical protein"
/codon_start=1
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/gene="T22F11.4"
complement(<7046. .>10140)
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complement(8674. .8705)
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9519. .9594
                                                                                                                                                                                         2309. .2358
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complement(2929. .3001)
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9523. .9654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="(TAAA)n"
9707. .9793
                                                                                                                                                                                                                                                                                                                                                                             'product="tRNA-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (6658
                                                                                                                                                  CLKIWLETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene.chspene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (sea Eddy. Simple repeats are identified by repeatmasker (Arian Smit. http://ftp.genome.washington.edu/kW/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are anotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD23652.1"
/db_xref="G1:4567238"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The institute for Genomic Research
9712 Medical Center Dr.
9712 Medical Center Dr.
9712 Mideligar. USA
e-mail: Xin@tigar.org
BAC clone T22F11 is from Arabidopsis chromosome II and is near the
molecular marker GPA1.
                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-APR-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Apr 6, 1999 this sequence version replaced g1:445441.
Address all correspondence to:
Lin,X: and Kaul,S.

Direct Submission
Submitted (12-MAR-1999) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 86017)
Lin,X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The orientation of the sequence is from SP6 to T7 end of the BAC
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foote="exon predicted by xgrail, quality marginal"
foote="exon predicted by xgrai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1026,1124. .1295,1815. .1853,2757. .2867,
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/note="exon predicted by xgrail, quality marginal"
complement(384..444)
/rpt_family="(Th)n"
complement(408..532)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="hypothetical protein"
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/db_xref="taxon:3702"
/chromosome="II"
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/rpt_family="AT_rich"
complement(715..778)
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Naratas, P., Heatoru, A., HORTON, L., HOWLENG, L., JODGE, Y., Macdonald, P., Maratas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Maratas, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Mella, M., Morlis, W., Morlis, P., Mychalecky, J., Naloff, M., O'Connor, T., O'Donnell, P., Pevlin, B., Stanger Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Whan, D., Ye, W.J. and Zody, M.

Direct Submission

NL Submitted (27-Aug-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 3, 1999 this sequence version replaced gi:5788096.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker: html.

* Nord: This record contains 113 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* arbitrary. Low-pass sequence sampling is useful for

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* voverlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* he preserved.
Kann, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown length
gap of unknown length
contig of 822 bp in length
gap of unknown length
contig of 801 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.
7.
                                                                         somplement(join(<11079. .11215,11357. .11526,11611. .12335,
                                                                                                                                                                                                                                                                                              /profesin_id="Aad23655.1"
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/db_xref="G1:4567241"
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                                                                                                                                                                                                                                                                                                                                                                                                              HSDLSCAEVKKLHHDPLVDELKLKSLAKDKKWRQCKMCRHMIELSHACNHMTCRCGYQ
FCYQCEVEWKNDQKTCSSGCLLTGHGYYDDYDYNEPEYDFEVDTCNYYSDEEAMTRRE
MIRMWNTEQFFSEEENADGNDDNWDDYNNYGGLTVFWRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 03-SEP-1999
clone 358_I_19 map 11, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direction 1 to 99657)

Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Barren, B., Linton, J., Barna, M., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Depayre, E., Devon, K., Dewar, R.,
Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
                                                                                                                                                /note="predicted by genscan; contains In figer domain (RING finger)"
                                                                                                                                                                                                 complement(join(11079. .11215,11357. .11526,11611. .12335,
12502. .12591)
/gene="T22F11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<13249, .13371,13455, .13545,13635, .137
14210. 14306,14651. 14707,16298. .16483,16607. .16849,
16970. .17134,17252. .18012,18142. .18250,18718. .18798,
19250. .19323,20863. .>20965))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12776. 12840
/note="exon predicted by xgrail, quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 86017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 99657)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone 358_1_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: ATAC007070 from: 1
                                                                                                                                                                                                                                                          /note="hypothetical protein"
/codon_start=1
                                                                                    12502. .>12591))
/gene="T22F11.5"
complement(<11079. .>12591)
/gene="T22F11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<13249. .>20965)
                                                       'rpt_family="(TAAAA)n"
               'rpt_family="AT_rich"
0479. .10576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AC009548 99657 bp DN.
DEFINITION Home sapiens chromosome 11
SAMPLING.
ACCESSION AC009548
VERSION AC009548.2 GI:5822701
KEYWORDS HTG: HTGS_PHASEO.
complement (9820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-20 x ATAC007070/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.00
3.636
91.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_htg3:AC009548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
 repeat_region
                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                           mRNA
                                                                                                                                    gene
                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
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ig of 855 bp in 1 of unknown length ig of 812 bp in 1 of unknown length ig of 816 bp in 1 of unknown length of unknown length ig of 822 bp in 1 of unknown length ig of 842 bp in 1 of unknown length ig of 842 bp in 1 of unknown length ig of 843 bp in 1 of unknown length ig of 815 bp in 1 of unknown length ig of 815 bp in 1 of unknown length ig of 813 bp in 1 of unknown length ig of 813 bp in 1 of unknown length	tig of 812  of unknown  of unknown  tig of 808  tig of 811  tig of 811  of unknown  tig of 814  tig of 804  tig of 804  tig of 808  of unknown  tig of 808  of unknown  tig of 808  tig of 808  of unknown  tig of 808  tig of 808  cof unknown  tig of 808  tig of 808  cof unknown  tig of 835  cof unknown  tig of 835	to of unknown length of unknown length tig of 801 bp in 10 of unknown length tig of 805 bp in 10 of unknown length tig of 824 bp in 10 of unknown length tig of 976 bp in 10 of unknown length tig of 976 bp in 10 of unknown length tig of 936 bp in 10 of unknown length tig of 936 bp in 10 of unknown length tig of 936 bp in 10 of unknown length tig of 972 bp in 10 of unknown length tig of 972 bp in 10 of unknown length	f unknown leng of 943 bp in f unknown leng of 876 bp in g of 876 bp in g of 876 bp in g of 876 bp in f unknown leng of 930 bp in f unknown leng g of 930 bp in
9792: 0604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 090604: 09	27148: 0 27956: 0 28761: 0 29572: 0 30373: 0 31177: 0 31982: 0 32791: 0 33626: 0 34496: 0 35333: 0	6800: 7601: 8406: 9214: 0038: 0945: 1921: 2857:	44705: 0.44705: 0.44705: 0.446548: 0.446524: 0.448319: 0.448319: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0.449249: 0
893 979 060 142 224 304 470 552	26337 27149 27957 29573 30374 31178 31983 32792 33627	5333 760 760 921 003 192 285	43830 44706 45649 46525 47466 48320 49250
*******	*********		******

*			gap of	unknown length
*	51106	52091:	tig	
*			4	unknown length
*	52092	53040:	tig	of 949 bp in length
*			4	unknown length
*	53041	53966:	contig	of 926 bp in length
*			gap of	nown lengt
*	53967	54835:	contig	
*			gap of	length
*	54836	55789:	contig	of 954 bp in length
*			gap of	lengt
*	55790	56674:	contig	of 885 bp in length
*			gap of	unknown length
*	56675	57631:	contig	of 957 bp in length
*			gap of	unknown length
*	57632	58514:	m	of 883 bp in length
*			•	unknown length
*	58515	59397:	tig	of 883 bp in length
*			•	unknown length
*	59398	60274:	tig	of 877 bp in length
*			•	unknown length
*	60275	61163:	contig	of 889 bp in length
*				unknown length
*	61164	62071:	contig	of 908 bp in length
*	,		44	angt
*	62072	62952:	tig	of 881 bp in length
*			44	unknown length
*	62953	63827:	tig	of 875 bp in length
*			gap of	know
*	63828	64798:	u	Д
*			O	_
*	64799	65764:	contig	Д
*			gap of	unknown length
unment scores	:			

alignment\_scores:
Quality: 40.00 Length: 13
Ratio: 4.000 Gaps: 0
Percent Similarity: 76.923 Percent Identity: 61.538

alignment\_block: US-08-653-294-20 x AC009548 Align seg 1/1 to: AC009548 from: 1 to: 99657

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```
Enterococcus faecalis EF110
Sequence of the CD28 gene. S
Rhodosporidium toruloides D-
Enterococcus faecalis gene E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes 3 Staphylococcus aureus proteins of The present sequence encodes 3 Staphylococcus aureus protein, that, based on homology with a unknown function and a protein, is believed to be an autolysin staphylococcus aureus protein, is believed to be an autolysin (EC 3.5.1.28) (N-acetylmuramoyl-1-alanine amidase).

The present sequence was obtained from a library of clones of S. aureus WCHH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of requiatory elements for the control of bacterial gene expression. The encoded protein may be used control of bacterial and host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                 DNA encoding an autolysin and 3 unknown proteins. Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p-PSDB; W28340, W28341, W28342, W28343.
Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate autimicrobial compounds, and in vaccines against S. aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997.
20-FEB-1997; UO2318.
20-FEB-1996; US-01188.
(SMIK ) SMITHKLINE BEECHAM CORP.
SMIK ) SMITHKLINE BEECHAM CORP.
Flack MT. Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
Pratt JM, Reichard RW, Rosenberg M, Ward JM;
WPI: 97-424969/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 14
Gaps: 0
Percent Identity: 35.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuAlaileArgile***ArgileLeuLeuArgTyr 14
242.58
244.01
258.05
289.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: T84234 from: 1 to: 3110
                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.

Key Costion/Qualifiers 679. 1272

CDS /+tag a /+tag a 1668. 1844

/+tag b /+tag b /+tag b 1865. 2064

CDS //+tag c 2326. 2832

CDS //+tag d /+tag d /+
106.68
106.63
106.20
105.30
                                                                                                                                                                                                                           T84234 standard; DNA; 3110 BP.
  34.00
34.00
34.00
                                                                                                                                                                                                                                                                               01-SEP-1998 (first entry)
                                                                                                                                          seq_name: N_Geneseq_36:T84234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.00
3.333
85.714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-20 x T84234
                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
N_Geneseq_36:X20213
N_Geneseq_36:Q28837
N_Geneseq_36:X19109
N_Geneseq_36:X20212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                     T84234;
                                                                                                                                                                                                                              | Pseudomonas pseudoalcaligenes
| Polynucleotide sequence from t
| Human placental calcium senso
| Human placenta calcium sensor
| Human parathyroid calcium sen
| Human kidney calcium sensor p
| Human kidney calcium sensor p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Human calcium sensor protein
| Human calcium protein sensor
| Mutant LAG1 coding sequence. Eu
| Alcohol acetyltransferase codi
| Tumor necrosis factor receptor
| TNF-R1-DD ligand protein clone
| LAG1 coding sequence. Eukaryot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type II topoisomerase database
Streptococcus pneumoniae genomi
CD28 cDNA. New xanthene derivat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF-R1-DD ligand protein clone
L.lactis DB1341 pf1 gene. Lact
Carbamoyl-phosphate-synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide sequence from | Polynucleotide sequence from
                                                                                                                                                                                                                   -MODEL-frame-primodel -DEV-xlp
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_16000
-GAPDXT=4 000 -MINMATCH=0.100 -LOOPENT=0.000
-GAPDXT=4 000 -MINMATCH=0.100 -CAPPOP=10.000 -KGAPEXT=0.500
-FGAPOP=4.500 -QGAPEXT=0.000 -YGAPDXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LCCAL -OUTFWT=Pfs -NORM=ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
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OM of: US-08-653-294-20 to: N_Geneseq_36:*
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115.48
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Database length: 125096042
Search time (sec): 590.520000
                                                      Date: Feb 8, 2000 1:28 PM
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Query: US-08-653-294-20
Query length: 14
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N_Geneseq_36:V05996
N_Geneseq_36:T28773
N_Geneseq_36:V05994
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Geneseq_36:V74331
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N_Geneseq_36:V23687
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_Geneseq_36:T07263
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N_Geneseq_36:T28774
N_Geneseq_36:V05995
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New nucleic acid sequences from Staphylococcus aureus WCHU29 -

1 useful in vaccines and for treatment of bacterial infections of e.g.

1 useful in vaccines and for treatment of bacterial infections of e.g.

2 useful in vaccines and for treatment of bacterial infections of e.g.

2 trespiratory tract and central nervous system

3 claim 1: Page 214-216; 390pp; English.

2 this sequence encodes 2 Staphylococcus aureus proteins of unknown

3 claim 1: Page 214-216; 390pp; English.

4 claim 2: Page 214-216; 390pp; English.

4 claim 3 conditions which may be treated include bacterial infections, especially crespiratory, cardiac, gastrointestinal, central nervous, eye, kidney, criminary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. Pylori infection.

3 cequence 3110 BP; 1111 A; 48B C; 676 G; 832 T;
                                                      30-OCT-1998 (first entry)

DNA encoding 2 Staphylococcus aureus proteins of unknown function.

Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus contig SEQ ID #20.
Computer readable medium; vaccine; S.aureus infection; immunodetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knowles DJC,
Reichard RW, Rosenberg M,
                                                                                                                                                                                                                                 Location/Qualifiers
1.208. .1300
/*tag a /note= "encoded protein shown in W77771"
1282. .1668
/*tag b /note= "encoded protein shown in W77772"
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Gaps: 0
Percent Identity: 35.714
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Lonetto MA, Nicholas RO, Pratt JM,
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                                                                                                                                                                                                 therapy; ss.
Staphylococcus aureus
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US-08-653-294-20 x V53557
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24-SEP-1997; 307485.
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WPI; 98-252940/23
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Ratio:
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Polynucleotide(s) and proteins derived from Staphylococcus aureus - Polynucleotide(s) and proteins derived from Staphylococcus aureus - Polynucleotide(s) and proteins derived from staphylococcus aureus Proteins anti-S.aureus vaccines

Parti-S.aureus vaccines

Protein anti-S.aureus presents one of 5191 Staphylococcus aureus DNA sequences

Claim 1: Page 271-277; 3271pp; English.

Claim 1: Page 271-277; 3271pp; English.

Commonyr (RAM), read-only memory (ROM) or CD-ROM, Homology searches using the saureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or that protein-encoding or regulatory regions of commercial, therapeutic or that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, evelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences contained on the computer readable medium.

Computer readable medium.

Sequence 10470 BP; 2804 A; 2009 C; 1550 G; 3742 T;
                                                                                                361. .420
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/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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are included to maintain the nucleotide numbering
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cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                 Location/Qualifiers
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.2220
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                                                                 Staphylococcus aureus.
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05-JAN-1996; US-009861.
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us-08-653-294-20.rng

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This nucleotide sequence Comprises novel human tumour rejection
antigen precursor (TRAP) MAGE-C1 cDNA (see also v69720). MAGE-C1
is a novel member of the MAGE family that may be recognised by
cytotoxic T cells, leading to lysis of the tumour cells which
express it. MACE-C1 and MACE-C2 (see W81546-47) are expressed in a
variety of tumours and in normal testis cells, but not by other
normal cells. The MAGE-C1 cDNA was isolated from a melanoma
LB373-MEL cDNA library using a probe generated from LB-373-MEL
RNA by PCR (see V69728-29). It shows homology to MAGE-A1 cDNA (see
V69719) and codes for a putative l072-amino acid protein. The
NACE-C1 gene was localised to chromosome region Xq26-q27. MACE-C1
and MACE-C2 cDNAS (see V69726) are claimed, as are: expression
vectors; transformed or transfected cell lines (e.g. cOS and CHO);
an isolated TRAP encoded by the cDNAs; a kit useful in a PCR based
assay comprising an oligonucleotide having a sequence of
nucleotides 18-34 of the 4031 by mACE-C1 cDNA and an oligonucleotide
having a sequence which is complementary to nucleotides 200-217 of
the 4031 by cDNA sequence; a method for determining expression of
a MACE-C1 gene using the kit; a polytope comprising at least one tumour rejection antigen derived
from MAGE-C1 or MAGE-C2 and at least one other tumour rejection
the presence of cytolytic T cells specific for complexes of a human
lenkcyte antigen. MACE-C1 and be used in a method for determining
the presence of cytolytic T cells specific for complexes of a human
lenkcyte antigen. HAGE-C1 and be used in a method for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour rejection antigen precursors - used for determining presence of cytolytic T cells specific for complexes of a human leukocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour rejection antigen precursor MAGE-C1 cDNA.
MAGE-C1; human; tumour rejection antigen precursor; TRAP; therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                        to reverse of: V74331 from: 1 to: 10470
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Percent Identity: 35.714
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                                                                                                                                                                                                                                                                                                                                                                                1 TyrArgLeuAlaIleArgIle***ArgIleLeuLeuArgTyr 14
                                        Length:
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257. .3475
/*tag= a
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24-APR-1998; U08493.
25-APR-1997; US-845528.
(LUDW-) LUDWIG INST CANCER RES.
BOON-Falleur T, De Smet C, Lucas S;
WPI; 99-024041/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID v69717 standard; cDNA; 4031 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    849 A;
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                                                                                                                                                                                        alignment_block:
US-08-653-294-20 x V74331/rev
                                                                            3.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V69717
                                        40.00
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                                                                                                                Percent Similarity:
                                        Quality:
                                                                                Ratio:
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alignment_scores
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US-08-653-294-20 x V69717
                 Length:
                                                                                                            39.00
3.545
84.615
                                                                                                            Quality:
                                                                                                           alignment_scores:
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Gaps: 0 Percent Identity: 46.154

Ratio: Percent Similarity:

alignment\_block:

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This nucleotide sequence encodes novel human tumour rejection
This nucleotide sequence encodes novel human tumour rejection
This nucleotide sequence encodes novel human tumour rejection
antigen precursor (TRAP) MAGE-C1 (see W81546). MAGE-C1 is a novel
Cells, leading to lysis of the tumour cells which express it.
CHACE-C1 and MAGE-C2 (see W81547) are expressed in a variety of
tumours and in normal testis cells, but not by other normal cells.
The MAGE-C1 cDNA was isolated from a melanoma L8373-MEL CDNA by
CPCR amplification (see V69732-33). It shows homology to MAGE-A1
CDNA (see V69719). The MACE-C1 gene was localised to Xq26-q27.
CMACE-C1 and MAGE-C2 CDNAS (see V69726) are claimed, as are:
expression vectors; transformed or transfected cell lines (e.g. COS)
CC and CHO); an isolated TRAP encoded by the CDNAS; a kit useful in a
CPCR based assay; a method for determining expression of a MAGE-C1
gene using the Kit; a polytope comprising a number of tumour
rejection antigens derived from MAGE-C2; and a polytope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mour rejection antigen precursors - used for determining presence cytolytic T cells specific for complexes of a human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising at least one tumour rejection antigen derived from a water-clar MAGE-Cl and at least one other tumour rejection antigen. MACE-Cl and MACE-C2 and be used in a method for determining the presence of cytolytic I cells specific for complexes of a human
                                                                                                                                                                                                                                                                                                                                                                           Tumour rejection antigen precursor MAGE-C1 cDNA.
MAGE-C1; human; tumour rejection antigen precursor; TRAP;
therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Ratio: 3.545 Gaps: 0
Percent Similarity: -84.615 Percent Identity: 46.154
                                                                                                 13
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                                                               1 TyrArgLeuAlaIleArgIle***ArgIleLeuLeuArg
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   to: 4031
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257. .3685
/*tag= a
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(LUDW-) LUDWIG INST CANCER RES.
BLOTS-Fallour T. De Smet C, Lucas S;
WPI: 99-024041/02.
Align seg 1/1 to: V69717 from: 1
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                                                                                                                                                                                                                                                  seq_documentation_block:
ID V69720 standard; cDNA; 4225 BP.
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                                                                                                                                                                                                                                                                                                                                                   01-MAR-1999 (first entry)
                                                                                                                                                                                        seq_name: N_Geneseq_36:V69720
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US-08-653-294-20 x V69720
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96 AGACTGGCCGTTCGAGTGACTCGGATCCAAGTGCGC 61

ВР

standard; DNA; 99

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This sequence encodes a monoclonal anti-hepatitis B antigen binder sequence encodes a monoclonal anti-hepatitis B antigen binder sequence from the R26 library which may be used in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The catcached to a functional surrogate of an analyte for a limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively can with the analyte for a limiting amount of its affinity acceptor. Functional surrogates are able to minic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as polypucties, polypuctleoting and a small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allegens, hormones related to fertility pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, foliace stimulating hormone, human growth hormone, immunoglobulin E, prolactin, parathyroid hormone, human placental lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotropin, human luteinising hormone, cytomegalovirus, chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CAL25 (a tumour marker). Sequence 99 BP: 14 A; 36 C; 28 G; 21 T;
                                07-NOV-1997 (first entry)
DNA encoding MAb anti-HBSAg binder sequence, B13, from R26 library.
Functional surrogate; analyte; affinity receptor; immunoreactive group;
minic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia.
cardiac marker; tumnour marker; allergen; hormone; fertility; myoglobin;
pregnancy; infectious disease; ferritin; myosin light chain; troponin;
follicle stimulating hormone; human; growth hormone; immunoglobulin E;
prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin
                                                                                                                                                                                                                                                                                                                                 /transl_except= pos:61. .63, aa:Arg
/transl_except= pos:70. .72, aa:Cys
/note= "No stop codon given"
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Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 51; Page 98; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.00
3.364
91.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carter JM, Lee-Own FV; WPI; 97-077284/07. P-PSDB; W10864.
                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996; U10498.
07-JUN-1995; US-476375.
                                                                                                                                                                                                                                                                                                1. .99
/*tag=
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66
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2
                                                                                                 2 ArgLeuAlaIleArgIle***ArgIleLeuLeuArg 13
                                                             from: 1
                                                           Align seg 1/1 to reverse of: T48660
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alignment_block:
US-08-653-294-20 x T48660/rev
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W09916900 Seq ID 7.
Gram positive bacteria; covalent coupling; pathogenicity factors
Gram positive bacteria; covalent coupling; pathogenicity factors
LPXTG-motif dependent C-terminal anchorage; cell surface; antibacterial;
therapeutic agent; extracellular matrix; ss.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17: Page 43-44; 58pp; German.

This invention describes a novel method for identifying a nucleic acid that encodes a polypeptide which affects covalent coupling of polypeptides to the surface of Gram-positive bacteria. The method identifies mutations in bacterial factors that (in)directly interact with the LPXTG-motif dependent C-terminal anchorage of polypeptides, particularly pathogenicity factors, to the cell surface. The products of the invention have antibacterial activity and are potentially useful as therapeutic agents, inhibiting binding of bacteria to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09916894 Seq ID 7.
Active agent, covalent coupling; Gram-positive bacteria; inhibitor; adhesion; extracellular matrix; LPXIG motif-dependent anchorage; pathogenicity factor; bacterial cell wall; therapeutic agent; ss. Unidentified.
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26-SEP-1998; E06137.
29-OCT-1997; EP-118840.
(EVOT-) EVOTEC BLOSYSTEMS AG.
(EVOT-) EVOLUC J, Strauss A, Thumm G;
WPI; 99-255102/21.
Identifying agents that affect adhesion of Gram positive bacteria Disclosure; Page 40-41; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                        (EVOT-) EVOTEC BIOSYSTEMS AG.
Goetz F. Pohlner J. Strauss A. Thumm G;
WPI; 99-255104/21.
Identifying nucleic acid that affects adhesion of Gram positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extracellular matrix.
This sequence is represented in the Seq ID listing but does appear in the specification.
Sequence 459 BP; 144 A; 80 C; 62 G; 170 T;
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Gaps: 0
Percent Identity: 50.000
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                                                                                                                          (first entry)
                                           seq_documentation_block:
ID X24237 standard; DNA; 459
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US-08-653-294-20 x X24237/rev
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seq_name: N_Geneseq_36:X24237
                                                                                                                                                                                                                                                                                                                 26-SEP-1998; E06136.
29-OCT-1997; EP-118755.
27-SEP-1997; EP-116841.
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Ratio:
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                                                                                                                       -JUL-1999
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888888888888888

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seq_documentation_block:
ID Q98553 standard; DNA; 1215 BP.
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3.700
76.923
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FR2715167-Al.
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Ratio:
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                                       NAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describe a novel method for identifying an active agent that affects covalent coupling of polypeptides to the surface of Gram-positive bacteria. The agents identified inhibit polypeptide-induced adhesion of bacteria to extracellular matrix in the host. The active agent effects the LPXTG motif-dependent anchorage of pathogenicity factors to the bacterial cell wall and are potentially useful as therapeutic agents, inhibiting binding of bacteria to extracellular matrix in the host.

This sequence is not described in the specification but is represented
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The promoter (T3364) of the arabinofuranosidase gene of Aspergillus niger 3M43 was identified in a full-length gene (T33646) isolated from a genomic DNA library. The promoter is strongly repressed by glucose and induced by intermediates of xylose metabolism. It can be used to control the expression of a gene of interest, e.g. A. niger arabinofuranosidase or a heterologous gene, in a host cell, pref. Aspergillus or a transgenic plant.

Sequence 869 BP; 224 A; 209 C; 193 G; 243 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus arabinofuranosidase - useful for degradation of
                                                                                                                                                                                                                                                                                                   170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                Length: 14
Gaps: 0
Percent Identity: 50.000
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Gaps: 0
Percent Identity: 58.333
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Promoter: arabinofuranosidase; AbfC; arabinoxylan;
Viscosity modifier; food; feedstuff; ss.
Aspergillus niger strain 3M43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 TATCAAGTCAGCAAAAAATTGAAAGAATACTTTTCAGATAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuAlaIleArgIle***ArgIleLeuLeuArgTyr 14
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Ö
                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 TACCAACTITTAGITCGATTGATCAGAATACTITIG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuAlaIleArgIle***ArgIleLeuLeu 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 869
                                                                                                                                                                                                                                                                                                80 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baruch A, Madrid SM, Rasmussen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: X24253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: T33641 from: 1
                                                                                                                                                                                                                                                              the sequence ID listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T33641 standard; DNA; 869 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                37.00
3.083
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-20 x X24253/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:T33641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-1996;
11-MAR-1996; E01009.
17-MAR-1995; GB-005479.
(DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-20 x T33641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96-443191/44.
                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arabinoxylan
                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                Sequence
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Protein: and related plasmids, transformed E.coli and recombinant protein: and related plasmids, transformed E.coli and recombinant protein: and related plasmids, transformed E.coli and recombinant proteins, useful in enanticoselective prodn of L-carnitine

T proteins, useful in enanticoselective prodn of L-carnitine decombinant proteins, useful in enanticoselective prodn of L-carnatine dehydratase (CDH) gene C Claim 1; Page 17-18; 32pp; French.

The nucleotide sequence of the E.coli L-carnatine dehydratase (CDH) gene designated calB. The sequence forms part of the carnatine operon which calforned sthe accessory protein CaiE encoded by the calE gene (Q98554).

The sequences were obtained from E.coli strain 044K74 which was isolated from rat intestine. The call gene was obtained by screening an E.coli chromosomal DNA library with the probes Q98555-7, based on the N-terminal sequence derived from the purified enzyme. The 1.3 kb Mul-MulI caiB sequence derived from the purified enzyme. The 1.3 kb Mul-MulI caiB sequence derived from the microbiological prodn. of L-carnatine from cortonobetaine. L-carnatine is an essential factor in long chain fatty acid transport across internal mitochondrial membranes. It can be used to treat L-carnatine-deficiency syndromes, haemodialysis and cardiac patients and to stimulate prodn. 313 A; 310; 311 G; 261 T;
28-FEB-1996 (first entry)
28-FEB-1996 (first entry)
E.coli L-carnatine dehydratase gene caiB.
E.coli, L-carnatine dehydratase; caiB; carnatine operon; CaiE; rat; intestine; chromsomal DNA library; probe; expression plasmid; Bacterium; crotonobetaine; long chain fatty acid; transport; mitochondrial membrane; haemodialysis; cardiac; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-NOV-1997 (first entry)
Coding sequence for alkaline liquefying alpha-amylase.
Coding sequence for alkaline liquefying alpha-amylase; detergent;
Starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;
alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;
dish.washing detergent; starch; ds.
Bacillus species KSM-AP1378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= alkaline liquefying alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
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                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1995.
20-JAN-1994; 000807.
20-JAN-1994; FR-000807.
(NASC-) INST NAT SCI APPLIQUEES LYON.
EICHLET K, RIEBER H, MANGRAND-BERTHELOT M;
WPI; 95-255580/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ArgLeuAlaIleArgIle***ArgIleLeuLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
145. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q98553 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [51339 standard; DNA; 1776 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-1996; J01641.
14-JUN-1995; JP-147257
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to reverse of: N60309 from: 1
alignment_block:
US-08-653-294-20 x N60309/rev
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                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                         terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                              DNA encoding alkaline liquefying alpha-amylase - useful in dish-washing and laundry detergents for removal of starch dirts claim 8. Page 23-26. 40pp. English.

This sequence represents the coding sequence for an alkaline liquefying alpha-amylase. Alpha-amylase is an enzyme that acts on starch-related polysaccharides. Nydrolysing the alpha-14-qlucoside bond of the polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit resistance to surfactants used in detergents, and decompose starch or starch-related polysaccharides in a highly random manner. The Bacillus species KSM-AP1378, from which this sequence was isolated, is an alkalophilic Bacillus strain. It was isolated from soil in the vicinity of the city of Tochigi. The enzyme is useful in improving the efficiency of dish-washing and laundry detergents, particularly on starch dirts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New equine and canine interferon - and recombinant DNA molecules coding for them, and transformed cells.

Disclosure: Fig 12: 149pp: German Disclosure: Fig 12: 149pp: German Microorganisms transformed with the recombinant sequence produce IFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is useful therapeutically in veterinary medicine. See also N60336-13 and N60938 4 476 C 471 C FF Sequence 2109 BP; 609 A: 476 C 471 C
                                                                                                                                                                                                                                                                              37.00 Length: 13
3.700 Gaps: 0
76.923 Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1986.
17-DEC-1985.
18-DEC-1984: DE-446122.
(BOEH ) BOEHRINGER INGELHEIM.
Humler A, Hauptmann R, Hauel N, Adolf G, Swetley
WPI: 86-170649/27.
P-PSDB: P60400.
                                                                                                                                                                                                                                                                                                                                                                                                                             1320 AGGTTACCCTTCCGTATTTTACGGTGATTACTACGGTAT 1358
                                                                                                                                                                                                                                                                                                                                                                                                    2 ArgLeuAlaIleArgIle***ArgIleLeuLeuArgTyr 14
             Ozaki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: T51339 from: 1 to: 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1421. .2005
/*tag= a
/product= IFN-omega-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1991 (first entry)
Equine IFN-omega-1 from pAH61.
IFN-omega-1; equine; interferon; ss.
Equus cabalus.
             Kawai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID N60309 standard; DNA; 2109 BP.
AC N60309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1421. 1490
/*tag= b
             Ito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.00
3.364
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:N60309
                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-20 x T51339
(KAOS ) KAO CORP.
Ara K, Hatada Y,
WPI; 97-118708/11.
                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal_peptide
                                        P-PSDB; W11326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-186098-A
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Aspergillus arabinofuranosidase - useful for degradation of arabinoxylan arabinoxylan Example; Page 52-55; 105pp; English.

Example: Page 52-55; 105pp; English.

The Aspergillus niger 3M43 arabinofuranosidase gene (T33646)

Crodes for the precursor form (W00810) of the arabinofuranosidase enzyme. It was isolated from a genomic DNA library by screening with a PCR clone obtd. by amplification of A. niger DNA using primers (see also T33644-45) based on an isolated peptide (W00806) con be used for prodn. of arabinofuranosidase (W04167) in transformed hosts, pref. Aspergillus or a transgenic plant. The promoter (see also T33641), terminator (133642) and signal sequence (T33643) may also be used to control expression of the arabinofuranosidase gene, or other gene of interest, in a host
                                                                                                                                                                                                        11-DEC-1996 (first entry)
Aspergillus arabinofuranosidase gene.
Arabinofuranosidase; AbfC; arabinoxylan; viscosity modifier; food;
feedstuff; ds.
1 TyrArgLeuAlaileArgile***ArgIleLeuLeuArgTyr 14
||| ::::::::|||
1896 TATTCTTCTCTGTCAGGTACAGACGGATTCTCCTGAAGTAC 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 TACCAACTTTAGTTCGATTGATCAGAATACTTTTG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TyrArgLeuAlalleArgIle***ArgIleLeuLeu 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T33646 from: 1 to: 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 C;
                                                                                                                                                                                                                                                                                                                               Aspergillus niger strain 3M43.
Key
Location/Qualifiers
promoter 1. .869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-1996.
11-MAR-1996; E01009.
17-MAR-1995; GB-005479.
(DANI-) DANISCO AS.
Baruch A, Madrid SM, Rasmussen P;
WPI; 96-443191/44.
                                                                                                                                                   seq_documentation_block:
ID T33646 standard; DNA; 2555 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          632 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
870 .947
/*tag= c
948 .1754
/*tag= e
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
870. .1757
/*tag= b
870. .947
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3.700
83.333
                                                                                                 seq_name: N_Geneseq_36:T33646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-20 x T33646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2555 BP;
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal_peptide
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PFENDS MONOGONE WAS AND MONOGONE WE ARE A PERSON WAS AND MONOGONE WE ARE A PENDS MONOGONE WAS A PENDS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protons across the cytoplasmic membrane, or vice versa. The proton gradient is used to drive ATP synthesis from ADP and Pi. The method can be used for optimising the formation of biomass or a desired product,
                                                                                                                                                                                                                                                                                                                                                             /gene= "atpA" "note= "atpA" "1260. 3129
                                                                                                                                                                                                                                                         /gene= "atpH"
/note= "delta subunit of the Fl portion of F0Fl ATPase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "gamma subunit of the Fl portion of FOF1 ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene= "atpD"
/note= "beta subunit of the Fl portion of F0Fl ATPase"
                                         04-AUG-1998 (first entry)
L. lactis soluble part (FI) exhibiting ATPase activity encoding DNA.
Biomass production; uncoupled ATPase; FOFI ATPase; membrane bound;
FI; Lactococcus lactis; ds.
Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          981 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ATPase subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
/product= "ATPase subunit"
                                                                                                                                                                                                                                /product= "ATPase subunit"
                                                                                                                                                                                                                                                                                                                                                 'product= "ATPase subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W56790, W56791, W56792, W56793.
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1491 A;
V29571 standard; DNA; 4815 BP.
V29571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "atpG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4710
                                                                                                                                                                                                                                                                                                     . 2244
                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snoep JL, Westerhoff HV; WPI; 98-193637/17.
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12-MAR-1998;
08-SEP-1997; DK0373.
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Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus

WPI; 98-272225/24.

30-OCT-1997; U19588. 31-OCT-1996; US-029960. (HUMA-) HUMAN GENOME SCI INC. Barash SC, Chol GH, Dillon PJ, Dougherty BA, Fannon M, Kunsch CA, Rosen CA:

Streptococcus pneumoniae genome fragment SEQ ID NO:104. Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.

Streptococcus pneumoniae WO9818931-A2.

ВР.

V52237 standard; DNA; 6735 23-OCT-1998 (first entry)

seq\_documentation\_block

seq\_name: N\_Geneseq\_36:V52237

1 TyrArgLeuAlaIleArgIle\*\*\*ArgIleLeuLeuArgTyr 14

to: 4815

from: 1

to: V29571

Align seg 1/1

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productions of the present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the nucleotide sequence at least 95% identical to 5EQ ID No: 1 to 391. The nucleotide sequence at least 95% identical to 5EQ ID No: 1 to 391. The nucleotide sequence at least 95% identical to 391 (V52134 to V52524) are genomic fragments from Streptococcus and 10 (V52134 to V52524) are genomic fragments from Streptococcus concerned (SEQ ID No: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating members or (b) isolating the nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the sequence is homologous to amplification primers derived from the isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the subject of the summary of the supplication and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the summary of the supplication and isolating the amplified system for identifying fragments of the supplied and system for identified system for identified system for identified system for ide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae. 1415 G; 2057 T; Sequence 6735 BP; 2122 A; 1141 C; 1415 G; 2057 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 12
Gaps: 0
Percent Identity: 66.667
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Gaps: 0 Percent Identity: 42.857

3.083 85.714

Ratio:

alignment\_scores: Quality: Percent Similarity: alignment\_block: US-08-653-294-20 x V29571

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OM protein - protein search, using sw model

February 8, 2000, 01:29:43; Search time 133.56 Seconds (without alignments) 2.660 Million cell updates/sec Run on:

US-08-653-294-21 70 1 AYRLLIKVIRIVLKY 15 Title: Perfect score: Sequence:

Scoring table:

188963 seqs, 23686106 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Mouse CLK serine/t	Cellubrevin-4. Iso	Yeast transcriptio	B. malayi ankyrin	ρц	Tuberous sclerosis	D. immitis pDiAnkl	Lytic peptide with	D. immitis ankyrin	Ankyrin protein fr	Pseudomonas mendoc	Sequence encoded b	D. immitis ankyrin	Full length ankyri	HLA-B2702 CTL modu	HLA-B2702 84-75-84	Immunomodulating d			-	Human TRIO phospho	HLA-B2702 84-79-84	Peptide B2702.84-7	Immunomodulating d	Human derived pept	ASP-5 analogue (3)	S.thermophilus exo	S.thermophilus exo		cyclin C	Human secreted pro	n end	DP.7	vcle
	ID	6	18	W13825	W76777	W70609	R77223	W76789	W77378	W76774	W70606	W88282	P81184	W76776	W70608	R92907	R95428	W33778	W81351	W81349	Y00868	W27227	R95429	W33798	W33799	P90056	R15605	W22173	W14074	W41497	W41496	9	26	20	72
			141	226			784						594	745	745	_	_	_	_	_		861										374 1	443 1	62	41
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Result	No.	н	7	m	7	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
	Query	Query Score Match Length DB ID	Query Score Match Length DB ID  37 52.9 497 1 W49912 Mouse CLK ser	Query   Score Match Length DB ID   Description     St.9   497   W49912   Mouse CLK serin 36   51.4   141   W04183   Cellubrevin.4.	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Cell cycle checkpo Human ataxia and r	A human ATR protei Virulence gene clu	Human secreted pro	Sequence of artifi	Human secreted pro	Sequence of artifi	Feline infectious	Expressed antigen	H. pylori GHPO 127
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322	32 32	31.5	31	31	31	31	31	31
3.5	37 38	39	40	41	42	43	44	45

## ALIGNMENTS

19912 standard; Protein; 497 AA.  19912 standard; Protein; 497 AA.  19912.1998 (first entry)  10.30-109.1998 (first entry)  10.30-109.1098 (first entry)  10.30-109.1098 (first entry)  20.30-109.1009.1009.1099.1099.1099.1099.1099	RESULT W49912	912	
Wouse CLK serine/threonine kinase mCLK2 Mouse CLK serine/threonine kinase mCLK2; Substitute CLK; serine/threonine kinase; protein kinase; LAMMER kinstigned Lansaduction; cancer; contraceptive; mouse; therapy; signal transduction; cancer; contraceptive; mouse; therapy; Mus musculus.  Location/Qualifiers  Note= "nuclear localisation domain"  Note= "nuclear localisation domain"  Note= "catalytic domain"  163. 479  Domain  Note= "catalytic domain"  Note= "catalytic domain"  163. 479  Peptide  Note= "catalytic domain"  Note= "catalytic domain"  163. 479  Note= "catalytic domain"  163. 479  Note= "catalytic domain"  163. 479  Note= "catalytic domain"  164. 203426.  17-JUN-1997; 18046.  17-JUN-1997; 180-203486.  17-JUN-1996; US-030860.  17-NOV-1996; US-030860.  18-NOV-1996; US-030860.  18-NOV-1996; US-030860.  18-NOV-1996; US-030860.  18-NOV-1996; US-030860.  18-NOV-1996; US-030860.  18-NOV-1996; US-030860.  19-NOV-1996; US-030860.  19-NOV-1996; US-030860.  19-NOV-1996; US-030860.  19-NOV-1996; US-030860.  11-NOV-1996; US-030860.  11-NOV	e	19912 standard; Protein; 497	А.
Domain CartiorAchieonine kinase mCLK2.  MCLK2; CLK; serine/threonine kinase; protein kinase; LAMMER kirsignal transduction; cancer; contraceptive; mouse; therapy; diagnosis.  McLK2; CLK; serine/threonine kinase; protein kinase; LAMMER kirsignal transduction; cancer; contraceptive; mouse; therapy; diagnosis.  Key 28.45  Domain //note="nuclear localisation domain"	ų.	;	
MOUSE CLEAN SETTIBE/THEGOLINE KINASE MILAKA.  MOUSE CLEAN SETIBE/THEGOLINE KINASE MILAKA.  Signal transduction; cancer; contraceptive; mouse; therapy; diagnosis.  Mus musculus.  Mus musculus.  28. 45 muclear localisation domain"  Domain  Anote= "nuclear localisation domain"  Anote= "catalytic domain"  MOSTA8723-A2.  24-DEC-1997.  11-JUW-1997.  18-037.  11-JUW-1997.  11-JUW-1997.  11-JUW-1997.  11-JUW-1997.  11-JUW-1997.  11-NOV-1996.  12-NOV-1996.  13-NOV-1996.  13-NOV-1996.  13-NOV-1996.  14-NOV-1996.  15-NOV-1996.  15-NOV-1996	<u></u>	20-JUL-1998 (first entry)	
signal transduction; cancer; contraceptive; mouse; therapy; diagnosis.  Mus musculus.  Ecation/Qualifiers  Domain  78.479  700te= "unclear localisation domain"  78.479  700te= "catalytic domain"  78.33-479  700te= "catalytic domain"  78.393-80-90-90-90-90-90-90-90-90-90-90-90-90-90	<u>.</u> 33	•	
diagnosis.  May musculus.  Key 28. 45  Domain	3		
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Ney  28. 45  Domain  Cote="nuclear localisation domain"  Note="catalytic domain"  163. 479  Domain  163. 479  Note="catalytic domain"  Note="lawmer motif"  WO9748723-A2.  24-DEC-1997.  17-UNN-1997; 1B0946.  17-UNN-1996; US-019629.  17-UNN-1996; US-019629.  17-UNN-1996; US-019629.  17-UNN-1996; US-019629.  17-UNN-1996; US-019629.  17-UNN-1996; US-019629.  17-UNN-1996; US-019660.  17-NOV-1996; US-019660.  18-NOV-1996; US-019660.  18-NOV-19960.  18-NOV-1996; US-019660.  18-NOV-1906; US-019660.  18-NOV-19060.	ຶ	Mus musculus.	
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19-DEC-1996; US-034286. 19-DEC-1996; US-034286. 13-AUG-1996; US-030860. 13-NOV-1996; US-030860. 13-NOV-1996; US-030860. 13-NOV-1996; US-030964. (PLAC ) MAX PLANCK GES FOREDERUNG WISSENSCHAFTEN. Aoki N, Chen Z, Kharitonenkov AI, Kim YW, Nayler O, Ullrich A, Wang HY: WPI: 98-120302/11. New phosphatase and kinase enzyme(s) - useful in the diagnosis treatment of signal transduction disorders Claim 11: Fig 4: 138Pp; English. This polypeptide comprises novel mouse CLK serine/threonine kinase family of proteins regulate RNA splicing in cells. mCLK2 cDNA was cloned from a regulate RNA splicing in cells. mCLK2 cDNA was cloned from a membryo 11.5 p.c. 12Ap CDNA library. The invention discloses the discovery of novel protein kinases mCLK2, cDNA was cloned from a membryo 11.5 p.c. 12Ap CDNA library. The invention discloses the discovery of novel protein kinases mCLK2, mCLK3 (see W49912) an mCLK4 (see W49914) of mOl. Wt. 59.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins, methods for identify compounds that activate or inhibit the novel proteins, as well methods for the diagnosis and treatment of diseases associated the novel proteins. Overexpression of CLK serine/threonine kin has been implicated in certain types of cancer. Compounds that chair catalytic activity or disrupt their interactions with natural binding partners may act as anti-cancer therapeuti mCLK related molecules and compounds may also be useful as male contraceptives.	) [I	- TB097 - TB094	
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13-NOV-1996; US-030860.  15-NOV-1996; US-030860.  15-NOV-1996; US-030860.  15-NOV-1996; US-030860.  15-NOV-1996; US-030860.  Aoki N, Chen Z, Kharitonenkov AI, Kim YW, Nayler O, Ullrich A, Wang HY; WPI; 98-120302/11.  New phosphatase and kinase enzyme(s) - useful in the diagnosis treatment of signal transduction disorders  Claim 11; Fig 4: 138Pp; English.  This polypeptide comprises novel mouse CLK serine/threonine kin mcLk2, from the CLK serine/threonine kinase family of proteins regulate RNA splicing in cells. mCLk2 cDNA was cloned from a membryo 11.5 p.c. 12Ap CDNA library. The invention discloses the discovery of novel protein kinases mCLk2, mCLk3 (see W49912) and mCLk4 (see W49914) of mOl. Wt. 59.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins (see W49912) and mCLk4 (see W49914) of mOl. Wt. 59.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins (see W49912) and mcLk4 cellular signal transduction, and provides vectors, novel cellular signal transduction, and proteins, as well methods for the diagnosis and treatment of diseases associated the novel proteins. Overexpression of CLK serine/threonine kin has been implicated in certain types of cancer. Compounds that inhibit their catalytic activity or disrupt their interactions with natural binding partners may act as anti-cancer therapeutic mCLK related molecules and compounds may also be useful as male contraceptives.	; p	00-3470-1006- TO-00340F	
15.NOV-1996; US-030964.  (PLAC.) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. Acki N, Chen Z, Kharitonenkov AI, Kim YW, Nayler O, Ullrich A, Wang HY; WPI: 98-120302/11. New phosphatase and kinase enzyme(s) - useful in the diagnosis treatment of signal transduction disorders This polypeptide comprises novel mouse CLK serine/threonine kin mCLK2, from the CLK serine/threonine kinase family of proteins regulate RNA splicing in cells. mCLK2 cDNA was cloned from a rembryo 11.5 p.cIZAP cDNA library. The invention discloses th discovery of novel protein kinases mCLK2, and 57.2 kDa, respectively, as well as other novel proteins (see W49912) an mCLK4 (see W49914) of mol wt. 59.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins of mcludia cellular signal transduction, and provides vectors, host cells, purified recombinant proteins, methods for identify compounds that activate or inhibit the novel proteins. Overexpression of CLK serine/threonine kin methods for the diagnosis and treatment of diseases associated the novel proteins. Overexpression of CLK serine/threonine kin hobit their catalytic activity or disrupt their interapeuti mCLK related molecules and compounds may also be useful as male contraceptives.	4 ρ	13-NOV-1996; 03-025465.	
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WPI; 98-12302/11.  New phosphatase and kinase enzyme(s) - useful in the diagnosis treatment of signal transduction disorders Claim 11: Fig 4: 138pp; English.  This polypeptide comprises novel mouse CLK serine/threonine kin mCLK2, from the CLK serine/threonine kinase family of proteins regulate RNA spliting in cells. mCLK2 CDNA was cloned from a mCLK2 from the CLK serine/threonine kinase family of proteins regulate RNA spliting in cells. mCLK2 CDNA was cloned from a mCLK4 (see W49914) of mol.wt. 59.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins (see W49906-10) involved in cellular signal transduction, and provides vectors, host cells, purified recombinant proteins, methods for identify compounds that activate or inhibit the novel proteins, as well methods for the diagnosis and treatment of diseases associated the novel proteins. Overexpression of CLK serine/threonine kin has been implicated in certain types of cancer. Compounds that inhibit their catalythe activity or disrupt their interactions with natural binding partners may act as anti-cancer therapeuti contraceptives.  Sequence 497 AA;	-1 F	Chen 2,	Kim rw, Nayler
New phosphatase and kinase enzyme(s) - useful in the diagnosis treatment of signal transduction disorders Claim 11: Fig 4: 138pp; English. This polypeptide comprises novel mouse CLK serine/threonine kinase family of proteins regulate RNA splicing in cells. mCLK2 CDNA was cloned from a regulate RNA splicing in cells. mCLK2 CDNA was cloned from a membryo 11.5 p.c. 12Ap CDNA library. The invention discloses the discovery of novel protein kinases mCLK2, mCLK3 (see W49912) an mCLK4 (see W49914) of mol.Wt. 59.9, 58.5 and 57.2 kDa, respectively, as well as other novel proteins (see W49961-0) involved in Cellular signal transduction, and provides vectors, respectively, as well as other novel proteins (see W4996-10) involved in Cellular signal transduction, and provides vectors, host cells, purified recombinant proteins, methods for identify compounds that activate or inhibit the novel proteins. Overexpression of CLK serine/threonine kin has been implicated in certain types of cancer. Compounds that inhibit their catalytic activity or disrupt their interactions with natural binding partners may act as anti-cancer therapeuti contraceptives.  Sequence 497 AA;	46	CI 5, Wally	
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Treatment of signal transduction disorders  Claim 11: Fig 4: 139pp: English.  This polypeptide comprises novel mouse CLK serine/threonine kin mCLK2, from the CLK serine/threonine kinase family of proteins regulate RNA spliting in cells. mCLK2 CDNA was cloned from a mCLK2 (soe W49014) of mol.wt. 59.9, 58.5 and 57.2 kDa, volumenty of novel protein kinases mCLK2, mCLK3 (see W4906-10) involved in cellular signal transduction, and provides vectors, host cells, purified recombinant proteins (see W4906-10) involved in cellular signal transduction, and provides vectors, host cells, purified recombinant proteins, methods for identify compounds that activate or inhibit the novel proteins, as well methods for the diagnosis and treatment of diseases associated the novel proteins. Overexpression of CLK serine/threonine kin has been implicated in certain types of cancer. Compounds that inhibit their catalytic activity or disrupt their interactions with natural binding partners may act as anti-cancer therapeuti contraceptives.  Sequence 497 AA;	F	New phosphatase and Kinase enzy	tul in the diagnosis
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Claim 25; Page 37; 59pp: English.

W04180-83 are novel human cellubrevins (CB-1, -2, -3 and -4). CBs

can be used for the study and regulation of vesicle trafficking in

normal, and in acute and chronic disease situations, and for the

diagnosis and treatment of conditions caused by infection, traumatic

tissue damage, hereditary disease, e.g. asthma or arthritis, invasive

cancer, leukaemia and lymphoma or other physiologic/pathologic problems

associated with induced, and otherwise abnormal, membrane trafficking.

In particular, the CB-4 polynucleotide (isolated from a cerebellum

library (CRBLNOYCI) can be used in a diagnostic test for conditions or

diseases in which its expression is induced, e.g. cerebellar degenerative

diseases or brain tumours, while CB-4 inhibitors can be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SNI/SNF proteins
Claim 11; Fig 10a-b; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human cellubrevin polynucleotide(s) - useful to develop prods. for diagnosis and treatment of conditions involving abnormal
                                                                                                                                                                                                                                                                                                                                                                                              leukaemia;
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                                                                                                                                                                                                                                                                                                                                                  CB-1; CB-2; CB-3; CB-4; human; cellubrevin; study; regulation; vesicle trafficking; diagnosis; treatment; infection; leukaemitraumatic tissue damage; asthma; arthritis; cancer; lymphoma.
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04-JUN-1997 (first entry)
14-JUN-1997 (first entry)
17-Inscription regulatory factor SRB8.
17-Inscription regulatory factor; suppressor of RNA polymerase SRB8; RNA polymerase II; holoenzyme; SWI/SNF.
Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 141;
Pred. No. 12;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1995; US-521872.
11-CCT-1995; US-540804.
26-JAN-1996; US-590399.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
Chao DM, Koleske AJ, Thompson CM, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WI3825 standard; Protein; 1226 AA.
                                                                                                                                                                                                                 W04183 standard; Protein; 141 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such conditions or diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-1996.
22-MAR-1996; U03835.
23-MAR-1995; US-409373.
(INCY-) INCYTE PHARM INC.
Hawkins PK. Murry LE, Sei
WPI: 96-443183/44.
                                                                                                                                                                                                                                                                                       29-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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   |:|:|:|: | ||
188 RVLVKIIKNVEKY 200
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28-AUG-1996; U14192.
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Best Local Similarity
Matches 8; Conserv
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WO9629407-A2.
                                                                                                                                                                                                                                                                                                                        Cellubrevin-4
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Wi7676-W7677 represent ankyrin proteins isolated from the helminth parasites Dirofilaria immitis and Brugia malayi. The nucleic acids and recombinant products are useful for the nucleic and sa vaccines against parasitic helminth, e.g. D. immitis or B. malayi. They can also be used for therapy after infection, and to raise antibodies, also for use in therapeutics, as passive immunogens, or as therapeutics against helminths on conjugation to cytotoxic agents. The nucleic acids contained in viruses, may also be used as viral vaccines, and the nucleic acids themselves or in vectors may be used as genetic vaccines.
Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5, SRB6, SRB7, SRB8, SRB10 and SRB11 (W13821-28) are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity, and are components of the RNA polymerase II holoenzyme. They were identified using methods designed to identify transcription factors involved in RNA polymerase II ctranscription factors involved in RNA polymerase II ctranscription factors involved in RNA polymerase II STBS can be used to treat diseases resulting from alteration or deletion of the SRB gene, pref. by gene transfer technology. They come also be used in in vitro transcription of DNA and to identify sequence 1226 AA;
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N-PSDB; V63024.
Nucleic acids encoding ankyrins from helminth parasites - useful for recombinant production of the proteins for use as vaccines and treatments against helminth infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 1226; Pred. No. 1.1e+02;
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Pred. No. 40;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-0AN-1999 (first entry)
B. malayi ankyrin pBmAnk302 protein.
Ankyrin; helminth; parasite; vaccine; therapy; infection;
parayive immunogen; cytotoxic agent.
Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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60.0%;
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77.8%;
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21-JAN-1999 (first entry)
Ankyrin protein PBmAnk302.
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Best Local Similarity 60.0
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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27-OCT-1998.
24-APR-1997; 847429.
24-APR-1997; US-847429.
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999 YHLLIKIIR 1007
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Best Local Similarity
Matches 7; Conserv
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us-08-653-294-21.rag

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label- Phosphorylation note- "potential protein-kinase C phosphorylation
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note= "potential protein-kinase C phosphorylation
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note- "potential protein-kinase C phosphorylation
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note- "potential protein-kinase C phosphorylation
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/note- "potential protein-kinase C phosphorylation
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hote- "potential protein-kinase C phosphorylation
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note- "potential casein-kinase 2 phosphorylation
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note- "potential tyrosine-kinase phosphorylation
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note= "potential casein-kinase 2 phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                      phosphorylation
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note- "potential casein-kinase 2 phosphorylation
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note- "potential tyrosine-kinase phosphorylation
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note- "potential protein-kinase phosphorylation
                              label- Phosphorylation
potential protein-kinase C phosphorylation
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potential casein-kinase 2 phosphorylation
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note= "protein-kinase C phosphorylation
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note- "potential casein-kinase 2
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"potential casein-kinase 2
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                                                                                                                                                                                                                                                             .572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       Dirofilaria and Brugia ankyrin proteins and antibodies - useful for protection of animals from disease caused by parasitic helminth (Claim 5; Columns 137-140; 84pp; English.

The present sequence represents a Brugia malayi ankyrin protein. The ankyrin protein, or anti-ankyrin antibodies, may be used to protect an animal from disease caused by a parasitic helminth, especially where the disease is heartworm disease, elephantiasis or
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note- "potential protein-kinase C phosphorylation
ite"
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/note= "potential protein-kinase C phosphorylation
site"
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note= "potential protein-kinase C phosphorylation
ite"
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hote- "potential protein-kinase C phosphorylation
ite"
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/note= "potential casein-kinase 2 phosphorylation

    Phosphorylation
    "potential casein-kinase 2 phosphorylation

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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
nunyrin protein; parasitic helminth; heartworm disease; elephantiasis; hydrocele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R77223;
04-DEC-1995 (first entry)
Tuberous sclerosis 2 TSC2 gene product.
Tuberous sclerosis 2; TSC2 gene; gene therapy; tumor.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label = Membrane-spanning_region
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB ]
Pred. No. 40;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Leucine_zipper
71. .187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9. .107
label= Repeat_motif
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label- Repeat_motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R77223 standard; Protein; 1784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                               20-OCT-1998.
26-FEB-1998. 031485.
24-APR-1997: US-847429.
26-FEB-1998: US-011485.
(HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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site"
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Best Local Similarity
Matches 6; Conserv
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53 IKVVELLLKY 62
                                                                                                                                                                      Blehm ES, Tang L;
WPI; 98-593373/50.
                                                                                                                                                                                                                                                                                                                                                                302 AA;
                                                  Brugia malayi.
US5824306-A.
                                                                                                                                                                                                        N-PSDB; V63315
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                                                                                                                                                                                                                                                                                                                                                  hydrocele.
                                                                                                                                                                                                                                                                                                                                                                  Sequence
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us-08-653-294-21.rag

FT modified_site   /note= "potential casein-kinas site"   /label= Phosphorylation   /label= Phos	PF 24-APR-1997; 847429.  PR 24-APR-1997; US-847429.  PR 4(HESK-) HESKA CORP.  PI Blebm ES, Tang L;  DR WPL; 98-593922/50.  PT recombinant production of the proteins for use recombinant production of the proteins for use transments against helminth infection.  PS Example 2: Column 35-36, 84pp; English.  CC W76778-W76802 are ankyrin-like repeat peptide containth parasite Dirofilaria immitis publakilo contained acids and recombinant products are use production of the ankyrin polypeptides. These contained also be used for therapy after infect antibodies, also for use in therapeutics, as proceed and the nucleic acids contained in viruses, may also be therapeutics against helminths on conjugation contoined and the nucleic acids themselves or in vectors of sequence 33 AA;  Ouery Match  Ouery Match  Best Local Similarity 50.0%; pred. No. 6.1; Matches 5; Conservative 4; Mismatches  Oy 6 IKVIRIVLKY 15  Db 15 IKIVELLEKY 24  RESULT 8  W77378  ID W77378  ID W77378  ID W77378;  DT 14-DEC-1998 (first entry)
site"  // Jabel - Phosphorylation site" // Anote - "potential protein-kinase C phosphorylation site" // Jabel - Phosphorylation // Anote - "potential protein-kinase phosphorylation site" // Anote - "potential protein-kinase phosphorylation site" // Jabel - Phosphorylation // Anote - "potential tyrosine-kinase phosphorylation site" // Jabel - Phosphorylation	/label- Phosphorylation site"
	modified_site modified_site modified_site modified_site modified_site modified_site

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ide fragments isolated from the nkl075 protein. Such ankyrin useful for the recombinant use proteins can then be used 3. D. immitis or B. malayi. fection, and to raise as passive immunogens, or as lon to cytotoxic agents. The so be used as viral vaccines, tors may be used as genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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se as vaccines and
                                                                hase C phosphorylation
use 2 phosphorylation
                                                                                                                                 ase 2 phosphorylation
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y; infection;
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+02;
4; Indels (
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us-08-653-294-21.rag

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Gaps

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protection of animals from disease caused by parasitic helminth claim 5; Columns 79-82; 84pp; English.

The present sequence represents part of a Dirofilaria immitis ankyrin protein. The ankyrin protein, or anti-ankyrin antibodies, may be used to protect an animal from disease caused by a parasitic helminth, especially where the disease is heartworm disease, elephantiasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production of para-hydroxybenzoate - using pobA(-) Pseudomonas
strains which have a toluene degradation pathway and do not produce
para-hydroxybenzoate hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dirofilaria and Brugia ankyrin proteins and antibodies - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas mendocina para-hydroxybenzoate hydroxylase.
Para-hydroxybenzoate hydroxylase; para-hydroxybenzoic acid; PHBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 39-41; 60pp; English.

This is the amino acid sequence of a Pseudomonas mendocina para-hydroxybenzoate hydroxylase (PHBH). P. mendocina possesses two highly homologous pobA genes (see V84270-71), both of which encode PHBH enzymes (see W86281-82) able to convert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 303;
Pred. No. 62;
4; Mismatches 1; Indels
                       DB 1; Length 303;
62;
                                                                   Indels
                                                                                                                                                                                                                                                                                         W70606;
21-JAN-1999 (first entry)
Ankyrin protein fragment PDiAnk303.
Ankyrin protein; parasitic helminth; heartworm disease;
elephantiasis; hydrocele.
Dirofilaria immitis.
                                                                     ۲,
                                                                   Mismatches
                       Score 34;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1998; U12072.
03-JUN-1998; US-049556.
13-JUN-1997; US-049556.
(DUPO) DU PONT DE NEMOURS & CO E I. Chen KK, Grelak RL; WPI; 99-060332/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W88282 standard; Protein; 395 AA.
                                                                                                                                                                                                                                                                       W70606 standard; Protein; 303 AA
                                                                   4;
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50.0%;
                       48.6%;
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Query Match
Best Local Similarity 50.v.
-Lnc 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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24-APR-1997; US-847429.
26-FEB-1998; US-031485.
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                                                                                                             6 IKVIRIVLKY 15
                                                                                                                                         Blehm ES, Tang L;
WPI; 98-593373/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IKVIRIVLKY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 AA;
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20-OCT-1998.
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                                                                                                                                                                                                                             RESULT
W70606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note of a cids encoding ankyrins from helminth parasites - useful for recombinant production of the proteins for use as vaccines and recombinant production of the proteins for use as vaccines and recombinant production of the proteins.

Treatments against helminth infection
Claim 8: Column 79-82; 84pp: English.

W76769-W7677 represent ankyrin proteins isolated from the helminth parasites birofilaria immitis and Brugia malayi. The nucleic acids and recombinant products are useful for the recombinant production of the ankyrin polypeptides. These proteins can then be used as vaccines against parasitic helminth, e.g. D. immitis or B. malayi. They can also be used for therapy after infection, and to raise antibodies, also for use in the rapeutics, as passive immunogens, or as therapeutics against helminths or curuses, may also be used as viral vaccines, and the nucleic acids contained in themselves or in vectors may be used as genetic vaccines.
                                                                                                                                                                                                                                                                New modified peptide(s) - obtained by substitution with an amino acid which is modifiable by a reaction and replacing other amino acid which is modifiable by a reaction and replacing other amino acids which are not to be modified

Claim 7; Page 22; 33pp; English.

The peptides w77376-W77390 can be modified by the method of the cinvention by substituting at least one amino acid which is modifiable by a reaction and replacing other amino acids in the peptide with amino acids which are not modifiable by the reaction. The methods can be used for the modification of biologically active peptides such as hormones, drugs, toxins and peptides which act on lipid bilayer membranes. The modified peptides can be used e.g. in the body of an animal or plant or parts in corder to affect the structure or integrity or permeability of a foreign body such as a microorganism, parasite or virus present in the body of the animal or plant or within the cells of the body of the animal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D. immitis ankyrin pDiAnk303 protein.
Ankyrin; helminth; parasite; vaccine; therapy; infection; passive immunogen; cytotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.6%; Score 34; DB 1; Length 37; 41.7%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                       Lytic peptide with alterable function 3.
Biologically active peptide; hormone; drug; toxin;
lipid bilayer membrane; microorganism; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
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                                                                                        Synthetic.
24-SEP-1998.
18-MAR-1998; G00799.
18-MAR-1997; GB-005519.
(ANMA-) ANMAT TECHNOLOGY LTD.
Ajoula HS, Clarke DJ:
WPI; 98-521161/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W76774;
15-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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24-APR-1997; 847429.
24-APR-1997; US-847429.
(HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US5827692-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blehm ES, Tang L;
WPI; 98-593992/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RLLIKVIRIVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 AA;
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W76774
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27-0CT-1998.
24-APR-1997; US-847429.
PA A-PR-1997; US-847429.
PA Nocleic acids encoding ankyrins from helminth parasites - useful for recombinant production of the proteins isolated from the helminth are combinant products are useful for the recombinant products are useful for the recombinant production of the crombinant products are useful for the recombinant production of the arkyrin polypeptides. These proteins can then be used as vaccines against parasitic helminth, e.g. D. immitis or B. malayi. They can also be used for therapy after infection, and to raise antibodies, also for use in therapeutics, as passive immunogens, or as therapeutics against helminths on conjugation to cytotoxic agents. The nucleic acids contained in viruses, may also be used as viral vaccines, and the nucleic acids of themselves or in vectors may be used as genetic vaccines.
                                                                   15-JAN-1999 (first entry)
D. immitis ankyrin pDIAnk1745 protein.
Ankyrin; helminth; parasite; vaccine; therapy; infection; passive immunogen; cytotoxic agent.
Dirofilaria immitis.
W76776
ID W76776 standard; Protein; 1745 AA.
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W70608
                                 NAME PARTIES OF THE P
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Sisclosure: Fig 1: 13pp; English.

CDNA was prepd. from FIPV straim 79-1146. N81533 gives the sequence

of the peplomeric gene in three reading frames. The top reading

frame is an open reading frame of 4356 nucleotides and has a coding

capacity for a precursor polypeptide having a mol. Wt. of 160.470

(1452 AAs). The beginning and the end of the E2 gene are indicated

in the FT of N81533. The first 18 N-terminal AAs have a strong

hydrophobic character and presumably comprises a cleavable signal

ceptide. The extreme carboxy-terminal part comprises a region of 20

hydrophobic AAs, which presumably serves as a transmembrane anchor.

The FIPV peplomeric protein has 35 potential glycosylation sites,

of which 22 are in the N-terminal part (poss 1-790) which corresponds

to the S-part of the IBV E2 (see P81183). N.B. IBV = infectious

bronchitis virus. "X" in the AA sequence denotes the translation
para-hydroxybenzoic acid (PHBA) to protocatechuate. A claimed method for the production of PHBA comprises: (a) culturing a pobA(-) Pseudomonas strain in a medium containing an aromatic organic substrate (e.g. toluene or p-cresol), at least one C-source (e.g. qlucose or succinate) and an N-source, where the pobA(-) Pseudomonas strain comprises pobA genes encoding the toluene monoxygenase toluene degradation pathway and where the pobA(-) Pseudomonas strain does not produce any detectable PHBH activity config to pobA gene distruption, so that PHBA accounliates at a rate of about 0.01-1 g PHBA/G.cell.hr; and (b) recovering the PHBA. The PHBA is used as a monomer for liquid crystal polymers. Esters of PHBA and also be used as backbone modifiers in condensation polymers, e.g. polyesters, and are also used to make paraben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-1992 (first entry)
Sequence encoded by the 2nd reading frame of the peplomeric gene
of FIVP strain 79-1146.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 395;
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Pred. No. 3.5e+02;
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81;
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Pred. No. 81;
2; Mismatches
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Feline infectious peritonitis virus.
EP-264979-A.
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57.1%;
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Best Local Similarity 66.7
Matches 6; Conservative
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310 YRILVKVYR 318
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Best Local Similarity
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The present sequence represents a full length Dirofilaria immitis anky protein. The ankyrin protein, or anti-ankyrin antibodies, may be used to protect an animal from disease caused by a parasitic helminth, especially where the disease is heartworm disease, elephantiasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dirofilaria and Brugia ankyrin proteins and antibodies – useful for protection of animals from disease caused by parasitic helminth
                                            ;
0
Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1745;
                                                                                                                                                                                                                                                                                        21-JAN-1999 (first entry)
Full length ankyrin protein.
Ankyrin protein; parasitic helminth; heartworm disease;
elephantiasis; hydrocele.
  Score 34; DB 1; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1;
Pred. No. 3.8e+02;
                                            4; Mismatches
                                                                                                                                                                                                                                              W70608 standard; Protein; 1745 AA.
W70608;
  48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.6%;
Query Match 48.6
Best Local Similarity 50.0
Matches 5; Conservative
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24-APR-1997; US-847429.
26-FEB-1998; US-031485.
(HESK-) HESKA CORP.
Blehm ES, Tang L;
                                                                                                                                                                                                                                                                                                                                                                                   Dirofilaria immitis.
                                                                                                                       393 IKIVELLERY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1745 AA;
                                                                                        6 IKVIRIVLKY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n ES, Tang L;
98-593373/50.
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Best Local Similarity
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75.84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) Sequence 20 AA;
                                                                                                                                                                                                                             HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic rilymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extension of acceptance period of transplants from MHC unmatched donor hosts, - using Class I B75-84 MHC antigen of the recipient
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Best Local Similarity 40.0%; Pred. No. 5.5;
Matches 8; Conservative 4; Mismatches 2; Indels
 1; Indels
 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                       R92907 standard; peptide; 20 AA.
                                                                                                                                                                                                             16-MAY-1996' (first entry)
5; Conservative
                                                                                                                                                                                                                                                                                                                                            12-OCT-1995;
05-APR-1995; U04349
                                                           393 IKIVELLEKY 402
                                     6 IKVIRIVLKY 15
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WPI; 95-358582/46.
                                                                                                                                   RESULT 15
Matches
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Search completed: February 8, 2000, 04:05:40 Job time: 9357 sec

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Gaps

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Sequence 7, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 1, Appli
Patent No. 5223481
Patent No. 5223481
Patent No. 5223481
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  Sequence
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                                                                                                                                                                                                                                                                 Sequence 5, Application US/08756771

Patent No. 5817497

GENERAL INFORMATION:
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL GLUTATHIONE S-TRANSFERASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 POTTER DIVE
CITY: Palo Alto
STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; Length 222;
Pred. No. 16;
4; Mismatches 0; Indels
          US-08-343-4278-4
US-08-343-4278-7
US-08-343-4278-9
US-08-343-4278-9
US-08-343-4278-10
US-08-652-450A-4
US-08-652-450A-4
US-08-652-4278-11
US-08-652-450A-1
US-08-652-450A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARR: FESTSED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,771
FILING DATE: Herewith
                                                                                                                                               5223481-6
5223481-7
5455227-2
                                                                                                                                     223481-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 222 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: Genbank CLONE: 193710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 6; Conserv
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US-08-756-771-5
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                                                                                  February 8, 2000, 00:02:05; Search time 75.85 Seconds
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Sequence 1
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1: /cgnl_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgnl_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgnl_6/ptodata/2/iaa/PCTUS9_COMB.pep:*
4: /cgnl_6/ptodata/2/iaa/Packfilesl.pep:*
            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 1000000
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Sequence 12, Application US/08218265
Patent No. 592288
GENERAL INFORMATION
APPLICANT: Young, Richard A.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1226; 90;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPRY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/540,804

FILING DATE: 11-OCT-1995

CLASSIFICATION NUMBER: US/08/51,872

FILING DATE: 21-AUG-1995

PRIOR APPLICATION NUMBER: US 08/521,872

FILING DATE: 21-AUG-1995

FILING DATE: 25-AAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Particla

REGISTRATION NUMBER: 32,227

REFERENCAMORICATION NUMBER: 33,227

REFERENCAMORICATION NUMBER: 33,227

REFERENCAMORICATION NUMBER: 33,227

REFERENCAMORICATION NUMBER: 31,227

REFERENCAMORICATION NUMBER: 31,227

REFERENCAMORICATION NUMBER: 31,227

REFERENCAMORICATION NUMBER: 32,227

REFERENCAMORICATION NUMBER: 31,227

RELEPHONE: 617-861-6540

INFORMATION FOR SEQ ID NO: 12:

CENTRANT SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36;
Pred. No. 9
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APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                     CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: Inear
; MOLECULE TYPE: protein
US-08-540-804-12
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APPLICANT: KOLESKe, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 5919666el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
ADDRESSE:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 222;
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/756,771
FILING DATE:
ATTORNEY,AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0162
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08540804 Patent No. 5919666 GENERAL INFORMATION:
                                                                                                                                                                                                                          Sequence 5, Application US/09096571 Patent No. 5976528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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Best Local Similarity 60.0
Matches 6; Conservative
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213 VEVVRIVLKF 222
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US-09-031-485-72
Sequence 72, Application US/09031485
Sequence 72, Application US/09031485
Patent No. 5824306
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
DB 2; Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 302,
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                                                                                         1; Indels
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COMPUTER READABLE FORM:
MEDLUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429A
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                              Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                   US-08-847-429A-38
Sequence 38, Application US/08847429A
Patent No. 5827692
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
60.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
                              Query Match 50.0
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Fort Collins
STATE: Colorado
                                                                                                                                             6 IKVIRIVLKY 15
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53 IKVVELLLKY 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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Patent No. 5824306
GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DROFILARIA OF CALL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2;
Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                     CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/47,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 37,459
TELECHONE: 970/493-722
TELECHONE: 970/493-722
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-218-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-031-485-38
                                                                                                                                                                                                                                                                                                                                                     amino acid
)GY: linear
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999 YHLLIKIIR 1007
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US-09-031-485-38
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Gaps
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Patent No. 5824306
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILLARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2; Length 33; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDAER: US/08/847,429
FILING DATE: 24 APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.6%; Score 34;
                                  REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-F
TELECHANDIOLATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS:
LENGTH: 33. amino acids
TYPE: amino acids
  ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Tall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         Query Match 48.6
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 970/484-9505 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-847-429A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-031-485-23
                                                                                                                                                                                                                                                                                                                                                                                                                                              6 IKVIRIVLKY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::::|||
|5 ||KIVELLLKY 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 80525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DRESTHEREOF
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDIROFILARIA
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 33;
                                                                                                                                                                       COMPUTE READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION NUMBER: US/08/847,429A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34;
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 72, Application US/08847429A
Patent No. 5827692
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.6%;
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-031-485-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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|5 IKIVELLLKY 24
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                                                                                                                                  COUNTRY:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROFEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 1745; Pred. No. 2.9e+02; 4; Mismatches 1; Indels
                                                                                                                                               COUPUTE 803.2.

COUPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: 37,459
REGISCOMMULCATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Fort Collins
STATE: Colorado
COUWTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
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FILING DATE: 24-APR-1997
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US-08-847-429A-33
; Sequence 33, Application US/08847429A
; Patent No. 5827692
                                        STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 33 SEQUENCE CHARACTERISTICS: LENGTH: 1745 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 48.6
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-031-485-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 IKIVELLIKY 402
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                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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US-08-847-4294-23

US-08-847-429A-23

Sequence 23, Application US/08847429A

Sequence 23, Application US/08847429A

Setent No. 5827692

GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/09031485
Patent No. 5824306
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429A
FILING DATE: 24-APR-1997
ATTORNEY.ACTION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
Best Local Similarity 50.0%; pred. No. 49; Matches 5; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 49;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELEPHONE: 970/483-722
TELEPHONE: 970/484-9505
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 48.6
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-847-429A-23
                                                               6 IKVIRIVLKY 15
                                                                                                            54 IKIVELLLKY 63
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||54 || IKIVELLLKY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80525
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Gaps

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TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                       California
: USA
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PCT-US94-12985-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: KRENSKY, ALAN M.
APPLICANT: RAHAM, PETER
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ATTIVITY REGULATION BY CLASS I MHC PEPTIDES
TITLE OF INVENTION: 43
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9
                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 1745;
Pred. No. 2.9e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.1%; Score 33; DB 1; Length 20; 40.0%; Pred. No. 4.7; tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLIA.
STATE: DC
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,851
FILING DATE: 05-APR-1994
FILING ATON: A24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
RADRESSEE: MORNISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
CITY: WASHINGTON
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
INFORMATION FOR SEQ ID NO: 33:
LENGTH: 1745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/08222851
Patent No. 5723128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTOREX AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 28600
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 897-1500
TELEFAX: (202) 897-1500
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 YRLLIKV-----IRIVLKY 15
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.v.
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Best Local Similarity 40.03
Matches 8; Conservative
                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-847-429A-33
                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  393 IKIVELLLKY 402
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PETUTION 14

PETUTION 1294-1295-1

CORRESSOURCE ADDALESS:

CORRESSOURCE PETRIC MEMBERS 1200-1

PETUTION 1294-1295-1

CORPUTER PETATORIC CORPUTER 1200-1

PETUTION 1294-1295-1

CORPUTER PETATORIC CORPUTER 1200-1

PETUTION 1294-1295-1

CORPUTER PETATORIC CORPUTER 1200-1

PETATORIC CORPUTER 1294-1

PETATORIC CORPUTER
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us-08-653-294-21.rai

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COUNTRY: | USA

2 IP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12985
FILING DATE: 10-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/150,493
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND BETTAM I
REGISTRATION NUMBER: 20,015
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 20,015
TELEFAX: 910 277299
INFORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-12985-4
```

Search completed: February 8, 2000, 01:01:46 Job time: 3581 sec

6; Gaps

Query Match

47.1%; Score 33; DB 3; Length 20;
Best Local Similarity 40.0%; Pred. No. 4.7;
Matches 8; Conservative 4; Mismatches 2; Indels

2 YRLLIKW-----IRIVLKY 15 

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 11:54:34; Search time 111.22 Seconds (without alignments) 6.362 Million cell updates/sec Run on:

US-08-653-294-21 70 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 AYRLLIKVIRIVLKY 15 Scoring table: Sequence:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

pirl:\* pir2:\* pir3:\* PIR\_62:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### CITAMADIEC

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T15344	S48405 B71612	D72118 JC2565	S59101 H71343	T15213 H71689	S74051 S56260	G71697 A72079
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1867	3973	185	326 359	369 376	395 448	651 111
50.0	20.0	6.8	48.6	48.6 48.6	48.6 48.6	48.6
325	 	3 8 8 4 4 4	34	34 34	34 34	34 33
31	ლ ო ო ლ 4 ო	3.6	. 8 6 8 8 8 8	40	4 4 3 2	44 45

### ALIGNMENTS

RESULT 1 S67203 S67203 N.Alternate names: hypothetical protein 05635 C.Species: Saccharomyces cerevisiae) N.Alternate names: hypothetical protein 05635 C.Species: Saccharomyces cerevisiae C.Species: S67203 R.Cziepluch, C.; Jauniaux, J.C.; Kordes, E.; Poirey, R.; Pujol, A.; Tobiasch, E. Sabnitted to the Protein Sequence Database, July 1996 A.Residues: 1567203 A.Residues: 1567203 A.Residues: 146 call A.Specimental source: strain 5288C C.Generics: Scolsource: strain 5288C A.Gross-references: SGD:S0005825; MIPS:YOR299w A.Gr	Best Local Similarity 45.0%; Pred. No. 17; Matches 9; Conservative 5; Mismatches 1; Indels 5; Gaps 1;
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1 AYRLLIKVIRI -----VLKY 15 δλ g

RESULT 2
F64238
hypotherical protein MG349 - Mycoplasma genitalium (SGC3)
C;Species: Mycoplasma gentalium
C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 10-Oct-1997
C;Accession: F64238
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.
M; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346
A;Reference number: A64200
A;Residues: 1-404 <TIGR>
A;Residues: 1-404 <TIGR>
A;Residues: 1-404 <TIGR>
A;Cross-references: GB:U39719; GB:L43967; NID:g1046055; PID:g1046056; TIGR:MG349
A;Genetics:
A;Genetics:
A;Genetics:

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A Status: preliminary
A; Molecule type: DNA
Residues: 1.379 «KAW»
A; Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49446.1; PID:e151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-142 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50677.1; PID:e151
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PAB2010 - Pyrococcus abyssi (strain Orsay)
hypothetical protein PAB2010 - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: 675170
C;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Pyrococcus abyssi
Cibate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
Ciaccession: G75029
R:anonymous, Genoscope
submitted to the EmBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A75001
C; Accession: C3227
R; Wang, Y.; Moore, M.; Levinson, H.S.; Silver, S.; Walsh, C.; Mahler, I.
J. Bacteriol. 171, 83-92, 1989
A.Title: Nucleotide sequence of a chromosomal mercury resistance determinant from A, Reference number: A32227; MUID:89123092
A, Accession: C32227
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-98 < WAN>
A, Residues: 1-98 < WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB:M22708; NID:g143188; PID:g1129095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 2;
Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 26;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%;
60.0%;
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.9
Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: G75029
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: PAB1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: PAB2010
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Matches
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16254
R;Wu, X.
B;Wu, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the peroxisomal acyl CoA oxidase from the alkan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: POX4
C.Superfamily: acyl-CoA oxidase
C.Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
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Righli, D.E.; Boulay, R.; Rogers, D.
Righli, D.E.; Boulay, R.; Rogers, D.
Rucciec Acids Res. 16, 365-366, 1988
A;Title: Complete nucleotide sequence of the peroxisomal acyl CoA oxidase france number: A29441; MUD:88124223
A;Accession: A29441; MUD:88124223
A;Rocession: A29441
A;Koessidues: 1-709 cHIL>
A;Experimental source: ATCC 20184
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 3 (mer operon) - Bacillus sp.
C;Species: Bacillus sp.
C;Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 09-Sep-1997
                                                                                                                                                Gaps
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                                                              Length 404;
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Pred. No. 31;
                                     DB 18;
                                                              Score 38; DB Pred. No. 18; 3; Mismatches
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ilarity 57.1%;
Conservative
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Matches 7; Conservative
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322 YQLLDKVINLVLDF 335
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H Sclence 282, 1136-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743
A;Reference number: A71601
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: DAA
A;Residues: 1-186 < GAR>
A;Residues: 1-186 < GAR>
A;Cross-references: GB:AE001431; GB:AE001362; NID:g3845327; PID:g3845329; TIGR:PFB098
A;Cross-references: Clone 3D7
C;Genetics: A;Genetics: A;Gene
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probable TRNA methylase - Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Nov-1998
C;Accssion: E71464
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia theference number: A71570; MUID:99000809
A;Accession: E71464
A;Molecule type: DNA
A;Residues: 1-187 carn>
A;Coss.references: GB:AE001356; GB:AE001273; NID:93329299; PID:93329300
A;Coss.references: GB:AE001356; GB:AE001273; NID:93329299; PID:93329300
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;G
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A; Residues: 1-222 <211NA
A; Cross-references: GB:LO647; NID:g193709; PIDN:AAA37754.1; PID:g193710
A; Cross-references: GB:LO647; NID:g193709; PIDN:AAA37754.1; PID:g193710
R; Medh, R.D.; Saxena, M.; Singhal, S.S.; Ahmad, H.; Awasthi, Y.C.
Biochem, J. 278, 793-799; 1991
A; Title: Characterization of a novel glutathione S-transferase isoenzyme from mouse 1
A; Reference number: S17542; MUID:91378941
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Pred. No. 21;
3; Mismatches
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3; Mismatches
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145 AFILLIFIIHIVARY 159
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hypothetical protein aq_293 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Accession: 670326
C:Accession: 670326
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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                                                                                                                                                                                                                                                                                                                                                                             Alternate names: hypothetical protein XM9959.19
:Species: Saccharomyces cerevisiae
:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Nov-1997
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A;Cross-references: GB:AE000682; NID:g2982979; PID:g2982988; GB:AE000657
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:249939; NID:g887599; PID:g887618; MIPS:YMR237W A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                              probable membrane protein YMR237w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein YM9959.19
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C;Superfamily: Aquifex aeolicus hypothetical protein aq_293
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C;Keywords: transmembrane protein
F;666-682/Domain: transmembrane #status predicted <TMM>
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15;
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40.0%; Pred. No. 59;
live 6; Mismatches
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submitted to the EMBL Data Library, June 1995
R*Eference number: S57587
A;Accession: S57604
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Best Local Similarity
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A; Residues: 1-724 <SKE>
                                                                                         1 AYRLLIKVI 9
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A; Cross-references: EMBL:228222; NID:9486398; PIDN:CAA82067.1; PID:9486399; MIPS:YKLZ A; Experimental source: strain S288C
R; Alexandraki, D.; Teremia, M.
R; Alexandraki, D.; Teremia, M.
Sast 10(Suppl.A), S81-S91, 1994
A; Tittle: Sequencing of a 13.2 kb segment next to the left telomere of yeast chromosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluste C;Keywords: DNA binding; nucleus; zinc finger C;Keywords: DNA binding; nucleus; zinc finger E;19-57/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F;24-52/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                       probable finger protein YKL222c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein F705
C;Species: Saccharomyces cerevisiae
C;Dedte: 03.May.1994 #sequence_revision
C;Accession: S38066; S44510; S43548
R;Alternate, D:, Horatits, O:, Tzermia, M.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S38065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Status: translation not shown
A.Molecule type: DNA
A.Residues: 1-705 <AL2>
A.Cross-references: EMBL:X75950; NID:g473124; PIDN:CAA53551.1; PID:g473127
A.Experimental source: strain S288C
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 705;
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71;
       Pred. No. 51;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: $44508; MUID:94378726
A; Accession: $44510
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           50.08;
       Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                1 AYRLLIKVIRIVLK 14
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541 AFRALIQIYTIFLOY
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Best Local Similarity
Matches 7; Conserva
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A; Residues: 1-705 <ALE>
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N:Alternate names: hypothetical protein P1745
C:Species: Saccharomyces cerevisiae
C:Species: Saccharomyces cerevisiae
C:Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 06-Feb-1998
C:Accession: S65238
R:Rieger, M.: Mueller-Auer, S.; Schaefer, M.
Submitted to the Protein Sequence Database, May 1996
A:Reference number: S65202
A:Accession: S65238
A:Accession: S6523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
B69260
hypothetical protein AF0082 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998
C;Accession: B69260
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Frielschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S. Simith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: B69260
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-282 <kLE>
A;Cross-references: GB:AE001100; GB:AE000782; NID:92689423; PID:92650567; TIGR:AF0082
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25;
A;Residues: 106-114,'P',116-120 <MED>
A;Experimental source: lung
A;Accession: 317681
A;Molecule type: protein
A;Residues: 107-113;'G',168-178,'GE',181-184,'X',186-186 <MEW>
A;Experimental source: liver
C;Superfamily: glutathione transferase
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 282;
31;
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Pred. No. 31;
4; Mismatches
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Best Local Similarity 53.8%;
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213 VEVVRIVLKF 222
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 8, 2000, 01:00:00; Search time 68.63 Seconds
(without alignments)
6.527 Million cell updates/sec
Title: US-08-653-294-21
Perfect score: 70
Sequence: 1 AYRLIKVIRIVLKY 15

Perfect score: 70
Sequence: 1 AYRLLIKVIRIVLKY 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 segs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	ě	P05335 candida mal	P55642 rhizobium s	Q05029 saccharomyc	P24472 mus musculu	Sac															P43589 saccharomyc	-	_			P25298 saccharomyc	human cy	Q12572 candida alb	Q60610 mus musculu	33	7	059432 pyrococcus	9	
SUMMAKIES		ID	Y349_MYCGE	CAO4_CANMA	Y4RI_RHISN	YM76_YEAST	GTA4_MOUSE	YKW2_YEAST	SRB8_YEAST	RRPL_SENDE	RRPL_SEND5	RRPL_SENDF	RRPL_SENDZ	ATPB_MYCLE	ATPB_MYCTU	CAO3_CANTR	CAO2_CANTR	TSC2_HUMAN	TSC2_RAT	YIM9_YEAST	UREF_ACTPL	NU1M_CHOCR	YFH5_YEAST	YM17_PARTE	YC8A_METJA	MBI3_YEAST	CAO1_CANTR	RN14_YEAST	VCAP_HCMVA	LYS2_CANAL	TIAM_MOUSE	MOT1_YEAST	YAMB_SCHPO	RS8_PYRHO	RS8_SULAC	
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RL5_THEMA   P38517 thermotoga   YIGP_ECOLI   P27852 escherichia   P27852 escherichia   CGIC_MOUSE   P55168 gallus gallus GGIC_MOUSE   O62447 mus musculu   CGIC_MOUSE   O62447 mus musculu   CGIC_ANT   P24863 home sapien   SSAK_SALTY   O67260 aquifex aeo   VP61_MRDV   P38571 home sapien   LICH_HUMAN   P38571 home sapien   AFC3_ARATH   P51568 arabidopsis   ALIGNMENTS   P51568 arabidopsis	D; PRT; 404 AA. Created) Last sequence update) Gast annotation update)	MG349.  Mycoplasma genitalium.   copyright ute of Bi cs Instit thtions it is not se agreem se@isb-si	<pre>%; Score 38; DB 1; Length 404; %; Pred: No. 9.8; 3; Mismatches 3; Indels 0; Gaps 0;</pre>	
12222222222222222222222222222222222222	STANDARD; (Rel. 33, Creat (Rel. 33, Last (Rel. 34, Last	11um. tes; Bacill Mycoplasma / G-37; YNE J.D., W BULT C.J., W ERBACK T.R., ERTH B.A., TITH H.O., H COMPLEMENT	Iny is Instit Formati Instit Stateme Istance Istance Istance In.	54.3%; 57.1%; rative 15
444444444 60000000000000000000000000000		sma genitali am frimicute smataceae; M E FROM N.A. 596026346. C.M., GOGAYN MANN J.L., WEI D.T., UTTERB D.T., UTTERB N.S.N., SMIT N.S.N., SMIT N.S.N., SMIT N.S.N., SMIT N.S.N., SMIT N.S.N., SMIT N.S.N., SMIT N.S.N., SMIT	the Swiss Interest of the Swiss Interest of the Swiss Interest of the Swiss of the	Similarity 54. Similarity 57. 8; Conservative LIKVIRIVLKY 15
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                                                                                          HILL D.E., BOULAY R., ROGERS D.;
"Complete nucleotide sequence of the peroxisomal acyl CoA oxidase
from the alkane-utilizing yeast Candida maltosa.";
Nucleic Acids Res. 16:365-366(1988).
-:- CARALYTIC ACTIVITY: ACYL-COA + O(2) = TRANS-2,3-DEHYDROACYL-COA +
H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH
FROM 8 TO 18).
                                                                                                                                                                                     -!- COFACTOR: FAD.
-!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoproteln; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.
 Candida maltosa (Yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
D5E344D2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 44.0 KD PROTEIN Y4RI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       708 AA; 78242 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.38;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; X06721; CAA29901.1; -.
                                                                                                                                                                                                                            -! - SUBUNIT: HOMOOCTAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 SYRMLARVSTIALRY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AYRLLIKVIRIVLKY 15
                          Candidaceae, Candida.
                                                                                                                                                                                                                                                                                                                                                                                       A29441; OXCKPM
                                                                STRAIN=ATCC 20184;
MEDLINE; 88124223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 97305956.
                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y4RI_RHISN
P55642;
                                                                                                                                                                                                                 SYSTEM.
Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
Y4RI_RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / AB972;
SKEITON J., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
--: SIMILARITY: TO YEAST CSD3/CHS6 AND YEAST YKR027W.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
11-DEC-1999 (Rel. 39, Last annotation update)
GLUTATHIONE S-TRANSFERSE 5.7 (EC 2.5.1.18) (GST 5.7) (GST CLASS-ADPIA) (GST A4-4) (GSTA4-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     υ
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 82.0 KD PROTEIN IN RNA1-RNII INTERGENIC REGION.
                                                                                                                                                               Length 390;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              il protein.
724 AA; 82048 MW; 6CE22AD2 CRC32;
                                                                                         FOAF4E11 CRC32
                                                                                                                                                               Score 37; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 36.5; E
40.0%; Pred. No. 33;
tive 6; Mismatches
                                                                                                                                                                                                             Mismatches
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetaceae; Saccharomyces.
                                         EMBL; AE000094; AAB91834.1; -. Hypothetical protein; Plasmid. SEQUENCE 390 AA; 43978 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 AYKLLTEIVQITGWEQLLKY 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AYRLLIKVIRI ----VLKY 15
                                                                                                                                                               52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z49939; CAA90208.1; -.
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                    157 YRELLKIARTTLSY 170
                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
8; Conserva
                                                                                                                                    YMR237W OR YM9959.19
                                                                                                                                                                                                                                                        2 YRLLIKVIRIVLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 73
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P24472;
                                                                                                                                                                                                                                                                                                                                                                                                                   YM76_YEAST
Q05029;
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213 VEVVRIVLKF 222
    IKVIRIVLKY 15
                                                                                                                                                            YKW2_YEAST
P35995;
                                                                                                                RESULT 6
YKW2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCLIBERT ACCOUNTIES BELOKUED.

MISCELLANEOUS: ON THE BASIS OF IMMUNOLOGICAL AND KINETICS DATA,

MISCELLANEOUS: ON THE BASIS OF IMMUNOLOGICAL AND KINETICS DATA,

GST 5.7 IS DISTINCT FROM ALPHA, MU AND PI CLASSES OF GTS. HOWEVER

IT HAS BEEN POSTULATED THAT THIS PROTEIN MAY BE PART OF A DISTINCT
SUBGROUP WITHIN THIS ALPHA CLASS.

MISCELLANEOUS: THE VARIATIONS WERE FOUND FROM AA SEQUENCING AND

IMPLY THERE ARE MULTIPLE FORMS OF THIS PROTEIN. THESE VARIATIONS

ARE LIKELY TO BE SEX-LINKED AND TISSUE SPECIFIC.

SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LUNG;
MEDLINE; 98158566.
KRENGEL U., SCHROTER K.H., HOIER H., ARKEMA A., KALK K.H., ZIMNIAK P.,
DIJKSTRA B.W.;
                                                                                                                                                                                                       MEDH R.D., SAXENA M., SINGHAL S.S., AHMAD H., AWASTHI Y.C.; "Characterization of a novel glutathione S-transferase isoenzyme from mouse lung and liver having structural similarity to rat glutathione
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of a murine alpha-class glutathione S-transferase involved in cellular defense against oxidative stress."; FEBS Lett. 422:285-290(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 99438340.
XIAO B., SINGH S.P., NANDURI B., AWASTHI Y.C., ZIMNIAK P., JI X.;
"Crystal structure of a murine glutathione S-transferase in complex with a glutathione conjugate of 4-hydroxynon-2-enal in one subunit and glutathione in the other: evidence of signaling across the dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 38:11887-11894(1999).

-!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOCENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
-!- CATALYTIC ACTIVITY: RX + GLUTATHIONE = HX + R-S-GLUTATHIONE.
-!- SUBBUNT: HOMODIMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
MEDLINE; 93050245.
ZIMNIAK P., ECKLES M.A., SAXENA M., AWASTHI Y.C.;
As subgroup of class alpha glutathione S-transferases. Cloning of CDNA for mouse lung glutathione S-transferase GST 5.7.";
FEBS Lett. 313:173-176(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Multigene family; Polymorphism; 3D-structure. VARIANT 115 115 {\rm K} -> {\rm P}_{\rm c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%; Score 36; DB 1; Length 222; 60.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PL -> GE.
7158E30C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ν γ.
γ γ.
β.
                                                                                                                                                       STRAIN-CD-1; TISSUE-LUNG, AND LIVER; MEDLINE; 91,378941.
                                                                                                                                         SEQUENCE OF 106-120 AND 167-184
                                                                                                                                                                                                                                                                                                     Biochem. J. 278:793-799(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L06047; AAA37754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S27234; S27234.
PDB: 1GUK: 08-APR-98.
PDB: 1B48: 29-SEP-99.
MGD: MGI:95857; GSTA.
PFAM: PF00043; GST. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                  S-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interface.
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Gaps

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0; Indels

4; Mismatches

Conservative

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                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 30, Last annotation update)
PUTATIVE 82.2 RD TRANSCRIPTIONAL REGULATORY PROTEIN IN FRE2 5'REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALEXANDRAKI D., TZERMIA M.;
"Sequencing of a 13.2 kb segment next to the left telomere of yeast chromosome XI revealed five open reading frames and recent recombination events with the right arms of chromosomes III and V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
STRB OR YCR081W OR YCR81W.
Sacharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Sacharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast 10:S11-S91(1994).

-i - SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

-i - SUMILARIY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
705 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%; Score 36; 46.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0463; ZN2_CY6_FUNGAL_1; 1.
PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X75950; CAA53551.1; -. EMBL; Z28222; CAA82067.1; -. PIR; S38066; S38066. PIR; S43548; S43548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.4
Best Local Similarity 46.7
Matches 7; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| ||:: | |:|
541 AFRALIQIYTIFLQY 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94378726
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RRPL_SEND5
P27566;
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                                                                                                                                                                                                                                                                                                                                              RESULT 9
RRPL_SEND5
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"Sequence of the Sendai virus L gene: open reading frames upstream of the main coding region suggest that the gene may be polycistronic."; virology 154:31-40(1986).

-!- FUNCTION IN MENA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF NEWLY SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA EDITING OF THE P GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
-!- MISCELLANEOUS: THEY ARE FOUND IN CATALYTIC AMOUNTS (APPROXIMATELY 2) TO 30 COPIES PER SENDAI VIRLON) IN VIRAL NUCLEOCAPSIDS.
-!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
         MEDLINE; 95293223.
HENGARTNER C.J., THOMPSON C.M., ZHANG J., CHAO D.M., LIAO S.M.,
KOLESKE A.J., OKAMURA S., YOUNG R.A.;
ASSOCIATION Of an activator with an RNA polymerase II holoenzyme.";
Genes Dev. 9:897-910(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1427;
81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sendai virus (strain Enders).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
                                                                                                                                  Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1427 AA; 166859 MW; 6B732E51 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2048 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred: No.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X59720; CAA42268.1; -. PIR; S19496. TRANSFAC; T02152; -. SGD; L0003007; SRB8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 51.4%;
Similarity 77.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||||:||
1200 YHLLIKIIR 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 YRLLIKVIR 10
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SEQUENCE 1427
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P06829;
                                                                                                       REVISIONS
                                                                                                                       GROMADKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sendai virus.";
Virology 184:227-234(1991).
-!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
-!- FUNCTION IN MENA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA EDITING OF THE P
GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
-!- MISCELLAMEDUS: THEY ARE FOUND IN CAPALYTIC AMOUNTS (APPROXIMATELY
20 TO 30 COPIES PER SEMIAI VIRION) IN VIRAL NUCLEOCAFSIDS.
-!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE: 90266480
MIDDLENE: 90266480
MIDDLENE: Y. TASHIRO M., THAI T., OH J., SEYMOUR J., PRITZER E.,
KLENK H.D., ROTT R., SETO J.T.;
and L. proteins of two malyses of the genes encoding the HN, M, NP,
and L. proteins of two host range mutants of Sendal virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91335752.
TASHIRO M., JAMES I., KARRI S., WAHN K., TOBITA K., KLENK H.D.,
ROTI R., SETO J.T.;
"Pneumotropic revertants derived from a pantropic mutant, Fl-R, of
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                  Length 2048;
                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sendai virus (strain Z / host mutants).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 PIR; A24293; ZLNZSE.
PFRAM; PFC0946; Paramyx_RNA_pol; 1.
Transferose: RNA-directed RNA polymerase.
SEQUENCE 2048 AA; 231623 MW; 7FA48C13 CRC32;
                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1; I
Pred. No. 1.2e+02;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MUTANT F1-R / T-5 REVERTANT;
                                                                                                                                                                                                                                                                                                                                    53.8%;
                                                                                                                                                       EMBL; M14887; AAA69579.1;
EMBL; D00053; BAA00036.1;
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003 YRFLTKEIKILMK 2015
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Best Local Similarity
Matches 7; Conserv
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CC DR DR DR DR SG FT

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-!- SUBUNIT.
- SUBUNIT.
- SUBUNIT.
- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BEATA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SMITH D.R., ROBISON K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.4%; Score 36; DB 1; Length 2228; larity 53.8%; Pred. No. 1.3e+02; Conservative 3; Mismatches 3; Indels
                                                                                                                      Sendai virus (strain 2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A04120; ZLNZSV.
PFAM; PF00946; Paramyx RNA_pol; 1.
Transferase; RNA-directed RNA polymerase.
eronience 2228 AA; 252864 MW; DD9798FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
101-NOV-1995 (Rel. 32, Last annotation update)
ATP SYNTHASE BETA CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 AA.
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2183 YRFLTKEIKILMK 2195
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 86148492.
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ID ATPB_MYCLE
AC P45823;
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E03E1CF1 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
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0
                                                                                                                                                                         Score 36; DB 1; Length 2228;
Pred. No. 1.3e+02;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sendai virus (strain Fushimi).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
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PFAM; PFOG946; Paramyx_RNA_pol; 1.
Transferace; RNA-directed RNA polymerase.
SEQUENCE 2228 AA; 252770 WW; 7F139FB8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                            2228 AA.
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                              EMBL, M30203; AAB06289.1; -- MBL, M6046; AAB06299.1; -- PFAM; PF00946; Paramyx_RNA_pol; 1.
Transferase; RNA-directed RNA polymerase.
                                                                                                                      252748 MW;
               EMBL; M30204; AAB06201.1; -.
                                                                                                                                                                           51.4%;
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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2228 AA;
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                                                                                                                                                                                                                                                                                                                                                                          RRPL_SENDF
Q06996;
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RRPL_SENDZ
ID RRPL_SENDZ
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SEQUENCE
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RESULT 10 RRPL\_SENDF

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SEQUENCE FROM N.A.
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P11355;
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SEQUENCE
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CAO2_CANTR
ID CAO2_CI
AC P06598
DT 01-JAN
DT 01-NOV
DE ACYL-CC
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CAO3_CANTR
  CARRES ES
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COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TERALA F., DANJES K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DANJES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E., TAXLOR K., WHITEHEAD S., BARRELL BG.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT.
SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 485;
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42;
                                                                                                                                                                                                                                                                                                                             PFAM; PF00006; ATP-synt_ab: 1.

PFAM; PF00306; ATP-synt_ab_C: 1.

Hydrolase; ATP synthesis; CF(1); ATP-binding; Hydrogen ion transport.

Hydrogen in 170 170 ATP (POTENTIAL); SEQUENCE 485 AA; 53034 MW; 07216783 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ATPD SYNTHASE BETA CHAIN (EC 3.6.1.34).
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Pred. No.
                                                                                                                                                                                                                                                                                                               PROSITE; PS00152; ATPASE_ALPHA_BETA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         170 177 A:
485 AA; 53034 MW;
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Best Local Similarity 50.0°
"... 7; Conservative
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376 YRVAQEVIRILQRY 389
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Q10593;
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SMALL G.M., LAZAROW P.B.;
SMALL G.M., LAZAROW P.B.;
SIMOLL G.M., LAZAROW P.B.;
SIMOLL G.M., LAZAROW P.B.;
SMALL G.M., LAZAROW P.B.;
Dimonstrate of Candida tropicalis.";
J. Cell Biol. 105:247-250(1987).
-:- CATALYTIC ACTIVITY: ACYL-COA + O(2) - TRANS-2,3-DEHYDROACYL-COA + H(2)O(2).

H(2)O(2). (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH

    -!- COFACTOR: FAD.
    -!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: PEROXISOMAL.
PIR; A28584; OXCKAX.
Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
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P06598;
01-7AN-1988 (Rel. 06, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE II (EC 1.3.3.6) (ACYL-COA OXIDASE) (PXP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungl; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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01-ZUL-1989 (Rel. 11, Last sequence update)
01-XUV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE POX4-2 (EC 1.3.3.6) (ACYL-COA OXIDASE)
                                                                                                                                                                                                                                                                           Score 35; DB 1; Length 486;
Pred. No. 42;
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A8001B2F CRC32;
EMBL; Z73419; CAA97743.1; -.
HSSP; P07677; 1SKY.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
PFAM; PF00006; ATP-synt_ab; 1.
Hydrolase; ATP synthes1s; CF(1); ATP-binding;
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Pred. No. 43;
5; Mismatches
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                                                                                                                                                                                                     486 AA; 53094 MW;
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Best Local Similarity 40.0
Government of Conservative
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                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                  Hydrogen ion transport.
NP_BIND 171 178
SEQUENCE 486 AA; 5309
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libersib.ch).
                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 87280361.

SMALL G.M., LAZAROW P.B.;

SMALL G.M., LAZAROW P.B.;

"Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of Candida tropicalis.";

J. Cell Biol. 105:247-250(1987).

-!- CATALYTIC ACTIVITY: ACYL-COA + O(2) = TRANS-2,3-DEHYDROACYL-COA + H(2)0(2) (ACYS ON COA DERIVATIVES OF FATIY ACIDS WITH CHAIN LENGTH FROM 8 TO 18).

-!- COPACTOR: FAD.

-!- COPACTOR: FAD.
                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ATCC 20336 / PK233;
MEDLINE; 86149279.
OKAZAKI K., TAKECHI T., KAMBARA N., FUKUI S., KUBOTA I., KAMIRYO T.;
"Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida
tropicalis: primary structures deduced from genomic DNA sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:1232-1236(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 20336 / PK233;
MEDINE; 87248070.
MURRAY W.W., RACHUBINSKI R.A.;
"The primary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast Candida tropicalis pK233.";
Gene 51:119-128(1987).
AOX OR POX-4.
Candida tropicalis (Yeast).
Eukaryota, Fungi, Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
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REF. 2 AND 3).
REF. 2).
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REF. 2 AND 3).
CRC32;
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G -> A (IN R
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Q -> E (IN R
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P -> A (IN F
N -> K (IN F
FRAMESHIFT
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EMBL; M12160; AAA34362.1; -.
EMBL; Y00623; CAA68660.1; -.
EMBL; Y00623; CAA68661.1; ALT_INIT.
EMBL; Y00623; CAA68662.1; ALT_INIT.
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A29047; OXCKX.
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697
708 AA;
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306 SYRMLARMSTIALRY 320
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8, 2000, 01:25:56 Search completed: February Job time: 1556 sec

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Score 35; DB 1; Length 708; Pred. No. 61; 5; Mismatches 4; Indels

50.0%;

Query Match 50.0 Best Local Similarity 40.0 Matches 6; Conservative

1 AYRLLIKVIRIVLKY 15

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Q89074 variola vir Q17265 brugia paha Q6893 chlorobium Q94044 aeropyrum p Q76770 dictyosteli

O80962 arabidopsis Q9wuf6 mus musculu Q23891 dictyostel1 Q9xpi9 dictyostel1

042180 fugu rubrip 075275 homo sapten 017344 caenorhabdi 017487 caenorhabdi 061037 mus musculu 021488 caenorhabdi 097275 plasmodlum 017486 caenorhabdi 055528 sendal viru 055530 sendal viru 056204 plasmodlum 056204 plasmodlum 096204 plasmodlum 096204 caenorhabdi 096204 caenorhabdi 096204 caenorhabdi 096204 caenorhabdi 096204 caenorhabdi 096204 caenorhabdi

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MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., ANDERSON R., FOLTON J.,

CRANTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDIER A., GREEN P., HARKINS T., HILLIER M., JOHNSTON L.,

A JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LAITERILLE P.,

LIGHTRING J., LLOYD C., MCMORRAY A., MORTIMORE B., O'CALLAGHAN M.,

A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

A MALDON N., SMITH A., SONNHANMER E., STADEN K., SULSTON J.,

A HIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

A WATEN A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

ELEGARS.
                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 5; Length 2810;
Pred. No. 1.6e+02;
7; Mismatches 2; Indels
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Last annotation update)
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                                                                  023891
09XF19
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075275
017344
017487
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017488
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09WUF6
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EMBL; 266563; CAA91469.1; -

PFAM; PF00612; IQ; 2.

PFAM; PF00063; myosin_head; 4.

PFAM; PF00784; MYFH4; 2.

SEQUENCE 2810 AA; 323526 MW;
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Best Local Similarity 35.7%;
Matches 5; Conservative
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01-NOV-1998 (TEBMBLEEL. 0)
01-MAY-1999 (TEBMBLEEL. 1
HUM-4 PROTEIN.
                             PRELIMINARY;
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Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
020456
020456;
RESULT
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Q84185 human parai
Q20487 caenorhabdi
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Q08754 saccharomur
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caenorhabdi
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Q21436
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O66643
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O6096
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                225878 seqs, 69334122 residues
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Q20487
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Gapop 10.0 , Gapext 0.5
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U40941; AAA81709.1; -. SEQUENCE 771 AA; 87310 MW; 5AE2EE3F CRC32;
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LAYRELLLE P.,
LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN K., WALTESTON J.,
THIERRY-MIEG J., THOMAS K., VADULIN M., VAUGHAN K., WALTESTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CZIEPLUCH C., JAUNIAUX J.C., KORDES E., POIREY R., PUJOL A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOBIASCH E.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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1-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL 08, Last annotation update)
CODED FOR BY C. ELEGANS CDNA CEESB82F.
                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; 275207; CAA99528.1; -.
SEQUENCE 746 AA; 84829 WW; 01352AC2 CRC32;
                                                                                                                                                                                                                                               746 AA
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                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                              1102 FRLSVEIFKLILKY 1115
                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
       2 YRLLIKVIRIVLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   ORF YOR299W
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Q08754
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Q20026
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRAN-BROWN.
SPIRAN-BROWN.
MEDLINE; 89123092.
WANG Y., MOORE M., LEVINSON H.S., SILVER S., WALSH C., MAHLER I.;
WANG Y., MOORE M., LEVINSON H.S., SILVER S., WALSH C., MAHLER I.;
"Nucleotide sequence of a chromosomal mercury resistance determinant
"Irom a Bacillus sp. with broad-spectrum mercury resistance.";
J. Bacteriol. 171:88-92(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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BUBDLINE; 9819571.
BOGDANOVA E.S., BASS I.A., MINHAKHIN L.S., PETROVA M.A., MINDLIN S. VOLODIN A.A., KALYAEVA E.S., TIEDGE G.M., HOBMAN J.L., BROWN N.L., NIKIFIROV V.G.;
"HOTIZONIAL SPREAD OF MET OPERONS among gram-positive bacteria in natural environments."
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01-NOV-1996 (TIEMBLREL 01, Last sequence update)
01-NOV-1999 (TIEMBLREL 12, Last annotation update)
HYPOTHETICAL 10.9 KD PROTEIN.
Bacillus Sp., Bacillus megaterium, and Exiguobacterium sp.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98;
Score 38; DB 5; Length 771
Pred. No. 1.1e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF138877; AAA83975.1; -.
EMBL; X09907; CAA71043.1; -.
EMBL; X99457; CAA67820.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 98 AA; 10900 MW; F1D67BC1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MK64-1;
MINAKHIN L.S.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2;
Pred. No. 22;
2; Mismatches
                                                                                                                                                                                                                                                                       98 AA
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 144:609-620(1998)
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58.3%;
54.38;
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Best Local Similarity 58...
7; Conservative
  Query Match 54.3
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                            ::|:|::|
578 IVKIIRVLLEY 588
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                                                                                                5 LIKVIRIVLKY 15
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Gaps

; 0

Indels

Length 100;

Q21436 Q21436;

2

RESULT 021436

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STRAIN-VF5;
MEDLINE; 98196666.
DECKERT G, WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G, WARREN F.V., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 98221163.
ADVANI R.J., BAE H.R., BOCK J.B., CHAO D.S., DOUNG Y.C., PREKERIS R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX SERHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., I FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; Submitted (JUL. 1997) to the EMBL/GenBank/DDBJ databases. EMBL, AE006682; AAC06601.1; --
Hypothetical protein and A., 15393 MW; E36D7DD3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 15.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                             ;
                                                                                     100 AA; 11126 MW; 381D4576 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Aquificales; Aquificaceae; Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AA.
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                                                                                                                                                                             DB
34;
                                                                                                                                                                                                                                       Mismatches
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51.4%; Score 36; DB

Best Local Similarity · 28.6%; Pred. No. 44;

Matches 4; Conservative 8; Mismatches
                                                                                                                                                                             Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                          51.4%;
llarity 50.0%;
Conservative 3
EMBL; Y09024; CAA70222.1; -. EMBL; Y09027; CAA70244.1; -.
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12,
13,
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01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                              2 YRLLIKVIRIVL 13
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46 YRLLFSIVTIL 57
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                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquifex aeolicus
                                                         Plasmid.
SEQUENCE
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ID 06
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BEGDBANOVA E.S., BASS I.A., MINHAKHIN L.S., PETROVA M.A., MINDLIN S.Z., VOLDDIN A. WLYAEVA E.S., TIEDGE G.M., HOBMAN J.L., BROWN N.L., NIKIFIROV V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., WILSON R., AINSCOUGH R., CONBELL M., COPSEY T., COOPER J., COULSON A. CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., CARNER A., GREEN P. M., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSON J., PERCY C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWNKEEN R., SAUNDEN B., SHOWNKEEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN R., WATERSTON R., WALLING J., WOLLINGON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Horizontal spread of mer operons among gram-positive bacteria in natural environments."; Microbiology 144:609-620(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MINAKHIN L.S.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
PLASMID-PKLH302; TRANSPOSON-TN1546-LIKE, AND IN3-TYPE;
                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6EDE7750 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 5;
Pred. No. 3.3e+02;
4; Mismatches 3
                                                                                        PRT; 1696 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AA.
                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 249069; CAA88864.1; -.
SEQUENCE 1696 AA; 191324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.38;
                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1999 (TrEMBLrel. 09, K12D12.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JAN-1999 (TrEMBLrel. 09, TRANSPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.9
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|||| :| :||:
121 AHRLLIATMROMLKW 135
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Gaps

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Indels

069234; 069234

RESULT 069234

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A.L., HUBER R.,

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51.4%;
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Best Local Similarity 53.5
Processive 7; Conservative
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               050343;
01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
                                                                                                                                                                                                                   130 YNYLVNAITVMLKY 143
                                                                                                                                                                                              2 YRLLIKVIRIVLKY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281
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Science 0:0-0(1998).
                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 YRLLIKVIRIVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 YRHLMRLIRMTLK
                        SEQUENCE FROM N.A.
                                    STRAIN-D/UW-3/CX
                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 2
                                                                     DAVIS R.W.;
                                                                                                                                                                                                                                                                                     030154;
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050343
ID 050343
AC 050343
DT 01-JUN
DT 01-JUN
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STRAIN=D/UW-3/CX;
STRAIN=D/UW-3/CX;
STEPHENS S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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GARDNER M.J. TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAVIND L.,
GARDNER M.J.
SHALLOM S., MASON T., YU K., FUJII C., PEDERSON J.,
SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,
SALZBERG S., ZHOU L., SUTYON G., CLAYTON K., WHITE O., SMITH H.O.,
FRASER C. M., ADAMS M.D., VENTER J.C., HOFFWAN S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium
  YOO J.S., SCHELLER R.H.; "Seven novel mammalian SNARE proteins localize to distinct membrane compartments."; 273:10317-10324(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
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                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                  Length 141;
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                                                                                                                                        Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RRNA METHYLASE (POSSIBLE).
                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                J. Biol. Chem. 273:10317-10324(1998).

EMBL: AF044310; AAC24032.1; -.
PFAM: PF00957; synaptobrevin; 1.
SEQUENCE 141 AA: 16366 MW; 3C737E45 CRC32;
                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001431; AAC71985.1; -.
SEQUENCE 186 AA; 21961 MW; B165839F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                         186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 AA
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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Pred. No. 6
                                                                                                                  Score 36;
Pred. No.
                                                                                                                                                                                                                                                 096287;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAY-1999 (TrEMBLrel. 10, Last and
PREDICTED INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                  51.48;
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                                                                                                                Query Match 51.4
Best Local Similarity 53.3
Matches 8; Conservative
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125 AILLLVIILLIVMKY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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145 AFILLIFIIHIVARY 159
                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                              1 AYRLLIKVIRIVLKY 15
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                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE, 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRRIDES N.C.,

FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

PETERSON S., REICH C.I., WEIDHAN J.F., MCDONALD L., UTERRACK T.,

COTTON M.D., SPRIGES T., ARTIACH P., KAINE B.P., SYKES S.M.,

SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
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Nature 390:364-370(1997)
EMBL; AE001100; AAB91148.1; -.
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                                                                                                                                                                                                                                                              DB 2; Length 187;
61;
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Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
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                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                   to the EMBL/GenBank/DDBJ databases
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
HYPOTHETICAL 33.0 KD PROTEIN.
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Last sequence update)
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                                                                                                                                                                             9AF9D1A5 CRC32;
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Pred. No. 90;
4; Mismatches
                                                                                                                                                                                                                                                           Score 36; DB 2
Pred. No. 61;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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282 AA; 33040 MW;
                                                                                   Submitted (MAY-1998) to the EMI
EMBL; AEO01356; AAC68426.1; -.
Methyltransferase.
SEQUENCE 187 AA; 21768 MW;
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Gaps

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01-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
CHROMOSOME XVI READING FRAME ORF YPL219W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fundi: Ascomycota: Hemiascomycetes; Saccharomycetales; saccharomycetes.
  STRAIN=K24;
KIM S.1. LEEM S.-H., CHOI J.S., CHUNG Y.H., KIM S., PARK Y.-M.,
HA K.-S.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                 Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: 077659; AAC31700.1; -.
HSSP: P33164; 2PIA.
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
PFAM; PF00111; fer2; 1.
Hypothetical protein; Iron-sulfur.
EQUENCE 381 AA: 41377 MW; BE9CDICZ CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECTENCE FROM N.A. RIEGER M.; SCHAEFER M.; SUDmitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 273575; CAA97934.1; -.
SEQUENCE 492 AA; 55430 MW; 6C549DE0 CRC32;
                                                                                                                                                                                                                                                                                 Score 36; DB 2; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 3;
Pred. No. 1.5e+02;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA
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Job time: 21496 sec
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60.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             183 AYRLLKQEQRFVLHY 197
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Best Local Similarity
9; Conserve
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416 AHRIIISTIRIATK
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EMBL; AB009373; BAA75213.1; -.
HSSP; P33164; 2PIA.
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                      Plasmid pLH1.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
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STRAINS-ANA-18;
MEDILINE; 99132292.
MURAKAMI S., TAKASHIMA A., TAKEMOTO J., TAKENAKA S., SHINKE R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Moraxellaceae; Acinetobacter.
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                                                                                                                                                                                      STRAIN-ATCC15009;
THOMPSON K., MCCONVILLE K.J., MCREYNOLDS C., FOLEY S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ222725; CA119961.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 284 AA; 33632 MW; E77494B0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frateuria sp. ANA-18.
Bacteria; Proteobacteria; gamma subdivision; Frateuria.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 41.4 KLD PROFININ.
Acinetobacter lwoffil K24.
    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
ELECTRON TRANSFER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2;
Pred. No. 91;
3; Mismatches
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Pred. No. 1e+02;
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01-JUN-1998 (TrEMBLrel, 06, La
HYPOTHETICAL 33.6 KD PROTEIN.
Lactobacillus helveticus.
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Best Local Similarity 28.6%;
Matches 4; Conservative
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Best Local Similarity 60.0%
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| 127 AYRLLKQEQRFVLHY 141
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X78926 H.sapiens HZF3 mRNA
E06738 Rhizopus niveus chit
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YVSQFPILLHGGAVDPTEKFPSCKDEAVQNIRLASEITESQNRKMEIFRQKHWTYSY
CYDHMYKVVLSGRYNPADEARERRYDPVTFGGIPHGHRGKHRSRSRLARTESI"
527 c 516 g 1048 t 3 others
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Akamatsu,T., Hanzawa,Y., Ohtake,Y., Takahashi,T., Nishitani,K. and
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Arabidopsis thaliana
Bukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (30-JUN-1999) Division of Biological Sciences, Graduate
School of Science, Hokkaido University, NIO, W8, Sapporo 060-0810,
                                                                                                                                                                                                                                                                                                                                                                                            Expression of endoxyloglucan transferase genes in acaulis mutants
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LOCUS AF163820 3000 bp DNA PLN 01-DEC-1999
DEFINITION Arabidopsis thaliana endoxyloglucan transferase (XTR2) gene,
complete cds.

ACCESSION AF163820
VERSION AF163820.1 GI:5533310
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1. .3000
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2 (bases 1 to 3000)
Takahashi,T.
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gb_htg7:AC012083
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AUTHORS
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100 1 Continuation (3 of 4) of CEY

199 1 AC006917 Genomic sequence for

101 1 AC016012 Homo sapiens chaliana

101 1 AL0217067 Arabidopsis thaliana

101 1 AL021711 Arabidopsis thaliana

111 1 AL021711 Arabidopsis thaliana

112 1 AL021714 Arabidopsis thaliana

113 1 AL021714 Bacillus subtilis com

114 Bacillus subtilis com
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AC013247 Drosophila melanogas
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AC008181 Drosophila melanogas
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AC017008 Homo sapiens clone
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-MODEL-frame+_p2n.model_DEV-xlp
-Q-/cgnl_l/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
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-DB-Genembl_QFWT=fastap_STFFTX=rge -GAPOP=12.000 -GAPEXT=4.000
-GAPEXT=0.050 -KGAPOP=10.000 -KGAPEXT=0.500 -FGAPOP=6.000
-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-UST=45 -NORM=ext -MINLEN-1 -MATEN=1000000 -USER-US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
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                                                                      software, version 4.5,
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Query length: 15
Database: GenEmbl: B
Database sequences: 821193
Database length: -1518192014
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gb_htg6:AC011694
gb_ba1:BSUBD011
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gb_htg1:CEY53H1_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDQDLAARCSSWALQISSNSDTCDKTAAIIFKGLTSPVAAVRSNVHRSWLCRIITLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HESPEWAEYIDESMLKTFSAGFSQVFEEKKLEICQEKLEKFYPAEDLGRLNVHVDLSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMDLISSILSRPSTDFSISGFQMILYFFTRFHIGSMEFYPYNHLLIITKINPCHWSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEQKCAEFEEQRTKNYYGMDEVQAVRSGKTDVESYIKAQISKSGLSEQVEANRKEQNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(19032, 19201,1977). 19892,21407. .21732,
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EST
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yk607e1.3 comes from this gene; cDNA EST yk672a5.3 comes
from this gene"
    from
yk630h10.3 comes
s from this gene;
    from this gene; cDNA EST yk630h1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F56G4.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

SS Hilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
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9987. .11016

Join (9882. .9955,10019. .10840,10917. .11016)

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Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail:
jes6sanger.ac.uk or rw@nematode.wustl.edu
On Jun 13, 1998 this sequence version replaced gi:1665968.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                08-OCT-1999
                                                                                   Caenorhabditis elegans cosmid F56G4, complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368 (6466), 32-38 (1994)
94150718
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                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
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                                                                                                                          281552
281552.1 GI:3217528
        seq_documentation_block:
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                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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MEDLINE
REFERENCE
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JOURNAL
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100001 210000
200001 310000
300001 403554
of CEY53H1 from base 200001 (299775 Caenorhabditis elegans chro
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Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
1, complete sequence.
AC006917, 6 GI:4757662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chao.Q., Shinn.P., Dunn.P., Buehler,E., Kahn,S., Kim,C., Walker,M., Williams,S., Altafi,H., Araujo,R., Conn,L., Conway,A.B., Walliams,S., Hansen.N.F., Huizar,L., Kremenetskaia,I., Lenz,C., Li,J., Liu,S., Luros,S., Rowley,D., Schwartz,J., Toriumi,M., Vysotskaia,V., Yu,G., Davis,R.W., Federspiel,N.A., Theologis,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecker, J.R.
Genomic sequence for Arabidopsis thaliana BAC F1086 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thale cress.
Arabidopsis thallana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker.J.R.

Ecker.J.R.

Direct Submission

Direct Submission

Direct Submission

Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

Ecker.J.R.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-MAX-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA ON May 7, 1999 this sequence version replaced gi:4731042.

Location/Qualifiers
                   LOCUS CEY53H1 Accession 299775
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Gaps: 0
Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                       to: 110000
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2 (bases 1 to 132699)
                        Sequence split into 4 fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: CEY53H1_2
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US-08-653-294-21 x CEY53H1_2
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3.429
93.333
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LOCUS AC006917 1
                                         Fragment Name CEF53H1_0 CEF3H1_1 CEF3H1_1 CEF3H1_3 CEF93H1_3 COntinuation (3 of 4) or
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EQFSAEYGNATFLKVNCDVARDIVQRYNISAMPTFIFLKNRQQVDMVRGANQQAIAEK
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join(complement(1831. 1934), complement(899. .1205),
complement(227. .694), complement(83118.1:17580. .17700),
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AL117201.1:5096. 5173,AL117201.1:5220. 5345)
/gene="F5664.5"
/hote="similar to Thioredoxins; cDNA EST yk491h3.5
from this gene"
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/db_xref="G1:6018392"
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AL Unton.L. Nusbaum,C. and Lander,E. Home sapiens, clone RP11-25P5

Home sapiens, clone RP11-25P5

AL Unpublished

E Chases I to 68676)

Bliren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Banta,N., Beckerly,R., Boquslavkiy,L., Boukhqalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FilzHugh,M., Forrest,C., Fuke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehockwy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McCandald,P., Marquis,N., McTow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Kiley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vasley,R., Wo,A., Wheeler,J., Wu,X., Nyman,D., Ye,W.J., Zimmer,A. and Zody,M., Meeler,J., Wu,X., Direct Submission

Nyman,D., Ye,W.J., Zimmer,A. and Zody,M., All repeats were identified using RepeatMasker:

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Center Project name: 25_P-5

Center project name: 25_P-5
                                                                                                                                                                                                                                                                                                                                                                                      ACO16012 68676 bp DNA HTG 18-NOV-1999
Homo sapiens clone RP11-25P5, LOW-PASS SEQUENCE SAMPLING.
AC016012
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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140

Length: Gaps:

47.00

alignment\_scores: Quality: Ratio:

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Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
clone:MJC20.
Arabidopsis thaliana
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                  AB017067 83689 bp DNA PLN 20-NOV-1999 Arabidopsis thallana genomic DNA, chromosome 5, Pl clone: MJC20,
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LOCUS AF027868 87500 bp DNA BCT 15-NOV-1997
DEFINITION Bacillus subtilis chromosome region between terC and odhAB.
ACCESSION AF027868
VERSION AF027868.1 GI:2618993
KEYWORDS
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Unpublished (1998)
2 (bases 1 to 83689)
Nakamura,Y.
                                               Align seg 1/1 to reverse of: AC016012 from: 1 to: 68676
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/clone="MJC20"
/clone_lib="Mitsui P1"
15544 c 15663 g 25912 t
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                                                                                                                                                                                                                                                                     AB017067.1 GI:3510343
alignment_block:
US-08-653-294-21 x AC016012/rev
                                                                                                                                                                                                                                       complete sequence.
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3.538
92.857
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US-08-653-294-21 x AB017067
                                                                                                                                                seq_name: gb_pl1:AB017067
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LOCUS AB017067
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complament(4086.5070)
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Rayredeliollkatnatgliteldoytdsveasvpelsfyggcrgmesnvdyaaask
Rgipyrptpgrnaqayaemetgnytesferhtspsnowikdgebnsdytykrgne
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syyllppreeftgliidpgyfblakesalfyntsrayvynredlleylkehkisgaildy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"similar to Lactobacillus xylulose kinase (501 aa)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to B.subtilis D-3-phosphoglycerate dehydrogenase (419 aa) encoded by serA gene"
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5394. .7427
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           Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 59208 to 59540)
Muller,J., Walter,F., van Dijl,J.M. and Behnke,D.
Suppression of the growth and export defects of an Escherichia coli secA(Ts) mutant by a gene cloned from Bacillus subtilis
93062812
93062812
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KWDSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
4 (bases 1 to 87500)
Lapidus,A., Galleron,N., Sorokin,A. and Ehrlich,D.
Lapidus,A., Galleron,N., Sorokin,A. and Ehrlich,D.
Direct Submission
Submitted (01-OCT-1997) Laboratoire de Genetique Microbienne, INRA,
Domaine de Vilvert, Jouy-en-Josas cedex 78352, France
Location/Qualifiers
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                                                                                                                                                                                                                                   Wolf,M., Geczi,A., Simon,O. and Borriss,R.
Genes encoding xylan and beta-glucan hydrolysing enzymes in
Bacillus subtilis: characterization, mapping and construction of
strains deficient in lichenase, cellulase and xylanase
Microbiology 141 (Pt 2), 281-290 (1995)
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604. .1101
/gene="yoaA"
/note="syaA"
/note="syaA"
ribosomal protein alanine acetyltransferase (194 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   j (bases 1 to 87500)
Lapldus,A., Galleron,N., Sorokin,A. and Ehrlich,D.
Sequence analysis of the Bacillus subtilis chromosome region
between the terc and odhAB loci cloned in a yeast artificial
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complement (9379. .11027)
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11755. .12910
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LOCUS ATF13C5 119111 bp DNA PLN 23-SEP-1999
DEFINITION Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSA
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Percent Identity: 69.231
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complement(9379. .9406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL021711
AL021711.2 GI:5738363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /citation=[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="yoaI
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Ratio: 3.538
Percent Similarity: 100.000
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US-08-653-294-21 x AF027868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AF027868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pl2:ATF13C5
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                                                                                                                 terminator
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VERSION
KEYWORDS
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                                                                        gene
                                                                                                                                                              CDS
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KSLYLKRELNRIGTKENNKVRVFSPRASEKCRVKAIEDLKKAKQRAREHELLIETADG
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RGUDBRARLEDEMBERNVESWIFMISSYAAAGLVKEAKEPYDSMPVRDVSWIPAMYT
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thale cress.
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Magnoliophyta, eudicotyledons, core
euphyllophytes, Spermatophyta, Magnoliophyta, eudicotyledons, core
eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="positions 1-4494 are not included within BAC clone F13C5"
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-5EP-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-83152 Martinsried, FRG, E-mail: Stochelledmips.blochem.mpg.de Project Condinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, On Aug 18, 1999 this sequence version replaced gi:2832611. Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="weak similarity to MICROTUBULE ASSOCIATED PROTEIN
1A (FRAGMENT) - HOMO SAPIENS, EMBL:095643"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-"similarity to hypothetical proteins - Arabidopsis
                                                                                                                                                                                   1 (bases 1 to 119111)
Bevan,M., Pohl,T., Weizenegger,T., Bancroft,I., Mewes,H.W.,
Mayer,K.F.X., Lemcke,K. and Schueller,C.
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                                                                                                                                                                                                                                                                                               Unpublished to 119111)

C (bases 1 to 119111)

EU Arabidopsis sequencing, project.

Direct Submission
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DEPMIEENKTCVVVREEGSTSPSSHTREHQVEOLESSIAIWENLVSDSCESMLOSRSM
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/note="similarity to heat shock transcription factor, Zea mays, PIR2:S61448"
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LOCUS AC011694 160557 bp DNA HTG 03-DEC-1999

DEFINITION Homo sapiens clone RP11-19D19, *** SEQUENCING IN PROGRESS ***, 33

ACCESSION AC011694
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Join(17543. .17758,19390. .20028)

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/gene="FiloS:60"
/foree="similarity to predicted protein, Arabidopsis thaliana, PID:G3834322"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52045 CATCATATATAATAAAAACATTCGTGTAATATTAAGTTAC 52004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 14
Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: ATF13C5 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                   .13598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(13599.
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HTG; HTGS_PHASE1.
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US-08-653-294-21 x ATF13C5/rev
                                                                                                                                                                                                                                                                                                                                                                                             GHLTSSERS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'number=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 3.286
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                     intron
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                            CDS
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Arabidopsis thaliana, PIR2:S52641"
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# 28483 31592: contig of 3110 bp in length # 31593 34072: contig of 2480 bp in length # 34073 38004: contig of 2480 bp in length # 38005 43296: contig of 3932 bp in length # 43297 48099: contig of 5292 bp in length # 43297 48099: contig of 4803 bp in length # 48100 52664: contig of 4803 bp in length # 52655 56856: contig of 4192 bp in length # 56857 61932: contig of 4192 bp in length # 61933 67427: contig of 5076 bp in length # 61933 67427: contig of 5076 bp in length # 61934: contig of 8076 bp in length # 61935: contig of 5076 bp in length # 61934: contig of 5076 bp in length # 61935: contig of 5076 bp in length # 61936: contig of 5076 bp in length # 61946: contig of 5462 bp in length # 71295: 76756: contig of 5462 bp in length	** 76757 82155:  ** 82156 90085:  ** 90086 98690:  ** 98691 107744:  ** 107745 116715:  ** 116716 132246:  ** 132247 145974:  ** 145975 160557:  Location/Quality:  ** 145975 160557:  Location/Quality:  ** 14597 16057:  Location/Quality:  ** 14597 16057:  A4509 a 35116 c 3  Battlo:  Dlock:    1/1 to reverse of: AC    1/1	ACCESSION 299114 AL009126 VERSION 299114.1 GT:2634230 KEYWORDS
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26-NOV-1997 of 21): from 2000171

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszerépasteur.fr,
adanchinépasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete genome sequence of the gram-positive bacterium Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
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1. .207730
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Neurospora intermedia mitochondrial plasmid DNA for DNA polymerase and RNA polymerase.
X52106 847059
X52106.1 GI:3089
DNA polymerase; RNA polymerase.
Neurospora intermedia.
Neurospora intermedia.
Witochondrion Neurospora intermedia
Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGSGEEFQAMLAFIDKHKLRPVIDRIYPLEKACEAYKRMOEGROFGNIGIVME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="glutamate synthase (small subunit)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to alcohol dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="glutamate biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 207730
                                                                                                                                                                             /protein_id="CAB13735.1"
/db_xref="G1:2634236"
                                                   complement(5627. .6484)
/gene="yofA"
/gene="yofA"
complement(5535. .5559)
/gene="yofA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="gltB"
complement(7611. .7625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="gltB"
complement(7658. .9139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7611. .9139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /EC_number="1.4.1.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                        function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                               /transl_table=11
                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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/gene="yogA"
6612. .7601
/gene="yogA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="gltB
                                                                                                                                                                                                                                                                                                                                         LDEINEMKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 46.00
Ratio: 3.538
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: BSUB0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-21 x BSUB0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pl1:NIMIDRPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS NIMIDRPM
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                      terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              terminator
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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4 (bases 7161 to 7293)
Vierula, P.J. and Bertrand, H.
A deletion derivative of the kalilo senescence plasmid forms
hairpin and duplex DNA structures in the mitochondria of Neurospora
Mol. Gen. Genet. 234 (3), 361-368 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TENEODKYVPENGEMYFESENYKTSFIKKITRODI.NEENRKITTDLETRSYPIHP
IKEGKOCKEGKVDSIMFPILMSVYNGKFVKSFIFKSOSAWFTEMNARKSIMLEKYDGY
KVYTHNFSFDGIFILDLSKLGEVRPFMRNGKILKIFFFTPDNSKRYTLYPMSCL
LILPDSLDKLSNFFRNKVKKLFFPHSFLDDWTIPINVYGKCPDYKYPFKAYTBDFTIE
QYQEYANKFKNNWDLKKELIKYCEIDTIALYQVLVSFQRKIYEKFWIDCTKYPTIS
MKAFRINDSGIPKYVGGTLQNIYNTKLSYFGGOICELXFRFGOVNIKSYBYBAR
MKYFRANDSGIPKYVGGTLQNIYNFTDSICEVPFGFYNWKWRYPLNDKFLENYPFAPA
AGTRTAFPLGQWEGWYFSEEILNAMKHGYEFFIEBGYLFESSSMFDEYIDLLYNIKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPKESPWYTSKLAMNSLYGRFGLNSEGEETFITSEEEGDATIATKEYVTITPLSSGN
VLISAKLPEBERGDMISVPISSALAAYSRIHBHSFLYKYSNNIYYIDPOGIKVDIDL
VKDEVDSKELGKMKYEXYFEEYTSLGPKVYGGLLYDKKGKLIELVKLRGYSSKLPYNK
LKEGLVRDHTLELTQKKWKRKLSESTVYLKNTHLLFE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKLSLFLNNVSKILSEHKKDLHKAQEIIEREWLKLATPSTDVKSDITSTMYTKHRLIH
DRAFDLLKLYKSNGNLNKISKSLKDYIVNEKFIFIAMSYLLASYSKSSLTNLDYRIGY
SITRHIYTEYYKDEFMSFDDFSNYNKFDVGFFVKLGDIFINTFTSPLNPIFERVFENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYSLKINKEYENEIMESLVISPRALPMVCPPLPWGHGIRGGNLINLTDTQDESLVVGS
FHRHKIAITDRLYNVINKLNAFKEKINGDLLSYLQNEGSFILDFYKNYKKDTYINNN
TITDIARTYLNTPFYLNYDWRGKIYTYOSFYLDYQGSELSLALINLEGKKLDEKGL
FFFYYYGANIYNDGGKEKKKSFQDRFNWYVENLDNIIANDKEFLIKAESPTLFAAFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SWISS-PROT:P33538"
/translation="MMNLRGFISLYKKQFKEEKFFFMAKIKFNNNDIRSISTVQIGST
DPLEVLRLLEAITSIYMHTHTGISEAVSEPFEYELFSLGDGLPKGNIIFTFKPTSNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKTKYEAHKSNIKRNKNINLSKKNPLNKFKYNGYTIPNTMDLSOWPNIHFINDGKNAV
SLNNIIKSGYDNMTLSFFITINKKYNEITYLLNNTPIFKIKDEKIMSEDDLSSFKRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MSKFSFFNYRINMRNSHATSLRFIKFNYSEFKNIRNFSSEKKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                        an
                                                                                                    Direct Submission
Submitted (16-WAR-1990) Bertrand H., Department of Microbiology,
University of Guelph, Guelph Ontario NIG 2W1, Canada
2 (bases 1 to 8642)
Court.D.A. and Bertrand, H.
A method for sequencing uncloned termini of linear plasmids
Nucleic Acids Res. 19 (7), 1714 (1991)
                                                                                                                                                                                                                                                                                                     Chan, B.S., Court, D.A., Vierula, P.J. and Bertrand, H. The Kalilo linear senescence-inducing plasmid of Neurospora is invertron and encodes DNA and RNA polymerases Curr. Genet. 20 (3), 225-237 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .8642
.Coganism="Neurospora intermedia"
//mitochondrion
//db_xref="taxon:5142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="site of terminal protein"
|1541. .4222
|codon_start=1
|trans1_table=4
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Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 8642)
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/db_xref="G1:578158"
/db_xref="SWISS-PROT:P33541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="inverted repeat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="DNA polymerase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /plasmid-"Mitochondrial
/tissue_type-"mycelium"
/cell_line-"P561"
1. .1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4899. .7334)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                     Bertrand, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="PPZ1
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
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                                      EKIVISKGKEIKVYDYLVPTRNGDEVVLDTFEVETLASIINDNIFNQEPKLHSIYDYL
TRLAKIYLKLDIPLSMSTPDGLELTQRYNLSKVKKLTINFLGKNRTAYLRSWYNEKDS
RREVQAIIPNIINSLDASHLTMIIDSWDSYILPIHECFGTHPNDMYKLAEQVRECFIL
LYSKNDFLMKIDYKFRENLKDYKIEIVNKNGEDFVXIKGNKRYEYLPVLPVLPQMGELN
VEDIRDMGKYMIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barrell, B.G., Rajandream, M.A. and Walsh, S.V.
Direct Submission
Submitted (O2-JUW-1995) Saccharomycess cerevisiae chromosome XIII
sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI) is given for each CDS.

Cosmid 9571 overlapped at 5′ end by cosmid 8337, EMBL entry SC8337, accession no. 246659, and at the 3′ end by cosmid 8270, EMBL entry SC8270, accession no.448613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50\% of their length by a larger CDS have been omitted from this
FMRKLKENPDY PVFNP I FLDATC SGVQHFAAMLLDLELGKYVNL INSGESVNDFY SQL
FPA I NKA I NESAEKKFKNLKFSDI SLNRSLLKKV IMTKSYNVTTYGI TEQLKSKLEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.cerevisiae chromosome XIII cosmid 9571.
249810 271257
249810 1 G1:854472
ERG6; lactoyl glutathione lyase; MRPL39; PARI; PDR4; PPZ1; protein phosphatase; ribosomal protein; SED6; SNQ3; SPT5; transcription initiation protein; transfer RNA-Ser; YAPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Fungi: Ascomycota: Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 29366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 8642
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                                                                                                                                                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLN
                                                                                                                                                                                                                            terminal protein"
77 g 2996 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: NIMIDRPM from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ArgLeuLeuIleLysValIleArgIleValLeuLys 14
                                                                                                                                                            7278. .8642
/note="inverted repeat A'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4932"
/chromosome="XIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="cosmid 9571"
/map="131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="AB972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
                                                                                                                                                                                                                          /note="site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gentles, S. and Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished 29366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-21 x NIMIDRPM/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29366 bp
                                                                                                                                                                                                                                                  1327 c
                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 3.750
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                    45.00
                                                                                                                                                          7278.
                                                                                                                                                                                                       8642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              baker's yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS SC9571X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_pl1:SC9571X
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                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                    3042
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                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                               alignment_scores
                                                                                                                                                               repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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RSSTYRENALDDDDDDKDDDKDDTPSRSNINGRPSIRGSSVSRRKSDVHEEPNN
GSTYSRNIQERYLVQALTRSNSHASSLHSRKSSFGSONTRYSTDASFERSDVINGERYNNITDSK
KDPNEEPNDIMOSSTNINGRNINGPRESPINGSONTHASMENVDKNNNITDSK
KDPNEEPNDIMOSSTNINGRNINGPNINGSONTHASMENVDKNNNITDSK
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KDPNEEPNSTNINGSSCRNNAPKEKRFDIDEFTIQKLLDAGYAARRKNVOLKNNNITDSK
CARREITSROPSLLELSOPSLILESPNINGSCRUNDELLOFTICKGFPPSSNYLFLGDDVD
CONTRAFFINGSCRUNDELSOPSLILESPNINGSCRUNDELLOFTICKGFPPSSNYLFLGDDVD
CONTRAFFINGSCRUNDELSOPSLILESPNINGSCRUNDELLOFTICKGFPPSSNYLFLGDDVD
CONTRAFFINGSCRUNDELSOPSLILESPNINGSCRUNDELLOFTICKGFPPSSNYLFLGDDVD
CONTRAFFINGSCRUNDELSOPSLILESPNINGSCRUNDELLOFTICKGFPPSSNYLFLGDDVD
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WKLQMLRTGGTSINNOLINKYPKYKYGKTRINGODEDSINKYPENLIPPODILOGOTON
SNYEDTWINEDENEKLAQDEGFKLLYTNLDKDGTNRFEFFRRTSLNKTQVKKLASTVA
NQTISENIRYFLQAPKKIYAGEIIELAMIYKNKWLTSGWCIEFDKRTKIKKKYLK
KLTFSIIENQQYKQDYGSDSVPEDEPDFYFDDEEVDKRETTLGNSLLGSKSLQOSDHN
SQDLKLQLIEQTNKLVLQFNKLDVSIEKYNNSPLLPEHIREAWRLYRLQSDTLPNAYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7287. :8126

//note="YM571.04, unknown, len: 279, CAI: 0.13, similar to WP:C1481.5 CE00902 Diphtheria toxin resistance protein (39.4% identity in 155 aa overlap) and WP:C35D10.12 CE01193, (30.8% identity in 208 aa overlap)"
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YTSRDMDKILNYWTTPLKEIYHITTAPAEFEDFKDYSTKVKLLTDPKDDAGKPPITKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPNEWEDNERGYSYCYNKVAINKFLNKFGFDLYCRAHMYVEDGYEFFNDRSLYTVES
PNYCGEFDWGAYWSYSEGLLCSFELLDPLDSAALKQYMKKGRQERKLANQQQMMET
SITNDNESQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRSKSNPFGSAKPVDTQSKILDIEEKMENLHVEDTTTLRASLIPSSDSMATTATGSKI
TILKKQTPTEEESHSATPTPKPLSYSEVVERSVVNETSKKGTPLSKLDSPALELQSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKSDEFKGGDEQGFEKGGDDKAQLDVSNDKDKGSETDVDKQFTFKNVEREHSMSRTKY
NGNRNNNNGRFRGSNRYRGPRGSSYKGGHNNRGDRGGYRGGSSYNNNNNNTNDNNNN
NNNSSSNNNNGSREGGELSDSSLDASGNKRNDFTNSTSNTQDYSFRPASG
FLGQGNNDSIRNNGRRYNSSGMNGGSRGRGFGRGFGRGFGAVNNNGSSGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGKOSLETILLLECKKIKYPENFFLLRGNHECANVTRVYGFYDECKRRCNIKIWKTFI
DTENTLPLAAIVAGKIFCVHGGLSPVLNSMDEIRHVVRPTDVPDFGLINDLLWSDPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="xM9571.02c, PP21 gene, len: 692, CAI: 0.17, % PP21 P26570 serine/threonine protein phosphatase PP-21; contains PS00125 Serine/threonine specific protein phosphatases signature"
1. .463
/note="overlap with cosmid 8337, positions 34044 34506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="PPZ1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatases signature"
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complement(6051. .7091)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SGD:S0004478"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3520. .5598)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLITLIKKWHELEPWILVARQLGVRNTPEIFLLANVANKASHSFTLPSGRLSIJGKLKV
NSLNRFLØSLTNVVBKYTPELVVNKTEMHELEMSREIKKLQEDAYKKSLEMDRIKAIE
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I IEELGHIINNELTSFDLERGKLEFDFELVSPFRYTVHPNEHMSVDQVPQLMPNGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mskstnvsyervelfenpxvpievedeilekyaessldhdmtvn
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Smlirngrdvdfpqvalrdhvlsvkdlokisnligadqssgtiemiscatdgkrlem
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ATLNTDSSEANEIVKKEEGSDERKRPREEDTKNSDGDTKDEGDNKDEDDDDDDD
                                                                                                                                                                                                                                                           SLDDNDEKQQQDQEQEREEVKYRYYHLYREGELAEDCRQAGAAVHSEGFERDNWWVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10178. .10813
/note="YM9571.06, len: 211, CAI: 0.22, potential
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SW:G35L_CANFA P27869 glycoprotein 25L precursor (24 4%
identity in 168 aa overlap) and to SW:P348_YEAST P32803
P24B protein precursor (26.0% identityin 131 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                          contains
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/note="YM9571.05, unknown, len: 584, CAI: 0.14, conta
PS00225 Crystallins beta and gamma 'Greek key' motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA89940.1"
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11739. .14930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown"
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11739. .14930
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                                                                                                                                                                                                                                                                                                                                                                                                                                            signature"
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CDS

gene

CDS

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ITANILSERSTDTTATSSEYALHDIVELSARWAGIIOPERVDETGKVSSTITKG
SILSKINTARARVSSVDANGNEIKIGDTIVEKVGSRREGQVLYIQTOOIFVVSKKIVB
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FLLPSVDTATIWGVRCRPGKEKELIRKLKKKFNLDRAMGKKKLKILSIFQRDNYTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA HTG 16-NOV-1999
*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (16-NoV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210956 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins:
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 29459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23408 TATCGCTACTCGTTCAAAAATTAAAATCGTTATCAATTAT 23449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
6592 c 6879 g 8142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                     Length: 14
Gaps: 0
Percent Identity: 57.143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 29366
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1. .29459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AC015353 29459 bp D
DEFINITION Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
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Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC015353
AC015353.1 GI:6435982
HTG: HTGS_PHASE2.
fruit fly.
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US-08-653-294-21 x AC015353/rev
                                                                                                                                                                                                                                                                                                                                               Quality: 45.00
Ratio: 3.462
Percent Similarity: 92.857
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: SC9571X
                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-21 x SC9571X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_htg5:AC015353
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ORIGIN
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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KEYWORDS
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DYYLIOENPY WINDODESISSKELPHONGELHISEDTESDUFSES HEREDIDIYTY
VSWILDDSDLOOPERREBELEWHSMLSSVLKGDVWOTERRELLTEPDGHSGTYISE
VWGLGLOALLOESDLOOPERREBELEWHSMLSSVLKGDVWOTERRELLTEPDGHSGTYISE
VWLGLOALLOESTRADOAEVIRS REGVEYLREVIDFOLODEETTR PPLEGVTEILE
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EFDLIMMPOFNOTGVENISSFVERIFRONTLITINRIHQAKOTISEN
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ALSTHWYSTLERNYGOTERFKILRESTRIKLATAYAK IKGPNFLIVDSMLDDFKI
YRKEIDFLENBWAFLNEHTYWIGGDIHMAGOFSYLSNSLLINVHRYVESHLNGFTER
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/tanslation="swicgethysytspuntslitypeaelicnretpetkwpewgas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVEEEALSIQLLQKETWLRIDELEIERNNTLLERLAICHVLDSSVFRNRDFIKLASSF
SNITIRWQQGHFVRSGMFGDVYTGVNMETGDLLAVKEIKLQDSRTFRSTVDQIHNEMT
VLERLNHPNVVTYYGVEVHREKVYIFWEFCQGGSLADLLAHGRIEDENVLKVYVVQLL
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HAGTPRWINAPEIILGTKOBFGAMIWSLGCVILEMWTGSTRWSENDHRWAINTHVA
AMHTPSIPQNEKISZLARDFIEQCFERDPEOGRPRAUDLLTHPWITDRFKKTIITMPPA
TITKKTSLSHTITEEKTAQLLAGRHDDSKAETDSLAASYKEESALPVASNVGLRQPNE
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AKLILIAGNCPPLRKSELEYYAMLSKANVHHYAGTNIDLGTACGKLFRVGVLAITDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:2770551"
/db_xref="SPTREMBL:014299"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSLMDNLVDSTESTKRSENFVSHIPLTPSHSGQSEKLMSTRTSHSPYISPTMSYTNHS
PANLTRNSSFNHQHYSTTLRSPPSMRGRGIDVNSSHYPHISRPRTSSDSQKMYTRAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry PF00069 pkinase, Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ctaactgagttattag, splice branch and acceptor"
complement(6677. .6682)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00108 Serine/Threonine protein kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(6533. .6623,6683. .6921))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="giaagt, splice donor sequence"
complement(6772. .6846)
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/profein_d="CABil499."
/db_xref="G1:2440209"
/db_xref="SWISS-PROT:P52808"
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/product-"hypothetical protein"
/protein_id-"CAB11487.1"
/db_xref-"GI:2370550"
                                                                                                                                                                                                                                 1985. 6190
/gene-wist"
/gene-wist"
/note-"SPAC9G1.02, len:140laa"
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/note="SPAC9G1.03c, len:109aa"
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5093. :5902
/gene="wis4"
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/gene="wis4"
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Protein coding regions (CDS) have been predicted with the help of protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CATTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system as SPATHIO.10: SP (S. pombe), A (chromosome 1), cSHIO (cosmid name), .01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapp between neighbouring submissions. Cosmid c9G1
                                                                                                                                                                                                                                                                                               beta-transducin; cdc12 homolog; cytochrome oxidase biogenesis protein; Homol D box; inositol metabolism; Inositol polyphosphate phosphatase: lysophospholipase; MAP Kinase Kinase Kinase; oxal; ribosomal protein L30e; rpl30; septin homolog; serine threonine protein kinase; spn4; src homology domain; vacuolar sorting; wakl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of yeast sequencing at the Sanger Centre are available on
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Barrell, B.G., Rajandream, M.A. and Wood, V.
Direct Submission
Submitted (26-8071997) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk
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P53242, hypothetical 34.0 kd protein, (292aa), fasta
scores, opt:210, E():4e-09, (32.7% identity in 159 aa
overlap), similarity: to YBR105C, YBV5_YEAST, P38263,
hypothetical 41.2 kd protein, (362aa), opt:159,
E():1.3e-08, (25.7% identity in 191 aa overlap)"
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/gene="Spac9G1.01"
/note="nominal overlap with EM_FUN:SPAC3H1 268144
position36460. .36920"
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Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                         PLN
   1853 GCCTACCGCCTCGTACGGATCGTTCGGATCGTC 1818
                                                                                                                                seq_documentation_block:
LOCUS SPAC9G1 30985 bp DNA
DEFINITION S.pombe chromosome I cosmid c9G1
ACCESSION 299763
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/chromosome="I"
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1 (bases 1 to 30985)
Churcher, C.M. and Gentles, S.
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                                                                                                                                                                                                                                                                       298763.1 GI:2370549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product_corrothcome oxidase biogenesis protein"
/protein_id="CABLI488.1"
/db_xref="G1:2370552"
/db_xref="G1:2370557"
/dc_xref="G1:2370557"
/dc_xref="G1:2370557"
/dc_xref="G1:237057"
/dc_x
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KTGDDYVEIDTDHKGSIFSISMSPDSSOFYSSAGASCKIMDAMTGSLIFEMLSSDKKO
LVGTWMPTRDLIIVNNSKGMLTYLMPSDCKYLDTIYGHQRSTTAATLSPDATHEYTAS
YDGTVLSWDIGKQKAFPLVGESHTNQVWQMIMADDHVITIGMDDTLRVIDIKQGCFAK
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GRITDLDWDGDSQRIIAVGEGKERYGHAFTADSGNSVGEIFGHSSVVNAVSLRKSRPF
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10423. .10468,10518. .11459,11506. .11928)
/gene="SPAC9G1.05"
/note="SPAC9G1.05, len:595aa, similarity: to WD42_DICDI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSSQLKSTWAPVPSTKPSQPCKIGTDFKGERIVYPANKAIIIRE
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9769. .11928
/gene="SPAC9G1.05"
/gene="rpl30"
/note="PS00709 Ribosomal protein L30e signature 1"
complement(6991. .6998)
/note="Homol D box"
/note="Homol E box"
/note="Homol E box"
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8997. .9002
/gene="oxal"
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join(8152. .8180,8246. .8996,9073. .9417)
/gene="oxal"
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9054. 9072
/gene="oxal"
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8233. .8245
/gene="oxal"
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/protein_id="CAB11489.1"
/db_xref="G1:2370553"
/db_xref="SWISS-PROT:014301"
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/gene="oxal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.00
3.750
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: SPAC9G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-21 x SPAC9G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                           promoter
                                                                                                                                                                promoter
                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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Caenorhabditis elegans strain=Bristol N2.

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida; Rhabditida;

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;

Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 42751)

88 Milson, R., Ainscough, R., Anderson, R., Baynes, C., Berks, M.,

Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,

Coulson, A., Craxton, M., Darson, S., Du, Z., Durbin, R., Favello, A.,

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,

Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laisten, N.,

Latrellle, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,

O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Sonnhammer, E.,

Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,

Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,

Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ďq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The 5' cosmid is C10F3, 200 bp overlap;3' cosmid is R01B10, 2200 overlap. Actual start of this cosmid is at base position 197 of CELF29G9; actual end is at 40555 of CELF29G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sections
                                                                                                     07-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not be the entire insert of this It may be shorter because we only sequence overlapping sectionce, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                     INV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Caenorhabditis elegans" /strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEIGHBORING COSMID INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of C. elegans cosmid F29G9
Unpublished (1997)
3 (bases 1 to 42751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence from more than one subclone
                                                                                                     Caenorhabditis elegans cosmid F29G9.
AF016440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (30-JUL-1997)
Submitted by:
                                                                                                                                                                                                          AF016440.1 GI:2315352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 42751)
seq_name: gb_in1:CELF29G9
                                                                    seq_documentation_block:
LOCUS CELF29G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Langston, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94150718
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NLLGRACQIWTTINKTILITGATOSIGKOTALDLAAHPDNEVIHGRTEERCIATR
DWIGKENGNCSNIDYVAGDFAVLKEVAIIABEVERRFPELNVLLCNAGVLYPRRLETK
                                                                                                                                                                                                                                                                                                         DGMESTFOVNYLAHYLLCNLLLPVLSHINRSNYIVVGSYLHTWPSLDWADYMATKEYEK
YLQYSRSKLMCHLMAFALHRRMNIARQHVNVNIIELGKEKEPNNIGKLRTTSALSSSM
STLSICRQAGNLAQLIEGPCLEKISGRYLDPSGKQMRSGSDATDERLQERLWAYSKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRTDVGPILRYDRAVLALMNTWVMMCSSYGVEHHMKKQLLFKAI
viclitkQQCsakGrPTEEEGTNDDGKKWTKGGDSMELWNEISLKRSRATMDRD
GSGWNDRFEDNRDRYGWIRGFGNDSGWIGMDRDGLGWIGMDRDGSEWVAMDRDGS
GWGKDRDGSVWIEMG[G]"
7983 c 7355 g 13922 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKWNKNLRNGCYIVLASLESIISKKTISSSKMRRIVRARALLFUGERSDHALSTQPPP
PIKFVILSYSPSQTVQWKPSVVSSVICRKKRQEQPTFERLLQLPPPAFANILKILGAV
KILELSQLSKRMCTLIQAANITFDHIMIAFSESSALPIIPKSVAMLQTLNLAYQPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(33753. .33916,34076. .34173,34222. .34536,35131. .35405,35616. .35934,35983. .36061,36467. .36485))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MPEXVPTLNFNFNSTSSIFKRSVKFGDLRLPIKYDPETATTGST
DNYEDCLQPCLDLFATIFSCRGGIAIVNLNECSLNVREHTAHRIFNKNLVVKLCGDVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLGTNNGSLQSFYPEYVLLEGIVADFHFLEEEFDPYEMFTRNRVSIMDAKWYLLYHLK
SLKFIWLVLYNSMLTERDVNEFIKLWLDGKWLQLHRFEIRHTSRGGFDLEVLKSGLNV
/note="contains similarity to the short chain type alcohol and other dehydrogenases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 14
Gaps: 0
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      јоди(39027. .39211,39749. .40103)
/gene="F29G9.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSTFSCIMCRAPONGELSLNKTILTITLW"
39027. .40103
/gene="F29G9.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(33753. .36485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F29G9.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.462 92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.00
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US-08-653-294-21 x CELF29G9
                                                                                                                                                                                                                                                                                                                                                                                                    CHEYL"
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence-not_experimental
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AVIGVILSDYDDPMAVSWHKLEKAPQEFTVANGGGLDQOGDERAFLPFTYERMG
IRPPKGVILYGCPGTGRTLLARAVANQTSATFLRIVGSELIQKYLGDGFKWNRELFRV
AEBNAPSIVFIDEIDAVGTRKYDSNSGGEREIQRTMLELLNQLDGFDSRGDVKVLMAT
NRIESLDPALIRPGRIDRKIEFPLPDEKTKRRIFQIHTSRMTLGKEVNLEEFITAKDE
LSGADIRAMCTPAGLLALRERRARVTWEDFQKSKENVLYRKKEGAPEELYL"
19.75
                                                                                                                              join(13017. .13124,13720. .14220,14274. .14475,15071. .15192)
/gene="F29G9.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            jóin(22980). .23133,23767. .23885,23939. .24070,24366. .24959,
25009. .25294,25342. .25634)
/qene="r2969.2"
/note="coded for by C. elegans cDNA CEESK57FB"
                                                                                                                                                                                                                                                                                                                                                                                                                                    LRVHPPRADSVPYSIRSGHSSSSEQHSPVEDYKPSIDQLLLPPISCIQNIKDRNINS
MPPPALPASTSAAGIHVITSIPVSHANSLHGRSENVFAEPERKIPKIELDQTLTSLTM
PDDVERPSALDTLSRIVENQPITTPSRPFRLGGEYQNQTPQSTGNGLFGGPPGPFDLL
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complement (15701. .17169)
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KMCAFLEYKDLKVYKRYAGILFCCA.EQNDNELITLEYJHRKYELDKYFGSVCELD
IIFNFEKAYFILDEFLLAGEIQETSKKQVLKAIAAQDLIQEEETPQGFFEDHGLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSTKOTPPRSPVIRYPTVVVSKNSIATPSSSLTPQGTPSYAVPVSRNOMOYSASKLOY
EHRHRCKMLDDENOKLMRMOSDVYNDANRRYOMHVNBIRMLAEDNRKLAISNKELRD
LSCFLDDDRQKTRKLAREWQKFGRYISSLMKOEVDSYHQKNVSIEEKLCTREREVDEL
ROLCMYLDEORQSLMONAAANVDCDRESEDLGGGSSEQSGGSEGHNDERKHHENNKCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKHKESTLRRIMATSWCSEPSEEERREVSKRERSRLGGYIOSLENRIKHLEMSONHE
SFWNSSSNVGSDCDEKTIIERGWLGEEVMSNSEDCHLELKPVMTTSSTSSSHIFGNDK
CPMFDSMTSNMTSSGCTTYASSGTDGDSVFVIGDEIDIGNLEVRTLSRIDEEATSASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(26014. .26095,26138. .26278,27281. .27361,
27421. .27531,28400. .28500,28853. .28975,29114. .29197,
29739. .29996,30057. .30269))
/gene="F29G9.6"
                                                                                                                                                                                                                                                                                                                                                                                                          NDKKMAECNNIRNKLNSLKNYLETHDCKLSREERTHEINRLIIPPSTVPPSQPYLQHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MSSESGSSASTVHYAKPVLRHVPMPSSTTPSSIGSSSSSSSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLKESARMPPKIAPPICSSLVLTNFDNMSEDCAPRLMRSASETCRPTTLLISSTQPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(15701. .15925,15972. .16694,16740. .16960,
17007. .17169))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17476. .18251
/gene="F2969.3"
join(17476. .17553,17602. .17705,17960. .18251)
/gene="F2969.3"
/note="Similar to clathrin coat assemble protein; coded
for by C. elegans CDNA ykl75h10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17007. 17109)
/gene="F2909.5]
/note="gtong similarity to the AAA family of ATPases"
/codon_start=1
                                                                                                                                                                                                                        /note="Similar to BZIP transcription factor"
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   /db_xref="taxon:6239"
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                                                                                                    13017. .15192
/gene="F29G9.4"
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                                                                /clone="F29G9"
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138. .1750
/*tag= a
/product= Chitinase
138. .242
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98. .760
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101.95
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Ratio: 3.231
Percent Similarity: 86.667
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US-08-653-294-21 x X13927
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  N_Geneseq_36:Q46292
N_Geneseq_36:Q46293
N_Geneseq_36:T78725
N_Geneseq_36:V89042
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                                                                                                                                                                                                                          2255 | Chitinase derivative gene. New is 2255 | Chitinase derivative gene. #1. 2255 | Chitinase derivative gene. #1. 2255 | Chitinase derivative gene. #1. 3721 | Enterococcus facealis genome 6 869 | Aspergillus arabinofuranosidase 8691 | Enterococcus facealis genome 7 8991 | Enterococcus pneumoniae genome 6 993 | Streptococcus pneumoniae genome 6 993 | Streptococcus pneumoniae genome 6 993 | Streptococcus pneumoniae genome 7 8 | Streptococcus pneumoniae genome 1 975 | Streptococcus pneumoniae genome 7 8 | Tumour rejection autigen precu 6 1 1000 | Continuation 6 | Colio of 1 1000 | Continuation 6 | Colio of 1 1000 | Continuation 6 | Colio of 1 1000 | Continuation 6 | Colio of 1 1000 | Continuation 6 | Colio of 1 1 1 | Human IL-Ira BAC contiguous DN 158 | Human IL-Ira BAC contiguous DN 16592 | Streptococcus aureus contiguation | Continuation 6 | Colio of 1 1 1 | Human IL-Ira BAC contiguous DN 16592 | Streptococcus aureus contiguation | Continuation 6 | Colio of 1 1 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7769 | Staphylococcus aureus contiguant 1 | Human Bacinia burgdorferi polynuc 7 | Human Bacinia burgdorferi polynuc 7 | Human Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Bacinia Baci
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1186 | Pythium oligandrum isolate 23-
1748 | Human testis secreted protein
3485 | Enterococcus faecalis genome
3907 | Enterococcus faecalis genome
16535 | Streptococcus pneumoniae gen
3768 | Enterococcus faecalis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110000 | Continuation (4 of 6) of v3 | 110000 | Continuation (2 of 17) of | 11000 | Continuation (9 of 10) of | 110000 | Continuation (4 of 6) of v3 | 110000 | Continuation (5 of 6) of v3 | 110000 | Continuation (5 of 6) of v3 | 110000 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continuation (5 of 6) of v3 | Continua
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-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
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-MODEL=frame+_p2n.model -MODEL=frame+_p4.model -MODEL=frame+_p4.model -GAPP==12.000
-GAPOP=4.500 -MINMATCH=0.100 -LOOPCL=0.000 -MODEL=frame+_0.500
-FGAPOP=4.500 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YARTR=LOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFNT=pfs -NORM=ext -MINLEN=0
-ALIGN=15 -MODE=LOCAL -OUTFNT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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                                                                                                              software, version 4.5,
     out_format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
  to: N_Geneseq_36:*
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Database sequences: 311585
Latabase length: 125096042
Search time (sec): 873.190000
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N_Geneseq_36:X20248_04 + N_Geneseq_36:X20248_04 + N_Geneseq_36:X20248_04 + N_Geneseq_36:X20248_08 + N_Geneseq_36:003147_0 = 3
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Query: US-08-653-294-21
Query length: 15
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  OM of: US-08-653-294-21
                                                        Date: Feb 8, 2000 7:30
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N_Geneseq_36:X20248_08
N_Geneseq_36:V30459_3
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_Geneseq_36:T58840_4
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N_Geneseq_36:T33641
N_Geneseq_36:T33646
N_Geneseq_36:X13195
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_Geneseq_36:V42962
_Geneseq_36:V07122
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N_Geneseq_36:T84234
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N_Geneseq_36:V69720
N_Geneseq_36:V74331
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N_Geneseq_36:V74364
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N_Geneseq_36:V74525
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1508 i PAL regulator gene. Regulat
415: i Phenrylalanine ammonia lysse
70: i SELEX generated lighad to hCG
320: i EST clone BV31. New polynucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PER 09-0CT-1998; U06371.

PER 1998; U06371.

PER 1998; U06371.

PER 29-JUL-1997; US-981257.

10-APR-19997; US-881227.

RA-JUN-1997; US-881227.

A (HUMA) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.

PER 542293/46.

PER 542293/46.

PER 64 diagnos1s, prevention and treatment of Helicobacter for the diagnos1s, prevention and treatment of Helicobacter for the diagnos1s, prevention and treatment of Helicobacter for the diagnos1s, prevention disconsers a Helicobacter for infections and gastrodudedanal diseases a Helicobacter infections, and gastrodudedanal diseases a Helicobacter infections, and gastrodudedanal diseases associated with these infections, including acute, chronic, and atroppic gastrifis, and peptic infections, including acute, chronic, and atroppic gastrifis, and peptic infections in diagnosis.

Defermine diseases, e.g. gastric and duodenal ulcers. They can also be used for detection and diagnosis.
                                                                                                                                                                                                                         seq_documentation_block:

ID X13927 standard; DNA; 810 BP.

AC X13927;

X13927;

DT 31-MAR-1999 (first entry)

DE H. pylori GHPO 635 gene.

KW GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;

KW Peptic ulcer disease; ss.

OS Helicobacter pylori.
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Chitinase derivative gene #1.
Chitinase, derivative; beta-1,4-glycoside bond; chitin;
beta-N-acetylhexosaminidase activity; yeast; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AlaTyrArgLeuLeulleLysVallleArglleValLeuLysTyr 15
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Gaps: 0
Percent Identity: 53.333
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444.90
1.5e+03
16.97
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arabinoxylan
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                                                                 infection.
                                                                                   Sequence
 88888888
                                                                                                                                                                                                                                                                                                                                                                      Claim 1: Page 1626-1628; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring
                                                                                                                                                                                 (KAGO) KAGOME XK.

WPI: 94-097015/12.

WPI: 94-097015/12.

WPI: 94-097015/12.

WPI: 94-097015/12.

New chitinase enzyme and coding sequence - cleaves beta-1,4-glycoside bond of chitin but has no beta-N-acetylhexosaminidase activity claim 11: Page 21-23: 66pp; Japanese.

The sequences given in Q56756-61 encode chitinase derivatives which cleave the beta-1,4-glycoside bond of chitin but have substantially no beta-N-acetylhexosaminidase activity. These sequences may be introduced into yeast and cultured for the production of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA.) HUMAN GENOME SCI INC.

Barash SC, Dillon PJ, Kunsch CA;

WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

- used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:411.
Enterococcus faecalis; contig; detection; Enterococcus infection; vaccine; attenuation; computer readable medium; ds.
Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                          747 T;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                          446 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q56758 from: 1 to: 2255
                                                                                                                                                                                                                                                                                                                                          448 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1867 AAAGTAATAAGAATTGTCTTAAAATAT 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LysvalileArgileValLeuLysTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X13348 standard; DNA; 3721 BP
                                                                                                                                                                                                                                                                                                                                          614 A;
                             /*tag= c
306. .498
/*tag= d
499. .566
/*tag= e
567. .1750
/*tag= b
243. .305
/*tag= c
                                                                                                               /*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:X13348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                     28-JUL-1992; 201427.
28-JUL-1992; JP-201427.
                                                                                                                                                                                                                                                                                                                                                                                                 42.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-21 x Q56758
                                                                                                                                                                                                                                                                                                                             chitinase proteins.
Sequence 2255 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                            J06046849-A
                                                                                                                                            22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection
                                                                                                                                                                                                                                                                                                                                            Sequence
                 intron
                                                                      intron
                                             exon
                                                                                                   exon
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used to
progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8: Page 48: 105pp; English.

The promoter (733641) of the arabinofuranosidase gene of Aspergillus niger 3M43 was identified in a full-length gene (733646) isolated from a genomic DNA library. The promoter is strongly repressed by glucose and induced by intermediates of xylose metabolism. It can be used to control the expression of a gene of interest, e.g. A. niger arabinofuranosidase or a heterologous gene, in a host sequence 869 BP; 224 A; 209 C; 193 G; 243 T;
                                                                                                                                                               954 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus arabinofuranosidase - useful for degradation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus arabinofuranosidase gene promoter.
Promoter: arabinofuranosidase: AbfC; arabinoxylan;
viscosity modifier; food; feedstuff; ss.
WO9629416-Al.
                                                                                                                                                               785 G;
                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TyrArgLeuLeuIleLysVallleArgIleValLeuLysTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 TACCAACTITIAGTICGAITGAICAGAATACTITIG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TyrArgLeuLeuIleLysValileArgileValLeu 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: X13348 from: 1
                                                                                                                                                               582 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DANI-) DANISCO AS.
Baruch A, Madrid SM, Rasmussen P;
WPI; 96-443191/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T33641 from: 1
                                                                                                                                                          1387 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID T33641 standard; DNA; 869 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID T33646 standard; DNA; 2555
AC T33646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133641,
11-DEC-1996 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-21 x X13348/rev
                                                                                                                                                                                                                                                                  41.00
3.417
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:T33641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:T33646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 3.333
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1996; E01009.
17-MAR-1995; GB-005479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-653-294-21 x T33641
                                                                                                                                                               3721 BP;
                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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The Aspergillus niger 3M43 arabinofuranosidase gene (T33646) codes for the precursor form (W00810) of the arabinofuranosidase enzyme. It was isolated from a genomic DNA library by screening with a PCR clone obtd. by amplification of A. niger DNA using primers (see also T33644-45) based on an isolated peptide (W00806) the enzyme. The mature enzyme coding sequence (see also T33640) can be used for prodn. of arabinofuranosidase (W04167) in transformed hosts, pref. Aspergillus or a transgenic plant. The promoter (see also T33641) therminator (T33642) may also be used to control expression of the arabinofuranosidase gene, or other gene of interest, in a host
Aspergillus arabinofuranosidase gene.
Arabinofuranosidase; AbfC; arabinoxylan; viscosity modifier; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:258.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                             Aspergillus arabinofuranosidase - useful for degradation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 3.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                    615 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 TACCAACTITIAGTICGATIGAICAGAATACTITIG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TyrArgLeuLeulleLysVallleArglleValLeu 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T33646 from: 1 to: 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                   651 C;
                                                                                                                                                                                                                                                                         arabinoxylan
Example; Page 52-55; 105pp; English.
                              Aspergillus niger strain 3M43.
Location/Qualifiers
promoter 1. 869
                                                                                                                                                                                                               (DANI-) DANISCO AS.
Baruch A, Madrid SM, Rasmussen P;
WPI; 96-443191/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  632 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID X13195 standard; DNA; 8991 BP.
                                                               /*tag a 870. 1757 /*tag b /*tag c 947 /*tag c 948. 1754 /*tag a 1755 /*tag e e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO985055-A2.
12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-046655.
                                                                                                                                                                              26-SEP-1996.
11-MAR-1996; E01009.
17-MAR-1995; GB-005479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:X13195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-21 x T33646
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2555 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                    signal_peptide
                                                                                                                                                                                                                                                  P-PSDB; W00810
                                                                                                                                                                     WO9629416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                         mat_peptide
                      feedstuff;
                                                                                                                                                terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash
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Claim 1: Page 1239-1244; 2084pp; English.
A computer readable medium has been developed which has recorded on it
Computer readable medium has been developed which has recorded on it
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as configs. The computer based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcal infection in an animal and monitoring
progression of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccines, drug screening, etc.

Claim 5; Page 156; 354pp; English.

X30724 to X30946 represent genomic DNA sequences isolated from
Streptococcus pneumoniae strain 0100993. These genomic DNA sequences
encode the novel proteins given in Y11114 to Y11367. The proteins,
isolated from Streptococcus pneumoniae, can be used in vaccines against
streptococcul infections and in assays for identifying compounds that
inhibit or activate the activity of the proteins. The antagonists can
be used to treat an individual having need to inhibit a bacterial
protein. Vectors expressing the proteins can be used to induce a
protective immune response in mammals.
Sequence 593 BP; 206 A; 76 C; 117 G; 194 T;
New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae genomic DNA sequence SEQ ID NO:169. Streptococcus pneumoniae strain 0100993; vaccine; immune response; streptococcal infection; pneumococcal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2683 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding pneumococcal polypeptide(s) - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1913 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 53.846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1946 TICGCCCTCCTCATCAAAIAGIACAGAIAGTCCTGCGC 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TyrArgLeuLeulleLysVallleArglleValLeuLys 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: X13195 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1478 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-0CT-1997.
01-APR-1997; U05306.
22-AUG-1996; US-025788.
02-APR-1996; US-014690.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2910 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X30892 standard; DNA; 593 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-653-294-21 x X13195/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 3.333
Percent Similarity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:X30892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8991 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stodola RK;
WPI; 97-503111/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seg_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; Y11310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block
                                                                                                                  infection
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alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T84234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E E E E E E
Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis Claim 1, Page 55; 181pp; English.

The sequence is that of a Streptococcal polypeptide coding region. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media. conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal filid. Sequence 1975 BP: 517 A; 524 C; 379 G; 555 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1998 (first entry)
Cytophaga drobachiensis kappa-carrageenase coding sequence.
cgkA: carrageenase; carrageenan; D-galactose; glycosidic linkage; ss;
                                                                                                                                                                                                                                          09-NOV-1998 (first entry)
Streptococcus pneumoniae polypeptide coding region.
Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremla; diagnosis; prophylaxis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.

(SMIK ) SMITHKLINE BEECHAM PLC.

Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO, Reid RH, Zarfos PN;
WPI; 98-322554/28.
          Length: 14
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 66.667
                                                                                                                              2 TyrArgLeuLeuIleLysValIleArgIleValLeuLysTyr 15
                                                                                                                                            ::
ئ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           959 CGCTTGCTCTGTCAAATCATGCGTATAGTCCTCAAG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ArgLeuLeulleLysValileArglleValLeuLys 14
                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1975
                                                                                                                                                                                                                                                                                                                        complement (1724. .1888)
                                                                                                                                                                                                                                                                                                                                               /note- "polypeptide"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                     Align seg 1/1 to reverse of: X30892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: V42962 from: 1
                                                                                                                                                                                                      seq_documentation_block:
ID V42962 standard; DNA; 1975 BP.
AC V42962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID V07122 standard; DNA; 2600 BP.
AC V07122;
                                                              alignment_block:
US-08-653-294-21 x X30892/rev
                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
          39.00
3.250
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.00
3.545
91.667
                                                                                                                                                                                  seq_name: N_Geneseq_36:V42962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:V07122
                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1997; U21976.
27-NOV-1996; US-031879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-21 x V42962
             Quality:
Ratio:
                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W62682
                                                                                                                                                                                                                                                                                                                                                             WO9823631-A1.
04-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
alignment_scores:
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Example: Page 20-23; Jipp; French.

Example: Page 20-23; Jipp; French.

This sequence represents the novel cgkA gene from the microorganism cytophaga drobachlensis the novel cgkA gene from the microorganism.

The sequence was isolated from a C. drobachlensis genomic library based on growth activity on medium containing carrageenan. From the screens of the library, 5 final positive clones were isolated, each contained the present sequence as an insert. The enzyme acts on kappa-carrageenans (polymers of Deglactose libred by beta(1-4) and alpha(1-3) glycosidic linkages and having 1 ester-sulphate groups per disaccharide unit) to produce oligo-carrageenans. The invention relates to the isolation of genes coding for glycosyl Mydrolases, which, when subjected to hydrophobic cluster analysis (WcA) together with Alteromonas carrageenovar kappa-carrageenase, give an HCA score of at least 75% in the domain between positions 17 and 262 of the kappa-carrageenase amino cald sequence. The enzymes can be used to convert carrageenase amino acid sequence. The enzymes can be used to convert carrageenase amino acid sequence. The enzymes can be used to convert carrageenase to sulphated oligocarrageenans which are immunomodulators, antiviral agents and growth factor binding antagonists. Oligocarrageenans to contractile power and adhesion, growth and protein synthesis in human call cultures, and elicit enzyme markers of growth or phenolic defence metabolism in plants. 874 A; 541 C; 522 G; 653 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1998 (first entry)
DNA encoding an autolysin and 3 unknown proteins.
Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression;
ester-sulphate; disaccharide; glycosyl hydrolase; immunomodulator;
hydrophobic cluster analysis; antiviral agent; growth factor; growth;
keratinocyte proliferation; fibroblast contraction; adhesion; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes coding for glycosyl hydrolases – useful for producing recombinant glycosyl hydrolases, especially Cytophaga drobachiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbeyron T, Henrissat B, Kloareg B, Potin P, Richard C; WPI; 98-233084/21.
P-PSDB; W50908.
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Gaps: 0
Percent Identity: 46.154
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/note- "putative signal sequence"
980. .2509
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                                                                                                                                                                                                                                                                                                /product= kappa_carrageenase
875. .979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: V07122 from: 1 to: 2600
                                                                                                                                                Location/Qualifiers
875. .2512
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ID T84234 standard; DNA; 3110 BP.
                                                                                                                                                                                                                        /*tag= a
/gene= "cgkA"
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3.250
92.308
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                                                                                                                 Cytophaga drobachiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1998.
07-0CT-1996; 012204.
07-0CT-1996; FR-012204.
03-FEB-1997; FR-001148.
(GOEM-) LAB GOEMAR SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                      sig_peptide
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alignment_scores:
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                                                                          CDS
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DNA encoding 2 Staphylococcus aureus proteins of unknown function.
DNA encoding 2 Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; uninary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              authors interprise the property of the present sequence encodes 3 Staphylococcus aureus proteins of The present sequence encodes 3 Staphylococcus aureus protein, that, based on homology with a known Staphylococcus aureus protein, is believed to be an autolysin (EC 3.5.1.28) (N-acetylmuramoy1-L-alanine amidase).

The present sequence was obtained from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.

Sequence 3110 Bp; 486 C; 675 G; 833 T;
                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
Bratt JM, Reichard RW, Rosenberg M, Ward JM;
WPI: 97-424969/39
P-PSDB: W28340, W38341, W28342, W28343.
Novel polypeptide(s) from Staphylococcus aureus strain WCUH29
to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 35.714
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                                                                                                                                                                                                                                                                                                /product= "autolysin"
                                                                     Location/Qualifiers
679. .1272
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Key Location/Qualifiers
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ID V53557 standard; DNA; 3110 BP.
                                                                                                                   /*tag= a
1668. .1844
/*tag= b
1885. .2064
                                                                                                                                                                                         1885. .2064
/*tag= c
2326. .2832
/*tag= d
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3.250
85.714
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20-FEB-1996 US-011888.
                                                Staphylococcus aureus.
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US-08-653-294-21 x T84234
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997
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  KKWW

SOUTH THE FETT THE PROPERTY THE FETT THE FETT THE PROPERTY THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT THE FETT T
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produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. splori infection sequence 3110 Bp; 1111 A; 488 C; 6/6 G; 832 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ward JM,
WPI; 98-25240/23.
WPI; 98-25240/23.
New Nucleic acid Sequences from Staphylococcus aureus WCHU29 -
New nucleic acid Sequences from Staphylococcus aureus WCHU29 -
New nucleic acid Sequences and for treatment of bacterial infections of e.g
useful in vaccines and for treatment of bacterial infections of e.g
claim i; Page 214-216; 390pp; English.
This sequence encodes 2 Staphylococcus aureus proteins of unknown
function, and represents a DNA Sequence of the invention.
The DNA sequences were isolated from Staphylococcus aureus WCHU29
(NCIMB 4071), Host cells containing the DNA sequences are used to
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Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                  24-SEP-1996; US-027032.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Burnham MRR, Hodgson JE, Knowles DJC,
Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M,
/*tag= b
/note= "encoded protein shown in W77772"
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30-007-1997; U19588.
31-007-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Dougherty BA, Fannon M,
WPI; 98-272225/24.
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3.250 Gaps: 0
85.714 Percent Identity: 35.714
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ID V52309 standard; DNA; 3984 BP.
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US-08-653-294-21 x V53557
                                                                                                                                                                                                                                                                                    24-SEP-1997; 307485.
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Ratio:
Percent Similarity:
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Claim 1; Page 1108-1110; 1409pp; English.

The present invention describes a computer readable medium which has the present invention describes a computer readable medium which has conclective sequences SEO ID No:1 to 391 (V52134 to V52524) recorded to SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No: 1 to 391. The nucleotide of any of the fragments of the S: pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S: pneumoniae genome (SED ID NO: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genome (DA library using as a probe a target sequence defined by any of the sequences in SEO ID NO: 1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating ment of the sequence of isolating members; or (b) isolating ments derived from the cramputer based system for identifying fragments of the S: pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S: pneumoniae genome. Products from the present computence is solations for S: pneumoniae genome. Products from the present compositions and vaccines for S: pneumoniae genome. Products from the present compositions and vaccines for S: pneumoniae genome. Solucine to Sequence S: 2124 T;
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This nucleotide sequence comprises novel human tumour rejection antigen precursor (TRAP) MAGE-C1 CDNA (see also V69720). MAGE-C1 is a novel member of the MAGE family that may be recognised by cytotoxic T cells, leading to lysis of the tumour cells which express it. MACE-C1 and MACE-C2 (see W81546-47) are expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The MAGE-C1 CDNA was isolated from a melanoma LB373-MEL cDNA library using a probe generated from LB-373-MEL RA by PCR (see V69728-29). It shows homology to MAGE-A1 cDNA (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour rejection antigen precursors - used for determining presence
of cytolytic T cells specific for complexes of a human leukocyte
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Tumour rejection antigen precursor MAGE-C1 cDNA.
MAGE-C1; humour rejection antigen precursor; TRAP;
therapy; diagnosis; ds.
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Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         867 C;
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257. .3475
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24-ARR-1998; U08493.
25-ARR-1997; US-845528.
BOON-Palleur T, De Smet C, Lucas S; WPI; 99-024041/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1241 A;
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Percent Similarity: 85.714
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WACE-C1 gene was localised to chromosome region Xq26-q27. MACE-C1 and MACE-C2 consists (see V69726) are claimed, as are: expression and MACE-C2 consists (see V69726) are claimed, as are: expression vectors; transformed or transfected cell lines (e.g. COS and CHO); an isolated TRAP encoded by the cDNAs; a kit useful in a PCR based assay comprising an oligonuclectide having a sequence of nuclectides 18-34 of the 4031 bp MACE-C1 CDNA and an oligonuclectide having a sequence which is complementary to nuclectides 200-217 of having a sequence; a method for determining expression of a MACE-C1 gene using the kit; a polytope comprising a number of tumour rejection antigens derived from MAGE-C1 or MAGE-C2 and at least one tumour rejection antigen derived from MAGE-C1 or MAGE-C2 and at least one tumour rejection antigen derived from MAGE-C1 or MAGE-C2 and at least one tumour rejection antigen derived comprising an expectation antigen. MACE-C2 and at least one other tumour rejection antigen (HLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nuclectide sequence concides movel human tumour rejection antigen precursor (TRAP) MAGE-C1 (see W81546). MAGE-C1 is a novel member of the MAGE family that may be recognised by cytotoxic T cells, leading to lysis of the tumour cells which express it.

MACE-C1 and MACE-C2 (see W81547) are expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The MAGE-C1 cDNA was isolated from a melanoma LB373-MEL CDNA by CR amplification (see V69732-33). It shows homology to MAGE-A1 cDNA (see V69719). The MACE-C1 gene was localised to MAGE-A2.

MACE-C1 and MACE-C2 cDNAs (see V69726) are claimed, as are: capman weetcors; transformed or transfected cell lines (e.g. COS and CHO); an isolated TRAP encoded by the CDNAs; a kit useful in a method for determining expression of a MACE-C1 cen was localized to determining expression of a MACE-C1 cen using the kit; a polytope comprising a number of tumour rejection antigens derived from MAGE-C1 or MAGE-C2; and a polytope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour rejection antigen precursors - used for determining presence
of cytolytic I cells specific for complexes of a human leukocyte
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Tumour rejection antigen precursor MAGE-C1 cDNA.
MAGE-C1; human; tumour rejection antigen precursor; TRAP;
therapy; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 13
Gaps: 0
Percent Identity: 38.462
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24-APR-1998; U08493.
25-APR-1997; US-845528.
(LUDW-) LUDWIG INST CANCER RES.
BOON-Fâlleur T, De Smet C, Lucas S; WPI: 99-024041/02.
P-PSDB; W81546.
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Claim 1: Page 48-50; 84pp; English.
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ID V69720 standard; cDNA; 4225 BP.
AC V69720;
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/*tag= a
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Percent Similarity: 100.000
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US-08-653-294-21 x V69717
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Location/Qualifiers
341. 420
/*tag= a
/note= "these bases represent a line of missing text in
/note the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence".
5820
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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Staphylococcus aureus contig SEO ID #20.
Computer readable medium; vaccihe; S.aureus infection; immunodetection;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome; ds.
comprising at least one tumour rejection antigen derived from MAGE-C1 or MAGE-C2 and at least one other tumour rejection antigen. MACE-C1 and MACE-C2 can be used in a method for determining the presence of cytolytic T cells specific for complexes of a human leukocyte antigen (HLA).

Sequence 4225 BP; 871 A; 1198 C; 923 G; 1233 T;
                                                                                                                                                      Length: 13
Gaps: 0
Percent Identity: 38.462
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ID V74331 standard; DNA; 10470 BP
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Ratio: 3.000
Percent Similarity: 100.000
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US-08-653-294-21 x V69720
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 SSSSSSS
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Tatti-S. aureus vaccines

Tatti-S. aureus vaccines

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

of the invention. The DNA sequences are recorded on a computer readable

medium, preferably selected from a floppy or hard disk, random access

menory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using

the S. aureus DNA sequences allows putative functions to be assigned so

that protein-encoding or regulatory regions of commercial, therapeutic or

industrial importance can be obtained "Specifically, sequences which are

likely to encode antigens have been identified and these polypeptides can

be used in a vaccine composition against S. aureus infection. The

collypeptides can also be used in a kitt for the immunodetection of

S. aureus in a sample. S. aureus is implicated in numerous human diseases,

including cellulitis, eyelid infections, food poisoning, osteomyelitis,

skin and surgical wound infections, scalded skin syndrome, toxic shock

syndrome, etc. Organisms transformed with the DNA sequences can be used

for recombinant production of the polypeptides. The new DNA sequences

computer readable medium.
                                                                                                             WPI; 97-374922/35. Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3742 T;
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                                                                     Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA
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Percent Identity: 35.714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2009 C;
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
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US-08-653-294-21 x V74331/rev
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3.250
85.714
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Ratio:
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